



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 172533

TO: Ruixiang Li
Art Unit: 1646
Location: rem/4D75/4C70
Serial Number: 10/712615

Monday, December 12, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

Published Applications Database - November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).



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STIC-Biotech/ChemLib

172533

ME

From: CR
Sent: FE
To: Li, Ruixiang
Subject: Sunday, November 27, 2005 12:02 PM
STIC-Biotech/ChemLib
Sequence search of Application No. 10/712,615

Please do a standard search on:

(i). SEQ ID NOS: 2 and 103 against both commercial and interference amino acid databases;

(ii). SEQ ID NO: 1 and 2 against both commercial and interference nucleic acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D75
Mail Box 4C70
(571) 272-0875

2 aa 508
103 aa 372
17 aa 1527

ME

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

Date completed: _____
Searcher: Beverly e 2528
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
☒ Other CBN

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: December 3, 2005, 06:22:00 ; Search time 155.286 Seconds
(without alignments)
1437.373 Million cell updates/sec

Title: US-10-712-615-2

Perfect score: 2644
Sequence: 1 MTSTCTNSTRSNSHTCMP.....GTGCTGKIVPSYDSTAFP 508

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*
9:	geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2644	100.0	508	ABR75712	Abb75712 G-protein
2	2644	100.0	508	AA015503	AA015503 Human G-P
3	2644	100.0	508	AAE25236	AAE25236 Human HGB
4	2644	100.0	508	ABR98721	ABR98721 Human G-P
5	2644	100.0	508	ABR57432	ABR57432 Human NOV
6	2644	100.0	508	ABR42865	ABR42865 Human G-P
7	2644	100.0	508	AEA33200	AEA33200 Human GPC
8	2644	100.0	508	AEA33070	AEA33070 Human G-P
9	2644	100.0	508	ADP70508	ADP70508 Oryz sat
10	2641	99.9	508	AAAB6428	AAAB6428 Human bra
11	2641	99.9	508	AAU25605	AAU25605 Human G-P
12	2641	99.9	508	AAU25605	AAU25605 Human G-P
13	2641	99.9	508	AAU25605	AAU25605 Human G-P
14	2641	99.9	508	AAU04369	AAU04369 Human G-P
15	2641	99.9	508	AAU11764	AAU11764 Human G-P
16	2641	99.9	508	AA015504	AA015504 Human G-P
17	2641	99.9	508	ABBB1923	ABBB1923 Human G-P
18	2641	99.9	508	ABP95640	ABP95640 Human GPC
19	2641	99.9	508	ABBB82501	ABBB82501 Human TGR
20	2641	99.9	508	ABW01566	ABW01566 Human G-P
21	2641	99.9	508	AD196462	AD196462 Human G-P
22	2641	99.9	508	AD109954	AD109954 Human G-P
23	2641	99.9	508	ADOC9034	ADOC9034 Human nov
24	2641	99.9	508	ADW44635	ADW44635 Human RUP
				AEA33109	AEA33109 Human GPC

25	2641	99.9	508	ABE20819	ABE20819 Human RUP
26	2641	99.9	926	AAU04387	AAU04387 GPCR-Ge f
27	2641	99.9	926	AD196550	AD196550 G protein
28	2641	99.9	926	ADW44723	ADW44723 Human RUP
29	2641	99.9	926	ABE20907	ABE20907 Human RUP
30	2637	99.7	508	ABE61982	ABE61982 Human G-P
31	2637	99.7	508	ABE81704	ABE81704 Human G-P
32	2637	99.7	508	ABE33111	ABE33111 Human GPC
33	2636	99.7	508	AAU04384	AAU04384 Human G-P
34	2636	99.7	508	AD196538	AD196538 Human mut
35	2636	99.7	508	ADW44711	ADW44711 Human RUP
36	2636	99.7	508	ADW44799	ADW44799 Human RUP
37	2636	99.7	508	AE331110	AE331110 Human GPC
38	2636	99.7	508	ABE20895	ABE20895 Human RUP
39	2629	99.4	508	ABR57433	ABR57433 Human NOV
40	2628	99.4	508	AAE25245	AAE25245 Human HGB
41	2628	99.4	508	AE331117	AE331117 Human GPC
42	2619	99.1	508	ABE07985	ABE07985 Human sev
43	2551	95.5	580	AD08310	AD08310 Novel pro
44	2518	95.2	485	AAE15642	AAE15642 Human G-P
45	2518	95.2	485	ADC86473	ADC86473 Human GPC

ALIGNMENTS

RESULT 1					
ID	ABR75712	standard, protein, 508 AA.			
XX	ABR75712;				
AC	ABR75712;				
XX	ABR75712;				
DT	24-JUN-2002	(first entry)			
XX					
DE	G-protein coupled receptor AXOR69.				
XX					
KW	G-protein coupled receptor; receptor; AXOR69; human; anti-HIV; virucide;				
KW	antimicrobial; analgesic; cytostatic; antidiabetic; anorectic; anabolic;				
KW	antisthmatic; antiparkinsonian; cardiant; cerebroprotective;				
KW	hypotensive; hypertensive; antidiabetic; antisthmatic; antiallergic;				
KW	antileptic; tranquilizer; neuroleptic; nootropic; anticonvulsant;				
KW	vaccine.				
OS	Homo sapiens.				
XX					
PN	GB2367295-A.				
PD	03-APR-2002.				
XX					
PF	12-JUN-2001; 2001GB-00014287.				
XX					
PR	16-JUN-2000; 2000US-00596400.				
XX					
PA	(SMIK) SMITHKLINE BEECHAM CORP.				
PA	(SMIK) SMITHKLINE BEECHAM PLC.				
PA	(SMIK) SMITHKLINE BEECHAM PLC.				
XX					
PI	Elshourbagy N, Gattu M, Shabon U;				
XX					
DR	WPI; 2002-294789/34.				
DR	N-PSDB; ABL53719.				
XX					
PT	An isolated human G-protein coupled (7TM) receptor AXOR 69 polypeptide,				
XX	for treating diseases such as obesity, stroke and anxiety.				
XX					
XX	Claim 1; Page 27; 34pp; English.				
CC	The present sequence is that of human AXOR69, a G-protein coupled				
CC	receptor (GPCR) that shows homology to other members of the GPCR family,				
CC	such as human adrenergic alpha-1a receptor. The invention provides AXOR69				
CC	polypeptides and polynucleotides, and methods for producing such				
CC	polypeptides by recombinant techniques. Also provided are methods for				
CC	using the AXOR69 polypeptides and polynucleotides to screen for compounds				

Yes, discloses SEQ ID NO: 1 and 2

CC that stimulate or inhibit AXOR69 levels or activity. The polypeptides,
CC polynucleotides, agonists and antagonists are used to treat conditions
CC associated with AXOR69 imbalance, including bacterial, fungal, protozoan
CC and viral infections, particularly HIV-1 and HIV-2 infections, pain,
CC cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's
CC disease, acute heart failure, hypotension, hypertension, urinary
CC retention, osteoporosis, angina pectoris, myocardial infarction, stroke,
CC ulcers, asthma, allergies, benign prostatic hypertrophy, migraine,
CC vomiting, psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, depression, delirium, dementia and
CC severe mental retardation, and dyskinesias such as Huntington's disease
CC and Gilles de la Tourette syndrome. AXOR69 polypeptides are also useful
CC in vaccines, and for raising specific antibodies

XX Sequence 508 AA;

Query Match 100.0%; Score 2644; DB 5; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.1e-233;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60
DB 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60
QY 61 QLLQVTRNFIRNLVTDLQISLVA PWVAVTSVPLFWPLNSHFCALVSLTHLPFASVN 120
DB 61 QLLQVTRNFIRNLVTDLQISLVA PWVAVTSVPLFWPLNSHFCALVSLTHLPFASVN 120
QY 121 TIVLVSVDRLYSIIHPLSPSKMTRRGYLLYGTVIAVLIQSTPPLVGMGOAFADEBNA 180
DB 121 TIVLVSVDRLYSIIHPLSPSKMTRRGYLLYGTVIAVLIQSTPPLVGMGOAFADEBNA 180
QY 181 LCSMIMGASPSYTIILSVSVFIVIPLIWIAACYSVFCAARQHALLVNKKHSLSEVRVYD 240
DB 181 LCSMIMGASPSYTIILSVSVFIVIPLIWIAACYSVFCAARQHALLVNKKHSLSEVRVYD 240
QY 241 CVENEDDEGAKEKEFEODESEFRROHGEVYAKGSRMEAKGSLAKAGSGTSTSSVEA 300
DB 241 CVENEDDEGAKEKEFEODESEFRROHGEVYAKGSRMEAKGSLAKAGSGTSTSSVEA 300
QY 301 RGSEEVRESSSTVVASGMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEODMEFGEDI 360
DB 301 RGSEEVRESSSTVVASGMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEODMEFGEDI 360
QY 361 NFESEDDVEAVNIPESLPSRRNSNSNPPLPRCYOCCA KAVFIIFSVYLSLGPYCFPLAV 420
DB 361 NFESEDDVEAVNIPESLPSRRNSNSNPPLPRCYOCCA KAVFIIFSVYLSLGPYCFPLAV 420
QY 421 LAVWVDVETQVPQWVITIIIMLFLOCCIHPRVYVGYMKTIKKEIQDMLKKFCKEKP 480
DB 421 LAVWVDVETQVPQWVITIIIMLFLOCCIHPRVYVGYMKTIKKEIQDMLKKFCKEKP 480
QY 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508
DB 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508

RESULT 2

AA015503

AA015503 standard; protein; 508 AA.

XX AA015503;

XX 24-OCT-2002 (first entry)

XX Human G-protein coupled receptor protein #1.

XX Human, G-protein coupled receptor protein; TGR34;

XX central nervous system disease; Alzheimer's disease; metabolic disease;

XX diabetes; cancer; breast cancer; circulatory disease; atherosclerosis;

XX inflammatory disease; arthritis; respiratory disease; bronchitis;

XX digestive disease; stomach ulcer; immune disorder; autoimmune disease;

XX infection; AIDS.

XX Homo sapiens.

XX WO200259304-A1.

XX 01-AUG-2002.

XX 22-JAN-2002; 2002WO-JP000405.

XX 23-JAN-2001; 2001JP-00015050.

XX 30-MAR-2001; 2001JP-00102560.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Miwa M, Ito T, Shintani Y, Miyajima N;

XX WPI. 2002-557949/59.

XX N-PSDB; AAL44179.

Human G-protein coupled receptor protein and DNA encoding it for design
of drugs and reagents for treatment and diagnosis of cancer or
respiratory and metabolic diseases.

Claim 1: Page 94-96; 109pp; Japanese.

The invention comprises the amino acid and coding sequences of two human
G-protein coupled receptor proteins (TGR34). The DNA and protein
sequences of: central nervous system diseases (e.g. Alzheimer's disease);
metabolic diseases (e.g. diabetes); cancer (e.g. breast cancer);
circulatory diseases (e.g. atherosclerosis); inflammatory diseases (e.g.
arthritis); respiratory diseases (e.g. bronchitis); digestive diseases
(e.g. stomach ulcer); immune disorders (e.g. autoimmune diseases); and
infections (e.g. AIDS). The present amino acid sequence represents a
human G-protein coupled receptor protein

XX Sequence 508 AA;

Query Match 100.0%; Score 2644; DB 5; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.1e-233;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60
DB 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60
QY 61 QLLQVTRNFIRNLVTDLQISLVA PWVAVTSVPLFWPLNSHFCALVSLTHLPFASVN 120
DB 61 QLLQVTRNFIRNLVTDLQISLVA PWVAVTSVPLFWPLNSHFCALVSLTHLPFASVN 120
QY 121 TIVLVSVDRLYSIIHPLSPSKMTRRGYLLYGTVIAVLIQSTPPLVGMGOAFADEBNA 180
DB 121 TIVLVSVDRLYSIIHPLSPSKMTRRGYLLYGTVIAVLIQSTPPLVGMGOAFADEBNA 180
QY 181 LCSMIMGASPSYTIILSVSVFIVIPLIWIAACYSVFCAARQHALLVNKKHSLSEVRVYD 240
DB 181 LCSMIMGASPSYTIILSVSVFIVIPLIWIAACYSVFCAARQHALLVNKKHSLSEVRVYD 240
QY 241 CVENEDDEGAKEKEFEODESEFRROHGEVYAKGSRMEAKGSLAKAGSGTSTSSVEA 300
DB 241 CVENEDDEGAKEKEFEODESEFRROHGEVYAKGSRMEAKGSLAKAGSGTSTSSVEA 300
QY 301 RGSEEVRESSSTVVASGMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEODMEFGEDI 360
DB 301 RGSEEVRESSSTVVASGMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEODMEFGEDI 360
QY 361 NFESEDDVEAVNIPESLPSRRNSNSNPPLPRCYOCCA KAVFIIFSVYLSLGPYCFPLAV 420
DB 361 NFESEDDVEAVNIPESLPSRRNSNSNPPLPRCYOCCA KAVFIIFSVYLSLGPYCFPLAV 420
QY 421 LAVWVDVETQVPQWVITIIIMLFLOCCIHPRVYVGYMKTIKKEIQDMLKKFCKEKP 480
DB 421 LAVWVDVETQVPQWVITIIIMLFLOCCIHPRVYVGYMKTIKKEIQDMLKKFCKEKP 480

Qy 481 EDSDPDLPTGEGTGGKIVPSYDSATFP 508
 |||||
 Db 481 EDSDPDLPTGEGTGGKIVPSYDSATFP 508

RESULT 3

AAE25236
 ID AAE25236 standard; protein; 508 AA.
 AC AAE25236;
 DT 30-OCT-2002 (first entry)
 XX
 DE Human HGPBMY8 protein #1.
 XX
 KW Human; G-protein coupled receptor; GPCR; HGPBMY8; drug screening;
 KW neurological disorder; brain; immunological; cell growth; cytostatic;
 KW neoplastic disease; CAMP; signalling pathway; immune disorder; cancer;
 KW gene therapy; tumour.
 XX
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 FH Misc-difference 124
 FT /note= "Leu at this position changes to Val due to single
 FT nucleotide polymorphism"
 FT Misc-difference 352
 FT /note= "Asp at this position changes to Gly due to single
 FT nucleotide polymorphism"
 FT Misc-difference 398
 FT /note= "Ala at this position changes to Asp due to single
 FT nucleotide polymorphism"
 FT Misc-difference 398
 FT /note= "Ala at this position changes to Thr due to single
 FT nucleotide polymorphism"
 XX
 PN MO200240670-A2.
 XX
 PD 23-MAY-2002.
 XX
 PF 14-NOV-2001; 2001WC-US043909.
 XX
 PR 14-NOV-2000; 2000US-0248285P.
 PR 14-FEB-2001; 2001US-0268581P.
 PR 27-JUL-2001; 2001US-0308285P.
 PR 04-SEP-2001; 2001US-0317166P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Batteglino P, Feder J, Mintier G, Ramathan C;
 PI Westphal R, Cacace A, Barber L, Hawken D, Kornacker M;
 XX
 DR MPI; 2002-519383/55.
 DR N-PSDB; AAD41159.
 XX
 PT A substantially purified human G-protein coupled receptor polypeptide,
 PT termed HGPBMY8, useful for treating a neurological disorder or brain
 PT disorder in a mammal.
 XX
 PS Claim 4; Page 161-163; 223pp; English.
 XX
 CC The invention relates to human G-protein coupled receptor (GPCR), termed
 CC HGPBMY8 and its corresponding nucleic acid. HGPBMY8 DNA is useful for
 CC screening for candidate compounds which are small molecules, biological
 CC agents, therapeutics or drugs. HGPBMY8 or its homologue is useful for
 CC treating a neurological disorder or a disease, a disorder or condition
 CC related to the brain in a mammal. It is used for treating or preventing
 CC neurological disorders, conditions or diseases and for inducing an
 CC immunological response in a mammal. HGPBMY8 DNA, protein and its
 CC antibody are useful in the diagnosis, treatment or prevention of
 CC disorders associated with aberrant or uncontrolled cellular growth and/
 CC or function, such as neoplastic diseases e.g., cancers and tumours and

CC diseases or disorders related to the brain, e.g., neurological disorders.
 CC HGPBMY8 DNA and protein are useful for modulating intracellular CAMP
 CC associated signalling pathways. An expression vector containing HGPBMY8
 CC DNA is useful to treat or prevent neoplastic disorders such as cancer or
 CC tumours, immune disorders or neurological disorders. HGPBMY8 DNA is used
 CC in gene therapy. The present sequence is human HGPBMY8 protein
 CC
 XX

SQ Sequence 508 AA;

Query Match 100.0%; Score 2644; DB 5; Length 508;
 Best Local Similarity 100.0%; Pred. No. 1,1e-233;
 Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTSTCTNSSTRESNSSHCTCMPLSKMPLSLAHGIIRSTVLVIFPAASFGVNIATLVQRP 60
 |||||
 Db 1 MTSTCTNSSTRESNSSHCTCMPLSKMPLSLAHGIIRSTVLVIFPAASFGVNIATLVQRP 60
 Qy 61 QLLQVYTNRIIFMLVTDLLQISLVA PWVAVTSVPLFWPLNSHFTALVSLTLPAPASVN 120
 |||||
 Db 61 QLLQVYTNRIIFMLVTDLLQISLVA PWVAVTSVPLFWPLNSHFTALVSLTLPAPASVN 120
 Qy 121 TIVLVSVDRYLSIHPSTPSKMTORRGYLLXGTWIVAAIIOSTPPLVGMGAARDERNA 180
 |||||
 Db 121 TIVLVSVDRYLSIHPSTPSKMTORRGYLLXGTWIVAAIIOSTPPLVGMGAARDERNA 180
 Qy 181 LGSMTWGAASPSYTTISVSVFIVPIVMACYSVFCARROHALLYNVGRSLERYVKD 240
 |||||
 Db 181 LGSMTWGAASPSYTTISVSVFIVPIVMACYSVFCARROHALLYNVGRSLERYVKD 240
 Qy 241 CVENBDEBGAKEKEFEODESEFRROHEGEVKAKEGMEAKDGLAKKEGSTGTSSESVBA 300
 |||||
 Db 241 CVENBDEBGAKEKEFEODESEFRROHEGEVKAKEGMEAKDGLAKKEGSTGTSSESVBA 300
 Qy 241 CVENBDEBGAKEKEFEODESEFRROHEGEVKAKEGMEAKDGLAKKEGSTGTSSESVBA 300
 |||||
 Db 241 CVENBDEBGAKEKEFEODESEFRROHEGEVKAKEGMEAKDGLAKKEGSTGTSSESVBA 300
 Qy 301 RQSEEVRESSTVAAOSGMEKSGSTKYVENSMAKDKGRVNVQCSIDLGEDDMEFEGDDI 360
 |||||
 Db 301 RQSEEVRESSTVAAOSGMEKSGSTKYVENSMAKDKGRVNVQCSIDLGEDDMEFEGDDI 360
 Qy 361 NFSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYOCKAAVIFIIIFSYVLSGPFYFLAV 420
 |||||
 Db 361 NFSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYOCKAAVIFIIIFSYVLSGPFYFLAV 420
 Qy 421 LAVWVDETOVPQWVITIIIMLFPLQCCIHPPVYGYMAKTIKKEIQDMLKKEFCCKEPPK 480
 |||||
 Db 421 LAVWVDETOVPQWVITIIIMLFPLQCCIHPPVYGYMAKTIKKEIQDMLKKEFCCKEPPK 480
 Qy 481 EDSDPDLPTGEGTGGKIVPSYDSATFP 508
 |||||
 Db 481 EDSDPDLPTGEGTGGKIVPSYDSATFP 508
 |||||
 RESULT 4
 ABB98721 ID ABB98721 standard; protein; 508 AA.
 XX
 AC ABB98721;
 XX
 DT 17-JUN-2003 (first entry)
 XX
 DE Human G protein coupled receptor, 50879.
 XX
 KW G protein coupled receptor; receptor; anorectic; antiparkinsonian;
 KW hypotensive; hypertensive; tranquiliser; neuroleptic; antidepressant;
 KW nootropic; anticonvulsant; antimigraine; human; 50879; hippocampus;
 KW hypothalamus; brain; obesity; bulimia; anorexia; Parkinson's disease;
 KW hypotension; hypertension; psychotic disorder; neurological disorder;
 KW anxiety; schizophrenia; manic depression; delirium; dementia; epilepsy;
 KW migraine; insomnia; circadian rhythm disorder; cognitive function.
 XX
 OS Homo sapiens.
 XX
 PN FR2822844-A1.
 XX
 PD 04-OCT-2002.

XX 27-MAR-2001; 2001FR-00004074.
XX
XX 27-MAR-2001; 2001FR-00004074.
XX
XX (SERV-) LES LAB SERVER SA.
XX
XX Galizzi JP, Coge F, Rigue H, Boutin JA;
XX WPI; 2003-021471/02.
XX N-PSDB; ABV74517.
XX
XX New nucleic acid encoding human G protein coupled receptors, useful for
XX creating e.g. obesity, also derived polypeptides, antibodies and
XX modulators.
XX
XX Claim 15; Page 27-29; 44pp; French.
XX
XX The present sequence is the protein sequence for human G protein-coupled
XX receptor, S0879. The receptor and its coding sequence can be used for
XX creating diseases associated with abnormal expression of the receptor,
XX particularly diseases involving the hippocampus or hypothalamus,
XX particularly obesity, bulimia, anorexia, Parkinson's disease, hypo- or
XX hyperextension, and psychotic or neurological disorders such as anxiety,
XX schizophrenia, manic depression, delirium, dementia, epilepsy, migraine,
XX insomnia, circadian rhythm disorders and loss of cognitive function. The
XX G protein-coupled receptor coding sequence was isolated from human brain
XX tissue

Sequence 508 AA;

Query Match 100.0%; Score 2644; DB 6; Length 508;
Beet Local Similarity 100.0%; Pred. No. 1.1e-233;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSCTNSTRSSNSHTCMPKPISLAHGIRSTVAVIFLAASFVGNIVATLVLRKP 60
DB 1 MTSCTNSTRSSNSHTCMPKPISLAHGIRSTVAVIFLAASFVGNIVATLVLRKP 60
QY 61 QLVQTNRFIFNLVTDLLQISLVAPVWVATSVFPMFPLNSHFCALVSLTLFPAFASV 120
DB 61 QLVQTNRFIFNLVTDLLQISLVAPVWVATSVFPMFPLNSHFCALVSLTLFPAFASV 120
QY 121 TIVAVSVDRYLSIHPISYPSKMTQRGVLVLTGTWIVALLQSTPPLVGMGQAPADERNA 180
DB 121 TIVAVSVDRYLSIHPISYPSKMTQRGVLVLTGTWIVALLQSTPPLVGMGQAPADERNA 180
QY 181 LCSMTWGSAPSTYLLSVSVFIVPIVIMACSVVPCARRHALLVYKRSLEVRKYD 240
DB 181 LCSMTWGSAPSTYLLSVSVFIVPIVIMACSVVPCARRHALLVYKRSLEVRKYD 240
QY 241 CVENEDDEGAEEKEFEFODESEFRROHEGSEVKAKEGRMEAKDQSLKAKGSTSTSSSEYA 300
DB 241 CVENEDDEGAEEKEFEFODESEFRROHEGSEVKAKEGRMEAKDQSLKAKGSTSTSSSEYA 300
QY 301 RGSSEVRESSTVASDGSMEKEGSTKVEENSMKADKGRTEVNOCSIDLGEDMEFGEEDI 360
DB 301 RGSSEVRESSTVASDGSMEKEGSTKVEENSMKADKGRTEVNOCSIDLGEDMEFGEEDI 360
QY 361 NFSEDDVAANVPELPPSRKNSNPNPLPRCYCKAKAVFIITFSYVLSIGPYCFPLAV 420
DB 361 NFSEDDVAANVPELPPSRKNSNPNPLPRCYCKAKAVFIITFSYVLSIGPYCFPLAV 420
QY 421 LAVWVDETOVPOWVITIIIMLFPOCCIHPRVYVGMHTIKKEIDMLKKFCEKPK 480
DB 421 LAVWVDETOVPOWVITIIIMLFPOCCIHPRVYVGMHTIKKEIDMLKKFCEKPK 480
QY 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
DB 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 5

ABR57432
ID ABR57432 standard; protein; 508 AA.
XX
XX ABR57432;
XX
XX 15-SEP-2003 (first entry)
XX
XX Human NOV14a protein SEQ ID NO:42.
XX
XX Human; NOVX; cytosolic; cardiant; antiinflammatory; immunosuppressive;
XX antiallergic; haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic;
XX anorectic; antiaesthetic; nephrotoxic; antiarthritic; hepatotropic;
XX neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
XX relaxant; anticonvulsant; hypotensive; vasotrophic; antiparkinsonian;
XX vulnerary; angiogenic; antilipogenic; gene therapy; vaccine; cancer;
XX cardiomyopathy; atherosclerosis; hypertension; diabetes; inflammation;
XX autoimmune disorder; allergy; blood disorder; AIDS; obesity; asthma;
XX acquired immunodeficiency syndrome; nephropathy; cirrhosis; arthritis;
XX Alzheimer's disease; Parkinson's disease; goitre; infection; stroke;
XX muscular dystrophy; epilepsy; wasting disorder; chromosome X.
XX
XX Homo sapiens.
XX
XX WO200294870-A2.
XX
XX 28-NOV-2002.
XX
XX 02-NOV-2001; 2001WO-US051580.
XX
XX 02-NOV-2000; 2000US-0245291P.
XX
XX 07-NOV-2000; 2000US-0245317P.
XX
XX 08-NOV-2000; 2000US-0246871P.
XX
XX 26-JAN-2001; 2001US-0264389P.
XX
XX 26-JAN-2001; 2001US-0264423P.
XX
XX 29-JAN-2001; 2001US-0264799P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Grose WM, Macdougall JR, Smithson G, Miller J, Stone DJ;
XX Gunther E, Ellerman K, Alsobrook JP, Lepley DM, Burgess CE;
XX Spytek KA, Edinger SR, Gangoli EA, Gorman U, Taupier RD, Li L;
XX Guo X, Fernandez ER, Verret CM, Tcherven VT, Caeman SJ, Shenoy S;
XX Mishra V, Furtak K, Baumgartner JC, Colman SD;
XX WPI; 2003-140359/13.
XX N-PSDB; ACF03567.
XX
XX New NOVX polypeptide useful for preventing or treating NOVX-associated
XX disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and
XX in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Claim 1; Page 130; 346pp; English.
XX
XX ACF03547 to ACF03570 encode the human NOVX proteins (I) given in ABR57412
XX to ABR57435. (I) have cytostatic, cardiant, antiinflammatory, nootropic,
XX immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiabetic,
XX antiarteriosclerotic, anorectic, antiaesthetic, nephrotoxic, virucide,
XX antiarthritic, hepatotropic, neuroprotective, antibacterial, relaxant,
XX antiparasitic, anticonvulsant, hypotensive, vasotrophic, antiparkinsonian,
XX vulnerary, angiogenic and antilipogenic activities, and can be used in
XX gene therapy and vaccines. The NOVX polypeptides and their antibodies can
XX be used to determine the presence or absence of (I) in a sample. The NOVX
XX polypeptides, polynucleotides encoding them, and antibodies against them,
XX are useful in manufacturing a medicament for treating or preventing a
XX syndrome associated with a NOVX-associated disorder such as hypertension,
XX cardiomyopathy, atherosclerosis, cancer, diabetes, asthma, inflammation,
XX autoimmune disorders, allergies, blood disorders, obesity, acquired
XX immunodeficiency syndrome (AIDS), immunoglobulin (Ig)A nephropathy,
XX cirrhosis, arthritis, Alzheimer's disease, Parkinson's disease, goitre,
XX infections (e.g. bacterial, viral, parasitic), stroke, muscular
XX dystrophy, epilepsy, and other wasting disorders associated with chronic
XX diseases. ACF03571 to ACF03644 represent PCR primers and probes for NOVX

Yes, SEQ ID NO:2 is present

CC sequence, which are used in an example from the present invention
SQ Sequence 508 AA;
Query Match 100.0%; Score 2644; DB 6; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.1e-233;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIRSTVLVIFLAASFGVNIVALVLRKP 60
DB 1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIRSTVLVIFLAASFGVNIVALVLRKP 60
QY 61 QLLQVTRNRFENLVLTDLQISLVAPWVAVTSVPLFWPLNSHFTALVSLTHLPFASVY 120
DB 61 QLLQVTRNRFENLVLTDLQISLVAPWVAVTSVPLFWPLNSHFTALVSLTHLPFASVY 120
QY 121 TIVLVSVDRYLSIHPLSPSKMTRRGYLLYGTMVAILLOSTPPLVGMGAAPDERNA 180
DB 121 TIVLVSVDRYLSIHPLSPSKMTRRGYLLYGTMVAILLOSTPPLVGMGAAPDERNA 180
QY 181 LCSMTWGAASPSYTIISVSVFIVPLIWMIACTSVVFCARROHALLVYKRSLEVRVD 240
DB 181 LCSMTWGAASPSYTIISVSVFIVPLIWMIACTSVVFCARROHALLVYKRSLEVRVD 240
QY 241 CVENEDDEGAKEKEEFQDESEFRROHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVYA 300
DB 241 CVENEDDEGAKEKEEFQDESEFRROHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVYA 300
QY 301 RSESEVRESSTVASDQSMGKSGSTVENSMAKDGRIEVENOCSIDLSEDMERGEDDI 360
DB 301 RSESEVRESSTVASDQSMGKSGSTVENSMAKDGRIEVENOCSIDLSEDMERGEDDI 360
QY 361 NSESDDEVAENIPESLPSPSRNSNPNPLPRCQCKAAVYFIIFISYVLSIGPYCLAV 420
DB 361 NSESDDEVAENIPESLPSPSRNSNPNPLPRCQCKAAVYFIIFISYVLSIGPYCLAV 420
QY 421 LAWVWDEVTQVQWVITIIIMFLQCCIHPPYVGYMHTIKKEIDMLKKEFCCKEPPK 480
DB 421 LAWVWDEVTQVQWVITIIIMFLQCCIHPPYVGYMHTIKKEIDMLKKEFCCKEPPK 480
QY 481 EDSHPDLPTGEGTEKIVPSYDSATFP 508
DB 481 EDSHPDLPTGEGTEKIVPSYDSATFP 508

RESULT 6
ABR42865
ID ABR42865 standard; protein; 508 AA.
XX
AC ABR42865;
XX
DT 22-SEP-2003 (first entry)
XX
DE Human G-protein coupled receptor OM_10.
XX
KW G-protein coupled receptor; GPCR; OM_10; human; receptor; cardiant;
KW hypertensive; hypotensive; antidiabetic; cytostatic; antiproliferative;
KW angiogenic; gynaecological; antidepressant; antisthmatic; osteoporotic;
KW neuroleptic; cranioillizer; nephrotoxic; antidiabetic; antiallergic;
KW neurotoxic; anticonvulsant; neuroprotective; antiparkinsonian;
KW gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 34..49
FT Domain /note= "predicted transmembrane domain"
FT Domain 86..90
FT Domain /note= "predicted transmembrane domain"
FT Domain 109..118
FT Domain /note= "predicted transmembrane domain"
FT Domain 155..162
FT Domain /note= "predicted transmembrane domain"

FT Domain 188..214
FT /note= "predicted transmembrane domain"
FT Domain 403..418
FT /note= "predicted transmembrane domain"
FT Domain 437..446
FT /note= "predicted transmembrane domain"
FT
PN WO2003044162-A2.
XX
PD 30-MAY-2003.
XX
PF 12-NOV-2002; 2002WO-US036204.
XX
PR 16-NOV-2001; 2001US-0332110P.
XX
PA (AMMP) WYETH.
XX
PI Blacher M, Paulsen JE, Bates BG.
XX
DR WPI; 2003-449811/42.
XX
DR N-PSDB; ACC42865.
XX
PT New polynucleotides encoding G-protein coupled receptor, i.e. OM-10 and
PT UP-11 polypeptides, useful for diagnosing, preventing and treating, e.g.
PT Parkinson's disease, acute heart failure, hypertension, cancer or
PT osteoporosis.
XX
PS Claim 27; Page 178-180; 190pp; English.
XX
CC The present sequence is the protein sequence of a novel human G-protein
CC coupled receptor (GPCR) termed OM_10. This orphan GPCR was identified
CC from a genome database search using the human 5-HT6 receptor sequence.
CC Identified regions of genomic DNA were used to predict full-length genes,
CC and these gene predictions were used to design probes and primers for the
CC isolation of a cDNA clone containing the predicted OM_10 open reading
CC frame. OM_10 is expressed predominantly in the putamen and caudate
CC nucleus. OM_10 and UP_11 polypeptides, polynucleotides, agonists and
CC antagonists of the invention are useful in drug screening assays.
CC pharmacogenomics, monitoring of effects during clinical trial, or for
CC diagnosing, preventing and treating diseases associated with enhanced or
CC inhibited GPCR activity, e.g. acute heart failure, hypertension,
CC hypertension, angina pectoris, myocardial infarction, hyperproliferative
CC diseases such as cancers and psoriasis, apoptotic diseases, pain,
CC endometriosis, anorexia, bulimia, asthma, osteoporosis, schizophrenia,
CC delirium, depression, anxiety, urinary retention, ulcers, allergies,
CC dyskinesias such as Huntington's disorder or Gilles de la Tourette's
CC syndrome, Alzheimer's disease, or Parkinson's disease
XX
SQ Sequence 508 AA;
Query Match 100.0%; Score 2644; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.1e-233;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIRSTVLVIFLAASFGVNIVALVLRKP 60
DB 1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIRSTVLVIFLAASFGVNIVALVLRKP 60
QY 61 QLLQVTRNRFENLVLTDLQISLVAPWVAVTSVPLFWPLNSHFTALVSLTHLPFASVY 120
DB 61 QLLQVTRNRFENLVLTDLQISLVAPWVAVTSVPLFWPLNSHFTALVSLTHLPFASVY 120
QY 121 TIVLVSVDRYLSIHPLSPSKMTRRGYLLYGTMVAILLOSTPPLVGMGAAPDERNA 180
DB 121 TIVLVSVDRYLSIHPLSPSKMTRRGYLLYGTMVAILLOSTPPLVGMGAAPDERNA 180
QY 181 LCSMTWGAASPSYTIISVSVFIVPLIWMIACTSVVFCARROHALLVYKRSLEVRVD 240
DB 181 LCSMTWGAASPSYTIISVSVFIVPLIWMIACTSVVFCARROHALLVYKRSLEVRVD 240
QY 241 CVENEDDEGAKEKEEFQDESEFRROHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVYA 300
DB 241 CVENEDDEGAKEKEEFQDESEFRROHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVYA 300

```
QY 301 RGSSEVRSSSTVASDGSMEKGGSTKVEENSMKADKGRTEVNOCSIDLGEDDMERGEDDI 360
D 301 RGSSEVRSSSTVASDGSMEKGGSTKVEENSMKADKGRTEVNOCSIDLGEDDMERGEDDI 360
QY 361 NFSSEDDVAANVIPESLPPSRNSNSNPPLPRCYCKAKAKVFIITIFSVLSLGPYCFPLAV 420
D 361 NFSSEDDVAANVIPESLPPSRNSNSNPPLPRCYCKAKAKVFIITIFSVLSLGPYCFPLAV 420
QY 421 LAWWDVETQVPQWVITITIIWLFPLQCCIHPRVYGYMKTIKKEIQDMLKKPFCKEKP 480
D 421 LAWWDVETQVPQWVITITIIWLFPLQCCIHPRVYGYMKTIKKEIQDMLKKPFCKEKP 480
QY 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
D 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 7
AEA33200
ID AEA33200 standard; protein; 508 AA.
XX
AC AEA33200;
XX
DT 11-AUG-2005 (first entry)
XX
DE Human GPCR HGRBMY8-related RAI-3 protein SegID134.
XX
KM protein purification; cytosolic; neuroprotective; antiparkinsonian;
KM triangulizer; hypotension; anti-HIV; vincristine; osteoporosis; cancer;
KM asthma; allergy; HIV infection; osteoporosis; Parkinson's disease;
KM anxiety disorder; hypertension; neurological disease; RAI-3.
XX
OS Homo sapiens.
XX
PN WO2005048951-A2.
XX
PD 02-JUN-2005.
XX
PF 12-NOV-2004; 2004WO-US038387.
XX
PR 13-NOV-2003; 2003US-00712615.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI Battaglin P, Feder JN, Mintier G, Nelson TC, Ramanathan CS;
PI Westphal R, Cacace AM, Barber LE, Hawken DR, Kornacker MG;
XX
DR WPI; 2005-395945/40.
XX
PT New isolated human G-protein coupled receptor, HGRBMY8, and encoding
PT polynucleotide, useful for diagnosing or treating cancer, asthma,
PT allergies, HIV, osteoporosis, anxiety, hypertension and neurological
PT diseases.
XX
PS Example 18; SEQ ID NO 134; 261bp; English.
XX
CC This invention relates to a novel isolated human G-protein and the DNA
CC sequence which encodes it. The invention may be useful for the
CC development of compounds with a cytosolic, neuroprotective,
CC antiparkinsonian, triangulizer, hypotension, anti-HIV, vincristine or
CC osteopathic activity acting as G-protein antagonists. The methods and
CC compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of the human G-protein coupled receptor,
CC HGRBMY8, such as cancer, asthma, allergies, HIV infections,
CC osteoporosis, Parkinson's disease, anxiety, hypertension and neurological
CC diseases. The present sequence is that of the human RAI-3 protein which
CC was used in the exemplification of the invention.
XX
SQ Sequence 508 AA;
Query Match 100.0%; Score 2644; DB 9; Length 508;
```

```
Beet Local Similarity 100.0%; Pred. No. 1,1e-233;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTSTCTNSTRESSNSHTCMPLSKMPLSLAHQIIRSTVLVIFLAISVGNIVLALVLRKP 60
D 1 MTSTCTNSTRESSNSHTCMPLSKMPLSLAHQIIRSTVLVIFLAISVGNIVLALVLRKP 60
QY 61 QLLQVNTNFENLLVTDLLQISLVAWVAVTSVPLFMPPLNSHFTALVSLTHLFAFASVN 120
D 61 QLLQVNTNFENLLVTDLLQISLVAWVAVTSVPLFMPPLNSHFTALVSLTHLFAFASVN 120
QY 121 TIVLVSDRYLSTIHPLSYPSKMTQRGTYLLYGTWIVAILQSTPPLVGMGOAIFDERNA 180
D 121 TIVLVSDRYLSTIHPLSYPSKMTQRGTYLLYGTWIVAILQSTPPLVGMGOAIFDERNA 180
QY 181 LCSMTWGSFSTYLLSVSFIVIPILVIMACYSVFCARQHALLVYVKHSLFVRVYKD 240
D 181 LCSMTWGSFSTYLLSVSFIVIPILVIMACYSVFCARQHALLVYVKHSLFVRVYKD 240
QY 241 CVENEDDEGAKEKEFODESEFFRRQHEGEVAKEGMEAKDGLKAKEGSTGTSSESVYA 300
D 241 CVENEDDEGAKEKEFODESEFFRRQHEGEVAKEGMEAKDGLKAKEGSTGTSSESVYA 300
QY 301 RGSSEVRSSSTVASDGSMEKGGSTKVEENSMKADKGRTEVNOCSIDLGEDDMERGEDDI 360
D 301 RGSSEVRSSSTVASDGSMEKGGSTKVEENSMKADKGRTEVNOCSIDLGEDDMERGEDDI 360
QY 361 NFSSEDDVAANVIPESLPPSRNSNSNPPLPRCYCKAKAKVFIITIFSVLSLGPYCFPLAV 420
D 361 NFSSEDDVAANVIPESLPPSRNSNSNPPLPRCYCKAKAKVFIITIFSVLSLGPYCFPLAV 420
QY 421 LAWWDVETQVPQWVITITIIWLFPLQCCIHPRVYGYMKTIKKEIQDMLKKPFCKEKP 480
D 421 LAWWDVETQVPQWVITITIIWLFPLQCCIHPRVYGYMKTIKKEIQDMLKKPFCKEKP 480
QY 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
D 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 8
AEA33070
ID AEA33070 standard; protein; 508 AA.
XX
AC AEA33070;
XX
DT 11-AUG-2005 (first entry)
XX
DE Human G-protein coupled receptor HGRBMY8 protein SegID2.
XX
KM protein purification; cytosolic; neuroprotective; antiparkinsonian;
KM triangulizer; hypotension; anti-HIV; vincristine; osteoporosis; cancer;
KM asthma; allergy; HIV infection; osteoporosis; Parkinson's disease;
KM anxiety disorder; hypertension; neurological disease; HGRBMY8;
KM G protein coupled receptor.
XX
OS Homo sapiens.
XX
PN WO2005048951-A2.
XX
PD 02-JUN-2005.
XX
PF 12-NOV-2004; 2004WO-US038387.
XX
PR 13-NOV-2003; 2003US-00712615.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI Battaglin P, Feder JN, Mintier G, Nelson TC, Ramanathan CS;
PI Westphal R, Cacace AM, Barber LE, Hawken DR, Kornacker MG;
XX
DR WPI; 2005-395945/40.
DR N-PSDB; AEA33069.
```

XX New isolated human G-protein coupled receptor, HGPBM78, and encoding
PT polynucleotide, useful for diagnosing or treating cancer, asthma,
PT allergies, HIV, osteoporosis, anxiety, hypertension and neurological
PT diseases.
XX
PS Claim 4; SEQ ID NO 2; 261pp; English.
XX
CC This invention relates to a novel isolated human G-protein and the DNA
CC sequence which encodes it. The invention may be useful for the
CC development of compounds with a cytostatic, neuroprotective,
CC antiparkinsonian, tranquilizer, hypotension, anti-HIV, virucide or
CC osteopathic activity acting as G-protein antagonists. The methods and
CC compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of the human G-protein coupled receptor,
CC HGPBM78, such as cancer, asthma, allergies, HIV infections,
CC osteoporosis, Parkinson's disease, anxiety, hypertension and neurological
CC diseases. The present sequence is that of the human HGPBM78 protein of
CC the invention.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 2644; DB 9; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.1e-233;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSSHTCMPISLKHGIIRSTVLVIFLAASFGNIVLALVQRP 60
DB 1 MTSTCTNSTRESNSSHTCMPISLKHGIIRSTVLVIFLAASFGNIVLALVQRP 60
QY 61 QLLQVTNRPIFNLTVDLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTLFPAFASV 120
DB 61 QLLQVTNRPIFNLTVDLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTLFPAFASV 120
QY 121 TIVLVSVDRYLSIIHPLSPSKMTQRGILLYGTWIVAILOSTPPLVYGMGAAPDERNA 180
DB 121 TIVLVSVDRYLSIIHPLSPSKMTQRGILLYGTWIVAILOSTPPLVYGMGAAPDERNA 180
QY 181 LCSMTWGSASPTIISVSVFIVPLIWMACYSVFCARROHALLYNKRHSLEVRVD 240
DB 181 LCSMTWGSASPTIISVSVFIVPLIWMACYSVFCARROHALLYNKRHSLEVRVD 240
QY 241 CVENDEDEGAEKKEFEFROHGEVKAKEGMEAKDQSLKAKEGSTGTSSESVYA 300
DB 241 CVENDEDEGAEKKEFEFROHGEVKAKEGMEAKDQSLKAKEGSTGTSSESVYA 300
QY 301 RGSSEVRESSTVASDQSGMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEDMEFGEDDI 360
DB 301 RGSSEVRESSTVASDQSGMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEDMEFGEDDI 360
QY 361 NSESDDEAVANIPESLPSPSRNSNSNPPLPRCYOCCAAYVIFIIIFSYLSLGPYCFILAV 420
DB 361 NSESDDEAVANIPESLPSPSRNSNSNPPLPRCYOCCAAYVIFIIIFSYLSLGPYCFILAV 420
QY 421 LAWVVDVETQVQWVITIIIMLPFLOCCIHPPYVGYGMHKTIIKEIDOMLKFFCCKEPPK 480
DB 421 LAWVVDVETQVQWVITIIIMLPFLOCCIHPPYVGYGMHKTIIKEIDOMLKFFCCKEPPK 480
QY 481 EDSDHDLPGTEGTEGKIIVSYDSATFP 508
DB 481 EDSDHDLPGTEGTEGKIIVSYDSATFP 508

RESULT 9
ADP70508
ID ADP70508 standard; protein; 746 AA.
XX
AC ADP70508;
XX
DT 12-FEB-2004 (first entry)
XX
DE Orphan receptor ligand-related human protein SegID131.

XX ligand; orphan receptor protein; fusion protein; fluorescent protein;
KW cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
KW GFPuv; Enhanced GFP; EGFP; human.
XX
OS Homo sapiens.
XX
PN WO2003071272-A1.
XX
PD 28-AUG-2003.
XX
PF 21-FEB-2003; 2003WO-JP001901.
XX
PR 22-FEB-2002; 2002JP-00045728.
PR 23-JUL-2002; 2002JP-00213949.
PR 11-OCT-2002; 2002JP-00298237.
XX
PA (TAKEDA) TAKEDA CHEM IND LTD.
XX
PI Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;
PI
XX
DR MPI: 2003-697654/66.
DR N-PSDB; ADP70610.
XX
PT Transformation of cells with a fusion protein of an orphan receptor
PT protein with a fluorescent protein useful for identification of ligands
PT to the orphan receptor.
XX
PS Disclosure; SEQ ID NO 131; 594pp; Japanese.

Query Match 100.0%; Score 2644; DB 7; Length 746;
Best Local Similarity 100.0%; Pred. No. 1.9e-233;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSSHTCMPISLKHGIIRSTVLVIFLAASFGNIVLALVQRP 60
DB 1 MTSTCTNSTRESNSSHTCMPISLKHGIIRSTVLVIFLAASFGNIVLALVQRP 60
QY 61 QLLQVTNRPIFNLTVDLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTLFPAFASV 120
DB 61 QLLQVTNRPIFNLTVDLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTLFPAFASV 120
QY 121 TIVLVSVDRYLSIIHPLSPSKMTQRGILLYGTWIVAILOSTPPLVYGMGAAPDERNA 180
DB 121 TIVLVSVDRYLSIIHPLSPSKMTQRGILLYGTWIVAILOSTPPLVYGMGAAPDERNA 180
QY 181 LCSMTWGSASPTIISVSVFIVPLIWMACYSVFCARROHALLYNKRHSLEVRVD 240
DB 181 LCSMTWGSASPTIISVSVFIVPLIWMACYSVFCARROHALLYNKRHSLEVRVD 240
QY 241 CVENDEDEGAEKKEFEFROHGEVKAKEGMEAKDQSLKAKEGSTGTSSESVYA 300
DB 241 CVENDEDEGAEKKEFEFROHGEVKAKEGMEAKDQSLKAKEGSTGTSSESVYA 300
QY 301 RGSSEVRESSTVASDQSGMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEDMEFGEDDI 360
DB 301 RGSSEVRESSTVASDQSGMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEDMEFGEDDI 360
QY 361 NSESDDEAVANIPESLPSPSRNSNSNPPLPRCYOCCAAYVIFIIIFSYLSLGPYCFILAV 420
DB 361 NSESDDEAVANIPESLPSPSRNSNSNPPLPRCYOCCAAYVIFIIIFSYLSLGPYCFILAV 420

QY 421 LAWVWVETQVPQWVITIIILWLFLLQCCIHPPYVGYMHTIKKEIQDMLKKFCEKXPPK 480
DB 421 LAWVWVETQVPQWVITIIILWLFLLQCCIHPPYVGYMHTIKKEIQDMLKKFCEKXPPK 480
QY 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
DB 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 10

AAB6428

ID AAB6428 standard; protein; 508 AA.

XX AAB6428;

XX 19-OCT-2001 (first entry)

XX Human brain SERALPHA protein.

XX SERALPHA; human; brain; G protein receptor; medicine.

XX Homo sapiens.

XX DE10004930-A1.

XX 09-AUG-2001.

XX 04-FEB-2000; 2000DE-01004930.

XX 04-FEB-2000; 2000DE-01004930.

XX (BRUE/) BRUES M.

XX (BOEN/) BOENISCH H.

XX Brues M, Boenisch H;

XX WPI; 2001-489887/54.

XX N-PSDB; AAH48673.

XX Gene encoding a protein of the G protein receptor super family, having

XX PT homology to neurotransmitter receptors is useful to develop new

XX PT medications.

XX PS Disclosure; Page 4; 8pp; German.

XX CC This invention describes a novel human brain-derived G protein receptor

XX CC gene and its encoding protein, designated SERALPHA. The receptor or cells

XX CC expressing the receptor are used to develop new medicines, chemicals and

XX CC technologies, and to devaluate existing medicines and technologies

XX SQ Sequence 508 AA;

Query Match 99.9%; Score 2641; DB 4; Length 508;

Best Local Similarity 99.8%; Pred. No. 2,1e-233;

Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSHTCMPLSKMPLSLAHGIIIRSTVLVIFLAASFGVGNIVLALVQRKP 60
DB 1 MTSTCTNSTRESNSHTCMPLSKMPLSLAHGIIIRSTVLVIFLAASFGVGNIVLALVQRKP 60
QY 61 QLLQVTNRFIFNLVTDLQISLVAWVAVTSVPLFWPLNSHFCALVSLTHLFAFASVN 120
DB 61 QLLQVTNRFIFNLVTDLQISLVAWVAVTSVPLFWPLNSHFCALVSLTHLFAFASVN 120
QY 121 TIVVSVDRYLSIHPILSPSKMQRGTLILGTYWIVAILDSTPPLVYGMAAFDERNA 180
DB 121 TIVVSVDRYLSIHPILSPSKMQRGTLILGTYWIVAILDSTPPLVYGMAAFDERNA 180
QY 181 LCSMTWGSAPSYTILSVSVFIVPLVIMACYSVFCAARQHALLYNKRHSLFVRVD 240
DB 181 LCSMTWGSAPSYTILSVSVFIVPLVIMACYSVFCAARQHALLYNKRHSLFVRVD 240

QY 241 CVENEDERGAKKEPFODESEFFRRQHGCEVYAKAKGRMEAKGSLKAKEGSTGTSSESYEA 300
DB 241 CVENEDERGAKKEPFODESEFFRRQHGCEVYAKAKGRMEAKGSLKAKEGSTGTSSESYEA 300
QY 301 RGESEVRESSTVASDGSMEGKEGSTKVBNEMKADKGRTEVNOCSIDLGEEDMERGEDDI 360
DB 301 RGESEVRESSTVASDGSMEGKEGSTKVBNEMKADKGRTEVNOCSIDLGEEDMERGEDDI 360
QY 361 NFSBDVEAVNIPESLPPSRNSNSNPPLPRCYOCCAIAVIFIIIFSYLSLGPYCFYAV 420
DB 361 NFSBDVEAVNIPESLPPSRNSNSNPPLPRCYOCCAIAVIFIIIFSYLSLGPYCFYAV 420
QY 421 LAWVWVETQVPQWVITIIILWLFLLQCCIHPPYVGYMHTIKKEIQDMLKKFCEKXPPK 480
DB 421 LAWVWVETQVPQWVITIIILWLFLLQCCIHPPYVGYMHTIKKEIQDMLKKFCEKXPPK 480
QY 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
DB 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 11

AAU25605

ID AAU25605 standard; protein; 508 AA.

XX AAU25605;

XX 18-DEC-2001 (first entry)

XX Human G Protein-coupled Receptor (GPCR) polypeptide #52.

XX Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia;

XX attention deficit disorder; anxiety; depression; bipolar disorder;

XX neurological disorder; Huntington's disease; dementia; obesity; anorexia;

XX metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis;

XX type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer;

XX cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV;

XX viral infection; immunostimulant; neuroleptic; nootropic; tranquiliser;

XX antidepressant; anorectic; gene therapy.

XX OS Homo sapiens.

XX W0200162797-A2.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-US005676.

XX 23-FEB-2000; 2000US-0184247P.

XX 23-FEB-2000; 2000US-0184303P.

XX 23-FEB-2000; 2000US-0184304P.

XX 23-FEB-2000; 2000US-0184305P.

XX 23-FEB-2000; 2000US-0184397P.

XX 02-MAR-2000; 2000US-0186457P.

XX 03-MAR-2000; 2000US-0186810P.

XX 09-MAR-2000; 2000US-0188064P.

XX 13-MAR-2000; 2000US-0188880P.

XX 03-APR-2000; 2000US-0194344P.

XX 23-JUN-2000; 2000US-0213861P.

XX 11-JUL-2000; 2000US-0213863P.

XX 11-JUL-2000; 2000US-0213863P.

XX 14-JUL-2000; 2000US-0218337P.

XX 20-JUL-2000; 2000US-0218492P.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Vogel I G, Wood LS, Parodi LA, Lind P;

XX WPI; 2001-570628/64.

XX N-PSDB; AAS42857.

XX New isolated nucleic acid encoding a new G-protein coupled receptor

XX polypeptide for detecting receptor modulators that can treat mental

PT disorders, such as schizophrenia, anxiety, depression, or obesity.
XX Claim 35; Page 90; 279pp; English.
XX
CC Sequences AAU2554-AAU25616 represent human G-protein coupled receptor
CC (GPCR) polypeptides of the invention. The proteins and their associated
CC DNA sequences can be used to identify compounds which bind to GPCR
CC polypeptides and in screening for compounds that modulate GPCR activity.
CC By screening a human subject for the presence of mutations in GPCR DNA, a
CC GPCR-related disorder or a genetic predisposition can be diagnosed. The
CC sequences can also be used for treatment and prevention of mental
CC disorders such as schizophrenia, attention deficit disorder, anxiety,
CC depression, dementia and bipolar disorder, neurological disorders such as
CC Huntington's disease, Parkinson's disease and Tourette's syndrome,
CC metabolic disorders such as obesity, anorexia and type 2 diabetes,
CC cardiovascular disorders such as thrombosis, myocardial infarction,
CC cardiomyopathy and atherosclerosis, viral infections caused by HIV and
CC cancers
XX
XX Sequence 508 AA;
SQ
Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 2.1e-233;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTSTCTNSTRESNSSHTCMPISLAKGIRSTVLVIFLAASFGNIVLALVQRKP 60
DB 1 MTSTCTNSTRESNSSHTCMPISLAKGIRSTVLVIFLAASFGNIVLALVQRKP 60
QY 61 QLLQVNTNRIFNLVTDLLQISLVAPWVAATVPFLWPLNSHCTALVSLTHLFAFASVN 120
DB 61 QLLQVNTNRIFNLVTDLLQISLVAPWVAATVPFLWPLNSHCTALVSLTHLFAFASVN 120
QY 121 TLVLSVDRYLSIIHPLSPSKTORRGYLLXGTMIVAILOSTPPLXGMOAAPDERNA 180
DB 121 TLVLSVDRYLSIIHPLSPSKTORRGYLLXGTMIVAILOSTPPLXGMOAAPDERNA 180
QY 181 LCSMWGASPSYTIISVSVFIYPLIWMACYSVFCARROHALLYNKRSHLEVRVND 240
DB 181 LCSMWGASPSYTIISVSVFIYPLIWMACYSVFCARROHALLYNKRSHLEVRVND 240
QY 241 CVENEDBGAKEKEEFODESEFRROHEGVKAKGEMKADGSLAKKESGTGTSSESVRA 300
DB 241 CVENEDBGAKEKEEFODESEFRROHEGVKAKGEMKADGSLAKKESGTGTSSESVRA 300
QY 301 RSESEVRRESSTVASDGSMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEDDMEFGEDDI 360
DB 301 RSESEVRRESSTVASDGSMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEDDMEFGEDDI 360
QY 361 NSESDVEAVNIPESLPSPRRNSNSNPPLPRCYOCCAAYVFIIFSYVLSLGPYCFLLAV 420
DB 361 NSESDVEAVNIPESLPSPRRNSNSNPPLPRCYOCCAAYVFIIFSYVLSLGPYCFLLAV 420
QY 421 LAVVWVDETOVPWMTIIIIIMLFLOCCHIPYVYGVMHTIKKEIDMLKKFCKCKPKPX 480
DB 421 LAVVWVDETOVPWMTIIIIIMLFLOCCHIPYVYGVMHTIKKEIDMLKKFCKCKPKPX 480
QY 481 EDSHPDLPGTEGTEGKIVPSYDSTAFP 508
DB 481 EDSHPDLPGTEGTEGKIVPSYDSTAFP 508
RESULT 12
AAG64126 standard; protein; 508 AA.
ID AAG64126;
XX AAG64126;
AC AAG64126;
XX
DT 25-SBP-2001 (first entry)
XX
DE Human G protein-coupled receptor GPRV72.
XX
KW Human; guanosine triphosphate binding protein-coupled receptor;

KW G protein-coupled receptor; GPRV8; GPRV12; GPRV16; GPRV21; GPRV40;
KW GPRV47; GPRV51; GPRV71; GPRV72; cancer; liver cirrhosis;
KW Alzheimer's disease; cytosolic; hepatotropic; neurotropic;
KW neuroprotective; gene therapy; peptide therapy.
OS Homo sapiens.
PN
XX WO200148188-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000MO-JP009408.
XX
PR 28-DEC-1999; 99JP-00375152.
PR 31-MAR-2000; 2000JP-00101339.
XX
XX (HELI-) HELIX RES INST.
XX
XX Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;
PI Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;
PI
XX WPI: 2001-425662/45.
DR N-PSDB; AAH73517.
XX
XX New DNA encoding guanosine triphosphate binding protein coupled receptors
PT and their expression products for screening potential anticancer and
PT neurotropic drugs and in diagnosis of these diseases.
XX
XX Claim 1; Page 135-138; 170pp; Japanese.
XX
XX The invention relates to nine human guanosine triphosphate binding
CC protein (G protein)-coupled receptors designated GPRV8, GPRV12, GPRV16,
CC GPRV21, GPRV40, GPRV47, GPRV51, GPRV71 and GPRV72, and to the genes
CC encoding them. These genes and proteins and antibodies against the
CC protein are useful in the treatment, prevention, diagnosis and
CC investigation of diseases associated with G protein-coupled receptors,
CC including cancer, cirrhosis of the liver and Alzheimer's disease. The
CC present sequence is a G protein-coupled receptor of the invention
XX
XX Sequence 508 AA;
SQ
Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 2.1e-233;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTSTCTNSTRESNSSHTCMPISLAKGIRSTVLVIFLAASFGNIVLALVQRKP 60
DB 1 MTSTCTNSTRESNSSHTCMPISLAKGIRSTVLVIFLAASFGNIVLALVQRKP 60
QY 61 QLLQVNTNRIFNLVTDLLQISLVAPWVAATVPFLWPLNSHCTALVSLTHLFAFASVN 120
DB 61 QLLQVNTNRIFNLVTDLLQISLVAPWVAATVPFLWPLNSHCTALVSLTHLFAFASVN 120
QY 121 TLVLSVDRYLSIIHPLSPSKTORRGYLLXGTMIVAILOSTPPLXGMOAAPDERNA 180
DB 121 TLVLSVDRYLSIIHPLSPSKTORRGYLLXGTMIVAILOSTPPLXGMOAAPDERNA 180
QY 181 LCSMWGASPSYTIISVSVFIYPLIWMACYSVFCARROHALLYNKRSHLEVRVND 240
DB 181 LCSMWGASPSYTIISVSVFIYPLIWMACYSVFCARROHALLYNKRSHLEVRVND 240
QY 241 CVENEDBGAKEKEEFODESEFRROHEGVKAKGEMKADGSLAKKESGTGTSSESVRA 300
DB 241 CVENEDBGAKEKEEFODESEFRROHEGVKAKGEMKADGSLAKKESGTGTSSESVRA 300
QY 301 RSESEVRRESSTVASDGSMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEDDMEFGEDDI 360
DB 301 RSESEVRRESSTVASDGSMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEDDMEFGEDDI 360
QY 361 NSESDVEAVNIPESLPSPRRNSNSNPPLPRCYOCCAAYVFIIFSYVLSLGPYCFLLAV 420
DB 361 NSESDVEAVNIPESLPSPRRNSNSNPPLPRCYOCCAAYVFIIFSYVLSLGPYCFLLAV 420

QY 421 LAWVDTVTOVPQWVITITIIIMLFLOCCIHPIYVGYMKTIKKEIDMLKKFCEKRPK 480
DB 421 LAWVDTVTOVPQWVITITIIIMLFLOCCIHPIYVGYMKTIKKEIDMLKKFCEKRPK 480
QY 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508
DB 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508

RESULT 13
AAU04369
ID AAU04369 standard; protein; 508 AA.
AC AAU04369;
XX 23-OCT-2001 (first entry)
DE Human G-protein coupled receptor, hRUP15.
KW Human; G-protein coupled receptor; GPCR; hRUP15; agonist;
XX inverse agonist; lung cancer.
OS Homo sapiens.
XX MO200136471-A2.
XX 25-MAY-2001.
XX 16-NOV-2000; 2000MO-US031509.
XX 17-NOV-1999; 99US-0166088P.
XX 17-NOV-1999; 99US-0166099P.
XX 17-NOV-1999; 99US-0166369P.
XX 23-DEC-1999; 99US-0171900P.
XX 23-DEC-1999; 99US-0171901P.
XX 23-DEC-1999; 99US-0171902P.
XX 11-FEB-2000; 2000US-0181749P.
XX 14-MAR-2000; 2000US-0189258P.
XX 14-MAR-2000; 2000US-0189259P.
XX 10-APR-2000; 2000US-0195898P.
XX 10-APR-2000; 2000US-0195899P.
XX 10-APR-2000; 2000US-0196078P.
XX 28-APR-2000; 2000US-0200419P.
XX 12-MAY-2000; 2000US-0203630P.
XX 12-JUN-2000; 2000US-0210741P.
XX 12-JUN-2000; 2000US-0210982P.
XX 21-AUG-2000; 2000US-0226760P.
XX 26-SEP-2000; 2000US-0235418P.
XX 26-SEP-2000; 2000US-0235799P.
XX 20-OCT-2000; 2000US-0242332P.
XX 20-OCT-2000; 2000US-0242343P.
XX 24-OCT-2000; 2000US-0243019P.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Chen R, Dang HT, Lowitz KP;
XX
XX MPI; 2001-355616/37.
XX N-PSDB; AAS07942.
XX
XX Endogenous and non-endogenous versions of human G-protein coupled
XX receptors for direct identification of candidate compounds as agonists,
XX inverse agonists or partial agonists for use as therapeutic agents.
XX
XX Claim 29; Page 102-104; 160pp; English.
XX
XX The sequence represents a human G-protein coupled receptor (GPCR),
XX hRUP15. The endogenous and non-endogenous, constitutively activated
XX versions of human G-protein coupled receptors (GPCR), are useful for
XX direct identification of candidate compounds as receptor agonists,
XX inverse agonists or partial agonists having applicability as therapeutic
XX agents for treating diseases related to GPCR, e.g. lung cancer. Non-
XX endogenous version of human GPCRs are also utilized in research settings

CC and in vitro and in vivo system, incorporating GPCRs, can be utilized to
CC elucidate and understand the roles these receptors play in the human
CC condition, both normal and diseased
XX
XX SQ Sequence 508 AA;
Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 2.1e-233;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNNSHTCMPKIPSLAHGIIIRSTVIVIFLASFVGNIVLALVQKRP 60
DB 1 MTSTCTNSTRESNNSHTCMPKIPSLAHGIIIRSTVIVIFLASFVGNIVLALVQKRP 60
QY 61 QLTQVTRNFIFNLVTDLLQISLVAWVAVTSVPLFMPNLNHFCTALVSLTHLFAFASVN 120
DB 61 QLTQVTRNFIFNLVTDLLQISLVAWVAVTSVPLFMPNLNHFCTALVSLTHLFAFASVN 120
QY 121 TIVVSVDRYLSIIHPLSYPSKMTQRCGYLLLYGTWIVALLQSTPPPLYGMCQAAFDERNA 180
DB 121 TIVVSVDRYLSIIHPLSYPSKMTQRCGYLLLYGTWIVALLQSTPPPLYGMCQAAFDERNA 180
QY 181 LCSMTWGAESPSTYLLISVSFIVIPLIWMIACYSVFCAARQHALLVNKHSLSEVRXKD 240
DB 181 LCSMTWGAESPSTYLLISVSFIVIPLIWMIACYSVFCAARQHALLVNKHSLSEVRXKD 240
QY 241 CVENEDDEGAARKEEFODESEFFRQHEGEVYAKEGRMKADGSLAKESGTGTSSESVYA 300
DB 241 CVENEDDEGAARKEEFODESEFFRQHEGEVYAKEGRMKADGSLAKESGTGTSSESVYA 300
QY 301 RGSEVERESTVYASGMEGKEGSTKVENSMKADKGTENVQCSIDLGEDDMERGEDDI 360
DB 301 RGSEVERESTVYASGMEGKEGSTKVENSMKADKGTENVQCSIDLGEDDMERGEDDI 360
QY 361 NPSDDVAVNIPESLPSRRNSNPNPLPRCYCKAKAVFIIFISVYLSIGPCFLAV 420
DB 361 NPSDDVAVNIPESLPSRRNSNPNPLPRCYCKAKAVFIIFISVYLSIGPCFLAV 420
QY 421 LAWVDTVTOVPQWVITITIIIMLFLOCCIHPIYVGYMKTIKKEIDMLKKFCEKRPK 480
DB 421 LAWVDTVTOVPQWVITITIIIMLFLOCCIHPIYVGYMKTIKKEIDMLKKFCEKRPK 480
QY 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508
DB 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508

RESULT 14
AAU11764
ID AAU11764 standard; protein; 508 AA.
AC AAU11764;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human alpha1a adrenergic receptor-like GPCR.
XX
XX Human; alpha1a adrenergic receptor; G protein-coupled receptor; GPCR;
XX peripheral nervous system disease; central nervous system disease;
XX urinary incontinence; benign prostatic hypertrophy; infection;
XX HIV infection; human immunodeficiency virus; pain; cancer; anorexia;
XX bulimia; asthma; Parkinson's disease; obesity; acute heart failure;
XX hypotension; hypertension; urinary retention; osteoporosis;
XX angina pectoris; myocardial infarction; ulcer; allergy; psychosis;
XX neurological disorder; anxiety; schizophrenia; manic depression;
XX delirium; dementia; severe mental retardation; dyskinesia;
XX Huntington's disease; Tourette's syndrome.
XX
XX Homo sapiens.
XX
XX WO20018126-A2.
XX PD 22-NOV-2001.

XX 11-MAY-2001; 2001WO-EP005383.
 PF
 XX 15-MAY-2000; 2000US-0204145P.
 PR
 PR 04-DEC-2000; 2000US-0250505P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Ramakrishnan S;
 XX
 DR WPI: 2002-106124/14.
 DR N-PSDB; AAS18898, AAS18899.
 PT
 PT New polynucleotide, useful for treating pain, cancer, Parkinson's
 PT (1a) adrenergic receptor-like G-protein coupled receptor (GPCR).
 XX
 PS Claim 25; Fig 3; 123pp; English.
 CC The invention relates to an isolated polynucleotide encoding an alpha
 CC adrenergic receptor-like G-protein coupled receptor (GPCR) polypeptide,
 CC the encoded polypeptide, fragments, derivatives and allelic variants.
 CC Also include are an expression vector comprising the polynucleotide, a
 CC host cell containing the vector, screening for therapeutic agents which
 CC decrease or increase the activity of the receptor by binding a test agent
 CC to the protein and determining whether the activity is decreased or
 CC increased. A modulator of the receptor is useful for treating alpha
 CC adrenergic receptor-like GPCR disorder such as peripheral or central
 CC nervous system disease, urinary incontinence or benign prostatic
 CC hypertrophy. The receptor, polynucleotide or modulator is useful for
 CC treating disorders such as bacterial, fungal, protozoan, and viral
 CC infections, particularly those caused by HIV (human immunodeficiency
 CC virus), pain, cancer, anorexia, bulimia, asthma, Parkinson's diseases,
 CC obesity, acute heart failure, hypertension, hypertension, urinary
 CC retention, osteoporosis, angina pectoris, myocardial infarction, ulcer,
 CC allergy, benign prostatic hypertrophy, and psychotic and neurological
 CC disorders, including anxiety, schizophrenia, manic depression, delirium,
 CC dementia, severe mental retardation, and dyskinesias, such as
 CC Huntington's disease and Tourette's syndrome. The polynucleotide is
 CC useful in diagnostic assays for detecting diseases and abnormalities or
 CC susceptibility to disease and abnormalities related to the presence of
 CC mutations in the gene. The protein is useful to identify test compounds
 CC which may act as agonists or antagonists, and for raising antibodies
 CC which can block the receptor and effectively prevent ligand binding. The
 CC present sequence is the alpha adrenergic receptor-like GPCR
 XX
 XX Sequence 508 AA;
 SQ
 Query Match 99.9%; Score 2641; DB 5; Length 508;
 Best Local Similarity 99.8%; Pred. No. 2.1e-233;
 Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSTCTNSTRESNNSHTCMPLSKMPLSLAHGIIIRSTVLVIFLAASFVGNIVLALVQRKP 60
 DB 1 MSTCTNSTRESNNSHTCMPLSKMPLSLAHGIIIRSTVLVIFLAASFVGNIVLALVQRKP 60
 QY 61 QILQVTNRIFNLVLDLQISLVAPWVAVTSVPLFWPLNSHPCITLVSLTHLFAASVND 120
 DB 61 QILQVTNRIFNLVLDLQISLVAPWVAVTSVPLFWPLNSHPCITLVSLTHLFAASVND 120
 QY 121 TLIVLSVDVRLIIFHPLSPSKMTORGILLYGTIVAILLOSTPLPYMGQNAFPERNA 180
 DB 121 TLIVLSVDVRLIIFHPLSPSKMTORGILLYGTIVAILLOSTPLPYMGQNAFPERNA 180
 QY 121 TLIVLSVDVRLIIFHPLSPSKMTORGILLYGTIVAILLOSTPLPYMGQNAFPERNA 180
 DB 121 TLIVLSVDVRLIIFHPLSPSKMTORGILLYGTIVAILLOSTPLPYMGQNAFPERNA 180
 QY 181 LGSMTWGAASPSYTIISVSPFIVPLIWMIACTSVFCAARQHALLYNKRSLLEVAVD 240
 DB 181 LGSMTWGAASPSYTIISVSPFIVPLIWMIACTSVFCAARQHALLYNKRSLLEVAVD 240
 QY 181 LGSMTWGAASPSYTIISVSPFIVPLIWMIACTSVFCAARQHALLYNKRSLLEVAVD 240
 DB 181 LGSMTWGAASPSYTIISVSPFIVPLIWMIACTSVFCAARQHALLYNKRSLLEVAVD 240
 QY 241 CTENEBEBAKKEEPODESSEPRROHEGYKAKEGMEAKDGLKAKESGTGSESSVVA 300
 DB 241 CTENEBEBAKKEEPODESSEPRROHEGYKAKEGMEAKDGLKAKESGTGSESSVVA 300
 QY 241 CTENEBEBAKKEEPODESSEPRROHEGYKAKEGMEAKDGLKAKESGTGSESSVVA 300
 DB 241 CTENEBEBAKKEEPODESSEPRROHEGYKAKEGMEAKDGLKAKESGTGSESSVVA 300
 QY 301 RSESEVRSSSTVAASDGSMEGKSGSTVYENSMKADKGRTEVNVQCSIDLGEDDMEFGEDDI 360
 DB 301 RSESEVRSSSTVAASDGSMEGKSGSTVYENSMKADKGRTEVNVQCSIDLGEDDMEFGEDDI 360

DB 301 RSESEVRSSSTVAASDGSMEGKSGSTVYENSMKADKGRTEVNVQCSIDLGEDDMEFGEDDI 360
 QY 361 NFESEDDVAVNIPESLPPSRNSNPNPLPRCYOCKAKAVFIILIFSVYLSIGPYCPLAV 420
 DB 361 NFESEDDVAVNIPESLPPSRNSNPNPLPRCYOCKAKAVFIILIFSVYLSIGPYCPLAV 420
 QY 421 LAWVDEVETOYVQWVITFIIMLFPOCCIHPPVYGYMHTIKKEIQDMLKPFCKEKP 480
 DB 421 LAWVDEVETOYVQWVITFIIMLFPOCCIHPPVYGYMHTIKKEIQDMLKPFCKEKP 480
 QY 481 EDSDHDLPGTEGTEGKTIVPYSYDSTFP 508
 DB 481 EDSDHDLPGTEGTEGKTIVPYSYDSTFP 508
 RESULT 15
 AAO15504
 ID AAO15504 standard; protein; 508 AA.
 XX
 AC AAO15504;
 XX
 DT 24-OCT-2002 (first entry)
 XX
 DE Human G-protein coupled receptor protein #2.
 XX
 KW Human; G-protein coupled receptor protein; TGR34;
 KW central nervous system disease; Alzheimer's disease; metabolic disease;
 KW diabetes; cancer; breast cancer; circulatory disease; atherosclerosis;
 KW inflammatory disease; arthritis; respiratory disease; bronchitis;
 KW digestive disease; stomach ulcer; immune disorder; autoimmune disease;
 KW infection; AIDS.
 XX
 OS Homo sapiens.
 XX
 PN WO200259304-A1.
 XX
 PD 01-AUG-2002.
 XX
 PF 22-JAN-2002; 2002WO-JP000405.
 XX
 PR 23-JAN-2001; 2001JP-00015050.
 XX
 PR 30-MAR-2001; 2001JP-00102560.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Miwa M, Ito T, Shintani Y, Miyajima N;
 XX
 DR WPI: 2002-557949/59.
 DR N-PSDB; AAL44180.
 PT Human G-protein coupled receptor protein and DNA encoding it for design
 PT of drugs and reagents for treatment and diagnosis of cancer or
 PT respiratory and metabolic diseases.
 PS Claim 2; Page 97-99; 109pp; Japanese.
 XX
 CC The invention comprises the amino acid and coding sequences of two human
 CC G-protein coupled receptor proteins (TGR34). The DNA and protein
 CC sequences of the invention are useful for the treatment, prevention and
 CC diagnosis of: central nervous system diseases (e.g. Alzheimer's disease);
 CC metabolic diseases (e.g. diabetes); cancer (e.g. breast cancer);
 CC circulatory diseases (e.g. atherosclerosis); inflammatory diseases (e.g.
 CC arthritis); respiratory diseases (e.g. bronchitis); digestive diseases
 CC (e.g. stomach ulcer); immune disorders (e.g. autoimmune diseases); and
 CC infections (e.g. AIDS). The present amino acid sequence represents a
 CC human G-protein coupled receptor protein
 XX
 XX Sequence 508 AA;
 SQ
 Query Match 99.9%; Score 2641; DB 5; Length 508;
 Best Local Similarity 99.8%; Pred. No. 2.1e-233;
 Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRP	60
Db	1	MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRP	60
Qy	61	OLLOVTNRFITNLVLTDLQISLVAPMVAATSVPLFWPLNSHCTALVSLTHLFAFASVN	120
Db	61	OLLOVTNRFITNLVLTDLQISLVAPMVAATSVPLFWPLNSHCTALVSLTHLFAFASVN	120
Qy	121	TIIVSVDRYLSIIHPLSYPSKMTORRGYLLLYGTWIVAILQSTPPLYGMOGAFAFDERNA	180
Db	121	TIIVSVDRYLSIIHPLSYPSKMTORRGYLLLYGTWIVAILQSTPPLYGMOGAFAFDERNA	180
Qy	181	LCSMIMGASPSYTIISVVSFIVIPLIIMACYSVVFCARQHALLYNVKHSLEVRVD	240
Db	181	LCSMIMGASPSYTIISVVSFIVIPLIIMACYSVVFCARQHALLYNVKHSLEVRVD	240
Qy	241	CVENDEDEGAEEKEEFODESEFRROHGEVKAKEGRMEAKDGLKAKEGSTGTSSESYEA	300
Db	241	CVENDEDEGAEEKEEFODESEFRROHGEVKAKEGRMEAKDGLKAKEGSTGTSSESYEA	300
Qy	301	RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMFEGEDDI	360
Db	301	RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMFEGEDDI	360
Qy	361	NFSEDDVEAVNIPESLPPSRNSNSNPPLPRCYCKAKAVIFIIIFSYYLSIGPYCFLAV	420
Db	361	NFSEDDVEAVNIPESLPPSRNSNSNPPLPRCYCKAKAVIFIIIFSYYLSIGPYCFLAV	420
Qy	421	LAVWVDVETQVPOWVITIIIMFLFLOCCIHPIYVGYMHTIKKEIQDMLKKFCEKEXPPK	480
Db	421	LAVWVDVETQVPOWVITIIIMFLFLOCCIHPIYVGYMHTIKKEIQDMLKKFCEKEXPPK	480
Qy	481	EDSHDLPCTEGTEGKIIVPSYDSATFP	508
Db	481	EDSHDLPCTEGTEGKIIVPSYDSATFP	508

Search completed: December 3, 2005, 06:30:43
 Job time : 160.286 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 10, 2005, 03:07:14 / Search time 595 Seconds
(without alignments)
5690.191 Million cell updates/sec

Title: US-10-712-615-2

Perfect score: 2644
Sequence: 1 MTSTCTNSTRESNSHTCMP.....GTEGTEGKIYPSYDSTATFP 508

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

MODEL=frame_plus_p2n.model -DEV=xlh
-O=/cgn2.1/USPTO_spool/US10712615/runat_02122005_103721_24052/app_query.fasta_1.647
-DB=N Geneseg -OFMT=faetap -SUFFIX=ring -MINMATCH=0.1 -LOOPEC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human4.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptlo -NORM=ext -HEAPSIZE=500 -MITLEN=0 -MAXLEN=2000000000
-USER=US10712615_@CGN_1_1_542_@runat_02122005_103721_24052 -NCPU=6 -ICPU=3
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseg 21.*
1: genesegn1980s.*
2: genesegn1990s.*
3: genesegn2000s.*
4: genesegn2001as.*
5: genesegn2001bs.*
6: genesegn2002as.*
7: genesegn2002bs.*
8: genesegn2003as.*
9: genesegn2003bs.*
10: genesegn2003cs.*
11: genesegn2003ds.*
12: genesegn2004as.*
13: genesegn2004bs.*
14: genesegn2005as.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2644	100.0	1524	6	AAL44179	Aal44179 Human G-P
2	2644	100.0	1527	4	AAH73517	Aah73517 Human G-P
3	2644	100.0	1527	6	ABL53719	Ab153719 G-protein
4	2644	100.0	1527	6	AAD41159	Aad41159 Human HGP

ALIGNMENTS

RESULT 1	ID	Score	Match	Length	DB	ID	Description
1	AAL44179	100.0	1527	10	ABV74517	ABV74517 Human G-P	
2	AAL44179	100.0	1527	14	AEA33069	Aea33069 Human G-P	
3	AAL44179	100.0	1580	6	AAD41170	Aad41170 Human HGP	
4	AAL44179	100.0	1580	14	AEA33115	Aea33115 Human GPC	
5	AAL44179	100.0	1584	8	ACF03567	Acf03567 Human NOV	
6	AAL44179	100.0	2241	10	ADP70610	Adp70610 Orphan re	
7	AAL44179	100.0	4718	9	ACC58886	Acc58886 Human G-P	
8	AAL44179	100.0	1524	6	AAL44180	Aal44180 Human G-P	
9	AAL44179	100.0	1527	4	AA542857	Aa542857 Human G-P	
10	AAL44179	100.0	1527	5	AA507942	Aa507942 Human G-P	
11	AAL44179	100.0	1527	6	AA188899	Aa188899 Human G-P	
12	AAL44179	100.0	1527	6	ABN86854	Abn86854 Human G-P	
13	AAL44179	100.0	1527	6	AB242914	Ab242914 Human GPC	
14	AAL44179	100.0	1527	8	AB242550	Ab242550 Human G-P	
15	AAL44179	100.0	1527	8	ABV73366	Abv73366 Human TGR	
16	AAL44179	100.0	1527	10	AA662687	Aa662687 Human G-P	
17	AAL44179	100.0	1527	11	ADL96461	Adl96461 Human G-P	
18	AAL44179	100.0	1527	12	AD140953	Ad140953 Human G-P	
19	AAL44179	100.0	1527	12	ADO29756	Ado29756 Human nov	
20	AAL44179	100.0	1527	14	ADW44634	Adw44634 Human RUP	
21	AAL44179	100.0	1527	14	AEA33113	Aea33113 Human GPC	
22	AAL44179	100.0	1527	14	AE820818	Aeb20818 Human RUP	
23	AAL44179	100.0	1527	14	AE86472	Aec86472 Human GPC	
24	AAL44179	100.0	1520	6	AA518898	Aa518898 Human alp	
25	AAL44179	100.0	1520	5	AA508274	Aa508274 CDNA enco	
26	AAL44179	100.0	2781	11	ADL96549	Adl96549 G protein	
27	AAL44179	100.0	2781	14	ADW44722	Adw44722 Human RUP	
28	AAL44179	100.0	2781	14	AE820906	Aeb20906 Human RUP	
29	AAL44179	100.0	4260	4	AAH48673	Aah48673 Human bra	
30	AAL44179	100.0	7524	6	ABN86855	Abn86855 Human G-P	
31	AAL44179	100.0	7524	10	AA662688	Aa662688 Human G-P	
32	AAL44179	100.0	1659	4	AA56818	Aa56818 Human G-P	
33	AAL44179	100.0	1659	6	AA598069	Aa598069 Human DNA	
34	AAL44179	100.0	1659	14	AEA33112	Aea33112 Human GPC	
35	AAL44179	100.0	1527	5	AA508265	Aa508265 Human GPC	
36	AAL44179	100.0	1527	11	ADL96537	Adl96537 Human RUP	
37	AAL44179	100.0	1527	14	ADW44710	Adw44710 Human RUP	
38	AAL44179	100.0	1527	14	AEA33114	Aea33114 Human GPC	
39	AAL44179	100.0	1527	14	AE820894	Aeb20894 Human RUP	
40	AAL44179	100.0	1550	8	ACF03568	Acf03568 Human NOV	
41	AAL44179	100.0	1527	6	AAD41171	Aad41171 Human HGP	

Human G-protein coupled receptor protein coding sequence #1.

Human: G-protein coupled receptor protein; TGR34; gene; de;
central nervous system disease; Alzheimer's disease; metabolic disease;
diabetes; cancer; breast cancer; circulatory disease; atherosclerosis;
inflammatory disease; arthritis; respiratory disease; bronchitis;
digestive disease; stomach ulcer; immune disorder; autoimmune disease;
infection; AIDS.

Homo sapiens.

Key Location/Qualifiers
CDS 1..1524
FT /*tag= a
FT /partial
FT /product= "Human G-protein coupled receptor protein #1"
FT /note= "No stop codon is given"

XX WO200259304-A1.

PD 01-AUG-2002.
XX
XX 22-JAN-2002; 2002WO-JP000405.
XX
XX 23-JAN-2001; 2001JP-00015050.
XX 30-MAR-2001; 2001JP-00102560.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Miwa M, Ito T, Shintani Y, Miyajima N;
XX WPI: 2002-557949/59.
XX P-PSDB; AAO15503.
XX
XX Human G-protein coupled receptor protein and DNA encoding it for design
XX of drugs and reagents for treatment and diagnosis of cancer or
XX respiratory and metabolic diseases.
XX
XX Claim 7, Page 99-100; 109pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequences of two human
XX G-protein coupled receptor proteins (TGR34). The DNA and protein
XX sequences of the invention are useful for the treatment, prevention and
XX diagnosis of: central nervous system diseases (e.g. Alzheimer's disease);
XX metabolic diseases (e.g. diabetes); cancer (e.g. breast cancer);
XX circulatory diseases (e.g. atherosclerosis); inflammatory diseases (e.g.
XX arthritis); respiratory diseases (e.g. bronchitis); digestive diseases
XX (e.g. stomach ulcer); immune disorders (e.g. autoimmune diseases); and
XX infections (e.g. AIDS). The present DNA sequence encodes a human G-
XX protein coupled receptor protein

XX Sequence 1524 BP; 346 A; 439 C; 418 G; 321 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9,136-244 Length: 1524
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-712-615-2 (1-508) x AML44179 (1-1524)

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DB 1 ATGAGCTCCACCTGCACCAACGACGCGGAGTAACAGACGACACCGTGCATGCC 60
QY 21 LeuSerLysMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
DB 61 CTCTCAAAATGCCATCAGCTGCGCCACGCGCATCATCCCTCAACCGTGGTATC 120
QY 41 PheLeuAlaIleSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLysPro 60
DB 121 TTCCTGGCGGCTCTTGTGCGCAACATAGTGGCGCTAGTGTTGAGGGCAAGCGG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuGln 80
DB 181 CAGCGCTGCAGGTACCAACCGTTTATCTTAACCTCTGTCACCACTGCTGCAG 240
QY 81 IleSerLeuValAlaProTyrValAlaAlaThrSerValProLeuPheTyrProLeuAsn 100
DB 241 ATTTCGCTGCTGGCCCCCTGGGTGGTGGCACTGTGCTCTTCTGGGCCCTCAAC 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheIleSerValAsn 120
DB 301 AGCCCTTCTGCACGCCCCCTGGTTAGCTCACCCACCTGTGTGCCCTTGCCAGCGTCAAC 360
QY 121 ThrIleValLeuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
DB 361 ACCATTGCTTGGTGTACGTGATCGTACTTGTGCATCATCAACCTCTCCACCCG 420
QY 141 SerLysMetThrGlnArgArgGlyTyrLeuLeuLeuTyrGlyThrTyrIleValAlaIle 160

DB 421 TCCAAGATGACCAAGCCCGCGGTAACTCTCTCTATGCGACCTGATGTGGCCATC 480
QY 161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlnAlaAlaPheAspGluArgAsnAla 180
DB 481 CTGCAGACACCTCCCTCACTCTACGCGCTGGGGCCAGGCTGCTTGAAGAGCGCAATGCT 540
QY 181 LeuCysSerMetIleTyrGlyAlaSerProSerTyrThrIleLeuSerValValSerPhe 200
DB 541 CTCTCTCATGATCTGGGGGGCCAGCCCCAGCTCACTAATTCATCGCTGGTCTTC 600
QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerSerValPheCysAlaIleArg 220
DB 601 ATCGTCATTCACATGATGATGATGATTCCTGCTACTCTCGTGGTGTCTGTCAGCCCCG 660
QY 221 ArgGlnHisAlaLeuLeuTyrAsnValIysArgHisSerLeuGlnValArgValLysAsp 240
DB 661 AGCGACATGCTCTGCTCTTCAATTCATGAGACACACCTTGGAGTCCGACTCAAGAAC 720
QY 241 CysValGluAsnGluAspGluGluGlyAlaGluLysGluGluPheGlnAspGluSer 260
DB 721 TGTGTGAGAAATGAGATGAGAGGAGACAGAGAAAGAGAGAGATTCCAGATGAGAGT 780
QY 261 GluPheArgArgGlnHisGluGlyGlyValLysAlaLysGluGlyArgMetGluAlaLys 280
DB 781 GAGTTTCGCCGCCACATGAAAGGTGAGGTCAAGGCCAAGAGGCGCAGATGAAACCCCAAG 840
QY 281 AspGlySerLeuLysAlaLysGluGlySerThrGlyThrSerGluSerSerValGluAla 300
DB 841 GACGGCACCTGMAAGCCMAAGMAAGACACGGGACCACTGAGAGTATGTTAGAGGCC 900
QY 301 ArgGlySerGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGly 320
DB 901 AGGGCAGCAGAGAGGTGAGAGAGAGCAGCAGGTGCGCAGCAGCAGCATGAGAGGT 960
QY 321 LysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
DB 961 AAGGAAGCACACCAAAAGTTGAGGAAACAGCATGAAGGAGACAAAGGTCGCAACAG 1020
QY 341 ValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
DB 1021 GTCAACCGATGACGATTTGATCTGGGTGAATGATCATGAGTTGGTGAAGACGACATC 1080
QY 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProProSerArg 380
DB 1081 AATTTCAGTGAAGATGAGTGAAGGCACTGAACATCCCGAGAGCTCCACCCAGTGTGT 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysLysAlaAlaLysVal 400
DB 1141 CGTAAACAGCAACAGCAACCTCTCTGCGCAGGTGCTACAGTGCMAAGCTGCTAAAGTG 1200
QY 401 IlePheIleIleIlePheSerTyrValLeuSerLeuGlyProTyrCysPheLeuAlaVal 420
DB 1201 ATCTTCATCATCATTTCTCTATGTGCTATCTCTGGGGCCCTTACCTGCTTTTACAGTC 1260
QY 421 LeuAlaValTyrValAspValGluThrGlnValProGlnTyrValIleThrIleIleIle 440
DB 1261 CTGGCGGTGGGTGATGATGGAACCCAGGTAACCCAGTGGGTATCAACCATATATCTC 1320
QY 441 TrpLeuPhePheLeuGlnCysCysIleHisProTyrValTyrGlyTyrMetHisLysThr 460
DB 1321 TGGCTTTTCTCTGCAATGCTGCATCCACCCCTATGTCTATGCTATCATGCACAAAGACC 1380
QY 461 IleLysLysGluIleGlnAspMetLeuLysLysPheCysLysGluLysProProLys 480
DB 1381 ATTAAGAAAGAAATCCAGACATGCTGAAGAAATTTCTCTGCAAGAAAGCCCCGAAA 1440
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyLysIleValPro 500
DB 1441 GAAGATACCAACCCAGACCTCCCGGAACAGAGGTGGAGATGAAAGCAAGATTCTCCT 1500
QY 501 SerTyrAspSerAlaThrPhePro 508
DB 1501 TCTTACGATTCGTACTTTTCT 1524

```
RESULT 2
AAH73517
ID AAH73517 standard; DNA; 1527 BP.
XX
XX AAH73517;
AC
AC AAH73517;
DT
DT 25-SEP-2001 (first entry)
XX
XX Human G protein-coupled receptor GPRV72 coding sequence.
DE
XX
XX Human, guanosine triphosphate binding protein-coupled receptor;
KW G protein-coupled receptor; GPRV8; GPRV12; GPRV16; GPRV21; GPRV40;
KW GPRV47; GPRV51; GPRV71; GPRV72; cancer; liver cirrhosis;
KW Alzheimer's disease; cytosolic; hepatotropic; neurotropic;
KW neuroprotective; gene therapy; peptide therapy; ds.
XX
XX Homo sapiens.
OS
XX WO200148188-A1.
XX
XX 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-JP009408.
XX
XX 28-DEC-1999; 99JP-00375152.
XX
XX 31-MAR-2000; 2000JP-00101339.
XX
XX (HELI-) HELIX RES INST.
XX
XX Matsu moto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;
XX Sugiyama T, Kishimoto T, Kanazaki K, Yasuda S, Inoue Y;
XX
XX MPI: 2001-425662/45.
XX
XX P-PSDB; AAG64126.
XX
XX New DNA encoding guanosine triphosphate binding protein coupled receptors
XX and their expression products for screening potential anticancer and
XX neurotropic drugs and in diagnosis of these diseases.
XX
XX Claim 1; Page 143-144; 170pp; Japanese.
XX
XX The invention relates to nine human guanosine triphosphate binding
XX protein (G protein)-coupled receptors designated GPRV8, GPRV12, GPRV16,
XX GPRV21, GPRV40, GPRV47, GPRV51, GPRV71 and GPRV72, and to the genes
XX encoding them. These genes and proteins and antibodies against the
XX protein are useful in the treatment, prevention, diagnosis and
XX investigation of diseases associated with G protein-coupled receptors,
XX including cancer, cirrhosis of the liver and Alzheimer's disease. The
XX present sequence is a G protein-coupled receptor coding sequence of the
XX invention
XX
XX SQ Sequence 1527 BP; 347 A; 439 C; 419 G; 322 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX
XX Pred. No.: 9,156-244 Length: 1527
XX Score: 2644.00 Matches: 508
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 4 Gaps: 0
XX
XX US-10-712-615-2 (1-508) x AAH73517 (1-1527)
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XX QY 1 MetThSeThrCyThraSenSerThraArgLusSerAsnSerSerThraCysMetPro 20
XX |||
XX 1 ATGACCTCCACCTGCACCAACAGACACGCGGAGATGAACAGCACCACGTCATGCCCC 60
XX |||
XX QY 21 LeuSerLyMetProIleSerLeuAlaHisGlyTlleIleArgSerThraValLeuValIle 40
XX |||
XX 61 CTCTCAAAATGCGCATCAGCCCTGGCCACGAGCATCATTCGCTCAACCGTGGTTATC 120
XX |||
XX QY 41 PheLeuAlaIaSerPheValGlyAenIleValLeuAlaLeuValLeuGlnArgLysPro 60
XX |||
```

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DB 121 TTCCTGCGCGCTCTTTCGTCGCAACATAGTGTGGCCGTAGTGTGAGGCAAGCCG 180
|||
QY 61 GlnLeuLeuGlnValThraSnaRPhelIlePheAsnLeuValThraSpleuLeuGln 80
|||
DB 181 CAGCTGCTGACAGTGAACCAACCGTTTATCTTTAACTCTCTGTCACCACTGCTGCGAG 240
|||
QY 81 IleSerLeuValAlaProIleValValAlaThrSerValProLeuPheIleProLeuAsn 100
|||
DB 241 ATTTGGCTGTGCGCCCTGGGTGGTGGCACCTGTGTCCTCTTCTGGCCCTCAAC 300
|||
QY 101 SerHisPheCyThraAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
|||
DB 301 ACCCACTTGCACCGCCCTGGTTAGCCCTACCCACCTGTTGCCCTCCCGACGCGTCAAC 360
|||
QY 121 ThrIleValLeuValSerValAsnRgryThreusSerIleHisProLeuSerTyPro 140
|||
DB 361 ACCATTGTCTGTGTGACGTGATGCTACTGTGTCATCATCACCTCTCTCTACCCG 420
|||
QY 141 SerLyMetThraGlnArgArgLysTyrIleLeuLeuTyrGlyThrTriIleValAlaIle 160
|||
DB 421 TCCAGATGACCCAGGCGCGCGGTTACCTGCTCTATGCGACCGATTTGTGGCCATC 480
|||
QY 161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlnAlaAlaPheAspGluArgAsnAla 180
|||
DB 481 CTGCAGAGCACTCTCCACTTACGCGCTGGGCGCAGGCTGCTGTGATGAGCGCAATGCT 540
|||
QY 181 LeuCySerMetIleTrpGlyAlaSerProSerTyrThrIleLeuSerValIaSerPhe 200
|||
DB 541 CTCTGCTCATATCTGGGGGCGCCAGCCCACTACATATTCAGCGGTGGTCTTTC 600
|||
QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerValValPheCysAlaAlaArg 220
|||
DB 601 ATCGTATTCACCTGATTTGATGATGCTGCTGCTACTCCGTGGTGTCTGTGAGGCCGG 660
|||
QY 221 ArgGlnHisAlaLeuLeuTyrAsnValLysArgHisSerLeuGlnValArgValLysAsp 240
|||
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|||
QY 241 CysValGluAsnGluAspGluGluGlyValIaGlyLysValGluPheGlnAspGluSer 260
|||
DB 721 TGTGTGAAGAAATGAGATGAAGAGGAGAGAGAGAAAGAGAGAGATTCAGAGATGAGAG 780
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QY 261 GluPheArgArgGlnHisGluGluGlyValLysAlaLysGluGlyArgMetGluAlaLys 280
|||
DB 781 GAGTTTCGCGCCAGCATTAAGTGAAGTCAAGGCCAAGAGGCGAATGGAAGCCAG 840
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QY 281 AspGlySerLeuLysAlaLysGluGlySerThrGlyThrSerGluSerSerValGluAla 300
|||
DB 841 GACGGCAGCCTGAAGGCCAAGAGAAAGAACACGAGGAGCATGATGATGAGAGGCC 900
|||
QY 301 ArgGlySerGluGluValArgLysSerSerThrValAlaSerAspLysSerMetGluGly 320
|||
DB 901 AGGGCAGAGGAGAGGTTCAGAGAGACAGACAGCGTGGCCAGCGACGACATGAGAGGT 960
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QY 321 LysGluGlySerThrIleValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
|||
DB 961 AAGGAAAGCAGACCAAGTTGAGGAAACAGATTAAGGACAGACAAAGGTCCACAGAG 1020
|||
QY 341 ValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyLysAspAspIle 360
|||
DB 1021 GTCACACAGTGACATTCGCTGGGTGAAGATGACATGAGATTGGTGAAGACGACATC 1080
|||
QY 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProProSerArg 380
|||
DB 1081 AATTTTACGATGAGATACGTCAGAGGAGTGAACATCCGAGAGCCTCCACCACTGCTGT 1140
|||
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysLysAlaAlaLysVal 400
|||
DB 1141 CGTAAACAGCAACGCAACCTCTCTGCCCAGGTGCTTACAGTGCAAAGCTGTAAAGTC 1200
|||
QY 401 IlePheIleIleIlePheSerTyValLeuSerLeuGlyProTyCysPheLeuAlaVal 420
|||
```

```
Db 1201 ATCTTCATCATCATTTTCTCCATATGCTATCCCTGGGGCCCTACTGCTTTTACGAGTC 1260
Qy 421 LeuAlaValITrpValAspValGluThrGlnValProGlnITrpValIleThrIleIleIle 440
Db 1261 CTGGCCGATGGGTGGATGTGAAACCCAGATACCCAGTGGGTATATACCATATATCATTC 1320
Qy 441 TrpLeuPhePheLeuGlnCysGlyIleHisIleProTyrValTyrGlyTyrMetHisIleThr 460
Db 1321 TGGCTTTTCTCTCCATGCTGATGCTGATCCACCCCTATGTCTATAGGCTACATGCAAGACC 1380
Qy 461 IleValSylValGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysProProLys 480
Db 1381 ATTAAAGAGAAATCCAGACATGCTGAAAGAACTTCTTGCAAGAGAAAGCCCCGANA 1440
Qy 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyLysIleValPro 500
Db 1441 GAAGATACCAACCCAGACCTGCCGGAACAGAGGTGGAGCTGAAGGCAAGATTGTCTCT 1500
Qy 501 SerTyrAspSerAlaThrPhePro 508
Db 1501 TCCTACGATTCTGCTACTTTCTCT 1524

RESULT 3
ABLS3719
ID ABL53719 standard; cDNA, 1527 BP.
XX
AC ABL53719;
XX
XX 24-JUN-2002 (first entry)
XX
DE G-protein coupled receptor AXOR69 cDNA.
XX
KW G-protein coupled receptor; receptor; AXOR69; human; anti-HIV; virucide;
KW antimicrobial; analgesic; cytostatic; antidiabetic; anorectic; anabolic;
KW antiasmatic; antiparkinsonian; cardiac; cerebroprotective;
KW hypotensive; hypertensive; antiulcer; antiasmatic; antiallergic;
KW antilemetic; tranquilizer; neuroleptic; nootropic; anticonvulsant;
KW vaccine; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 1..1527
FT FT /*tag= a
FT FT /product= "AXOR69"
XX
XX
XX GB2367295-A.
XX
XX
XX 03-APR-2002.
XX
XX 12-JUN-2001; 2001GB-00014287.
XX
XX 16-JUN-2000; 2000US-00596400.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Elahourbagy N, Gattu M, Shabon U;
XX
XX WPI; 2002-294789/34.
XX P-PSDB; ABB75712.
XX
XX An isolated human G-protein coupled (7TM) receptor AXOR 69 polypeptide,
XX for treating diseases such as obesity, stroke and anxiety.
XX
XX Claim 2; Page 27; 34pp; English.
XX
XX The present sequence is that of cDNA encoding a human G-protein coupled
XX receptor, termed AXOR69 (see ABB75712). AXOR69 shows homology to other
XX members of the G-protein coupled receptor family, such as the human
XX adrenergic alpha-1a receptor. The invention provides AXOR69 polypeptides
XX and polynucleotides, and methods for producing such polypeptides by
```

```
CC recombinant techniques. Also provided are methods for using the AXOR69
CC polypeptides and polynucleotides to screen for compounds that stimulate
CC or inhibit AXOR69 levels or activity. The polypeptides, polynucleotides,
CC agonists and antagonists are used to treat conditions associated with
CC AXOR69 imbalance, including bacterial, fungal, protozoan and viral
CC infections, particularly HIV-1 and HIV-2 infections, pain, cancer,
CC diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute
CC heart failure, hypotension, hypertension, urinary retention,
CC osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers,
CC asthma, allergies, benign prostatic hypertrophy, migraine, vomiting,
CC psychotic and neurological disorders, including anxiety, schizophrenia,
CC manic depression, depression, delirium, dementia and severe mental
CC retardation, and dyskinesias such as Huntington's disease and Gilles de
CC la Tourette syndrome. The polynucleotides can also be used for diagnosing
CC mutations, in chromosome localisation studies, in pharmacogenomics, and
CC to construct transgenic animals. The polypeptides and polynucleotides are
XX also useful as vaccines
XX
SQ Sequence 1527 BP, 347 A; 439 C; 419 G; 322 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9,15e-244 Length: 1527
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatch: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-712-615-2 (1-508) x ABL53719 (1-1527)
Qy 1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
Db 1 ATGAGCTCCACCTGACCCACAGCAGCGCGCAGAGTAAACAGACAGCACCGTGCATGCC 60
Qy 21 LeuSerLysMetProIleSerLeuAlaHisGlyIleIleArgSerThrValIleValIle 40
Db 61 CTCTCAAAAGGCCCATAGCCTGGCCCAAGGAGCATCATCCCTCAACCGTGTGGTATATC 120
Qy 41 PheLeuAlaAlaSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgHisPro 60
Db 121 TTCCTCGCGCGCTCTTTGTGGCAACATAGTGGCGGTAGTGTTCACGCGCAAGCCG 180
Qy 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuGln 80
Db 181 CAGCTGCTGAGGTGACCAACCGTTTATCTTAACTCTCGTCAACGACCTGCGAG 240
Qy 81 IleSerLeuValAlaProTrpValValAlaThrSerValProLeuPheTrpProLeuAsn 100
Db 241 ATTGCTGTGGCCCCCTGGGTGGTGGCACCTGTGTCTCTCTTCTGGCCCTCAAC 300
Qy 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
Db 301 AGCCACTTCTGACGCGCCCTGTAGCTCAACCAACCTGTTGCGCTTGCCAGCGCTCAAC 360
Qy 121 ThrIleValIleValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
Db 361 ACCATTGTCTGGTGTGAGTGAATGCTATCTGTTCATCATCAACCCCTCTCTCAACCG 420
Qy 141 SerLysMetThrGlnArgArgGlyTyrIleLeuLeuLeuTyrGlyThrTrpIleValAlaIle 160
Db 421 TCCAAAGTAGACCCAGCGCGCGTTACCTGTCTCTTATGGCACCTGGATTGTGGCCATC 480
Qy 161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlnAlaIlePheAspGlyArgAsnAla 180
Db 481 CTGCGAGACATCTCTCCACTTACGCGCTGGGGCCAGGCTGCTTGTAGAGCGCAATCT 540
Qy 181 LeuCysSerMetIleIleTrpGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200
Db 541 CTCTGCTCAAGATGTGGGGGGCCAGCCCGACATCACTATTTCCAGGTGTGTGCTTTC 600
Qy 201 IleValIleProLeuIleValIleMetIleAlaCysTyrSerValValPheCysAlaAlaArg 220
Db 601 ATCGCATTTCCATGATGTGATGATGCTGTCTACTCCGTGGTGTCTGTGACACCCGG 660
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QY 221 ArgGlnHisAlaLeuLeuTyrAnValLysArgHisSerLeuGluValArgValLysAsp 240
DB 661 AGGCAAGCATGCTCTGCTGACAAATGTCAGAGACACAGCTTGAGATGCGAGTCAAGAC 720
QY 241 CysValGluAsnGluAsnGluGluGluValArgLysLysGluGluGluGluGluGluGlu 260
DB 721 TGTGTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 261 GluPheArgArgGlnHisGluGluGluValLysAlaLysGluGluValArgMetGluAlaLys 280
DB 781 GAGTTTCGCGCCGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 281 AspGlySerLeuLysAlaLysGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 300
DB 841 GACGGCAGCCTGAGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 301 ArgGlySerGluGluValArgLysSerThrValAlaSerAspGlySerMetGluGluGly 320
DB 901 AGGGGCGAGGAGAGAGTCAAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAGGT 960
QY 321 LysGluGluSerThrLysValGluGluAsnSerMetLysAlaAspLysGluArgThrGlu 340
DB 961 AAGGAGGCGAGACCAAGGTGAGAGACAGCATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 341 ValAsnGlnCysSerLysAspLeuGluGluAspAspMetGluPheGlyLysAspAspIle 360
DB 1021 GTCAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 361 AsnPheSerGluAspAspValGluValAlaAsnIleProGluSerLeuProSerArg 380
DB 1081 AATTTCAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 381 ArgAsnSerAsnSerAsnProLeuProArgCysTyrGluCysValAlaAlaLysVal 400
DB 1141 CGTAACGAGCAACCACTCTCTGCGCAGGTCTACAGTCAAGTCAAGTCTCTAAAGTG 1200
QY 401 IlePheIleIleIlePheSerTyrValLysSerLeuGlyProTyrCysPheLeuAlaVal 420
DB 1201 ATCTTCATCATCTTTCTCTATATGCTATCCCTGCGGCCCTACAGCTTTTATGACATC 1260
QY 421 LeuAlaValTyrValAspValGluThrGluValProGlnTyrValIleThrIleIleIle 440
DB 1261 CTGGCCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 441 TrpLeuPhePheLeuGlnCysIleHisProTyrValTyrGluTyrMetHisLysThr 460
DB 1321 TGGCTTTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 461 IleLysLysGluIleGlnAspMetLeuLysLysPhePheCysLeuGluLysProPheLys 480
DB 1381 ATTTAAGAGGAATCCAGACATGCTGAAGAACTTTTTCGACGAGAAAGCCCGCGA 1440
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyTyrGluGlyLysIleValPro 500
DB 1441 GAAGATAGACCCAGACCTGCCCGGACAGAGGGTGGAGCTGAAGGCAAGATTGCTCCT 1500
QY 501 SerTyrAspSerAlaThrPhePro 508
DB 1501 TCTTACGATTCGCTACTTTCT 1524

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```

KW neoplastic disease; CAMP; signalling pathway; immune disorder; cancer;
KM gene therapy; tumour; gene; ss.
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1527
FT FT /*tag= a
FT FT /product= "Human HGPBMY8 protein"
FT FT /replace(370, G)
FT FT /*tag= b
FT FT /standard_name= "Single nucleotide polymorphism"
FT FT /replace(1055, G)
FT FT /*tag= c
FT FT /standard_name= "Single nucleotide polymorphism"
FT FT /replace(1192, A)
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FT FT /replace(1193, A)
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FT FT /standard_name= "Single nucleotide polymorphism"
FT FT /replace(1194, G)
FT FT /*tag= f
FT FT /standard_name= "Single nucleotide polymorphism"
XX MO200240670-A2.
XX PD 23-MAY-2002.
XX PF 14-NOV-2001; 2001WO-US043909.
XX PR 14-NOV-2000; 2000US-0248285P.
XX PR 14-FEB-2001; 2001US-0268581P.
XX PR 27-JUL-2001; 2001US-0308285P.
XX PR 04-SEP-2001; 2001US-0317166P.
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX PI Battaglini P, Feder J, Mintier G, Nelson T, Ramanathan C;
XX PI Westphal R, Cacace A, Barber L, Hawken D, Kornacker M;
XX DR WPI; 2002-519383/55.
XX DR P-PSDB; AAE25236.
XX PT A substantially purified human G-protein coupled receptor polypeptide,
XX PT termed HGPBMY8, useful for treating a neurological disorder or brain
XX PT disorder in a mammal.
XX PS Claim 1; Page 160-161; 223pp; English.
XX CC The invention relates to human G-protein coupled receptor (GPCR), termed
XX CC HGPBMY8 and its corresponding nucleic acid. HGPBMY8 DNA is useful for
XX CC screening for candidate compounds which are small molecules, biological
XX CC agents, therapeutics or drugs. HGPBMY8 or its homologue is useful for
XX CC treating a neurological disorder or a disease, a disorder or condition
XX CC related to the brain in a mammal. It is used for treating or preventing
XX CC neurological disorders, conditions or diseases and for inducing an
XX CC immunological response in a mammal. HGPBMY8 DNA, protein and its
XX CC antibody are useful in the diagnosis, treatment or prevention of
XX CC disorders associated with aberrant or uncontrolled cellular growth and/
XX CC or function, such as neoplastic diseases e.g., cancers and tumours and
XX CC diseases or disorders related to the brain, e.g., neurological disorders.
XX CC HGPBMY8 DNA and protein are useful for modulating intracellular CAMP
XX CC associated signalling pathways. An expression vector containing HGPBMY8
XX CC DNA is useful to treat or prevent neoplastic disorders such as cancer or
XX CC tumours, immune disorders or neurological disorders. HGPBMY8 DNA is used
XX CC in gene therapy. The present sequence is human HGPBMY8 cDNA
XX SQ Sequence 1527 BP; 347 A; 439 C; 419 G; 322 T; 0 U; 0 Other;
Alignment Scores: 9,15e-244 Length: 1527
Pred. No.: 2644.00 Matches: 508
Score:

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Human HGPBMY8 cDNA.
Human; G-protein coupled receptor; GPCR; HGPBMY8; drug screening;
neurological disorder; brain; immunological; cell growth; cyclostatic;

Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 6
 Gaps: 0

US-10-712-615-2 (1-508) x AAD41159 (1-1527)

Qy	1	MethSerThrCysThrAsnSerThraGluSerAsnSerSerHisThrCysMetPro	20
Db	1	ATGAGGTCCACCTGCACCAACGACGCGGAGAGAAACAGACGACACGTCATGCCC	60
Qy	21	LeuSerLysMetProHisSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle	40
Db	61	CTCTCAAAATGCCCACATGAGCTGGCCGACGATCATCCGCTCAACCGCTGGTTATC	120
Qy	41	PheLeuAlaAlaSerPheValGlyValenIleValLeuAlaLeuValLeuGlnArgLysPro	60
Db	121	TTCCCTCGCGCCTCTTTGCTGCGCAACATAGTGTGGCTAGTGTGGCGGCAACCGG	180
Qy	61	GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeuGln	80
Db	181	CAGCTGTCGAGGTGACCAACCGTTTATCTTTAACTCTCTGTCACCGACTGCTGAG	240
Qy	81	IleSerLeuValAlaProTrrPValAlaThrSerValProLeuPheTrrProLeuAsn	100
Db	241	ATTGGCTCGTGCGCCCTGGGGTGGGCGACCTCTGTGCTCTCTTCTGGCCCTCAAC	300
Qy	101	SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn	120
Db	301	AGCCACTTTCGACAGGCGCTGTTAGCTTACCTCAACCTCTTGGCTTGGCCAGCTCAAC	360
Qy	121	ThrIleValLeuValSerValAspArgTyrIleuSerIleIleHisProLeuSerTyrPro	140
Db	361	ACCATTGCTTGTGTGAGTGCATCTTGTCCATCATCATCACCTCTCTCTTACCCG	420
Qy	141	SerLysMetThrGlnArgArgGlyTyrIleuLeuLeuTyrGlyThrTrrIleValAlaIle	160
Db	421	TCCAGATGACCCGACGCGCGGTTACCTGCTCTTAAGGACCGTGGATTTGGCCACAC	480
Qy	161	LeuGlnSerThrProProLeuTyrGlyTrrGlyGlnAlaAlaPheAspGluArgAsnAla	180
Db	481	CTGCGAGACACTCTCCACTCTACGCGCTGGGCGCAGGCTGCTTGGATGAGCGCATGCT	540
Qy	181	LeuCysSerMetIleTrrPValAspSerProSerTyrThrIleLeuSerValIleSerPhe	200
Db	541	CTCTGCTCATGATCTGGGGGGCCAGCCCACTACATATTCTCAGCGTGTGCTCTTC	600
Qy	201	IleValIleProLeuIleValMetIleAlaCysTyrSerSerValIlePheCysAlaAlaArg	220
Db	601	ATCGTCATTTCCACTGATTTGTCATGATTGCTCTCTCTCCGTGTGTTCTGTGCACGCCG	660
Qy	221	ArgGlnHisAlaLeuLeuTyrAsnValIysArgHisAspSerLeuGlnValArgValIysAsp	240
Db	661	AGGCGACATGCTCTCTGTCATGATCAAGACACAGCTTGGAGTGGAGCTCAAGGAC	720
Qy	241	CysValGluAsnGluAspGluGluGlyAlaGluLysLysGluGluPheGlnAspGluSer	260
Db	721	TGTGTGGAATGAGAGATGAAGAGGAGCAGAGAGAGAGAGAGATTCACGATGAGAGT	780
Qy	261	GluPheArgArgGlnHisGluGlyGluValIleValIleValIleValIleValIleValIle	280
Db	781	GAGTTTCCGCGCACATGATGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	840
Qy	281	AspGlySerLeuLeuAlaLysGluGlySerThrGlyThrSerGluSerSerValGluAla	300
Db	841	GACGCGACCTTAAGGCGCAAGAGAGAGACACGAGGAGCAGTGAAGATGATGAAGGCGC	900
Qy	301	ArgGlySerGluGluValArgLysSerSerThrValAlaSerAspGlySerMetGluGly	320
Db	901	AGGCGCAGGAGAGAGTCAAGAGAGACACGAGGAGGAGGAGGAGGAGGAGGAGGAGG	960
Qy	321	LysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu	340

Db	961	AAGGAGCGACGACCAAAAGTTGAGAGAAACGATGAAGGACGACAGGCTCCACAGAG	1020
Qy	341	ValaGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle	360
Db	1021	GTCACACAGTGAAGATTCATGCTGGTGAAGTGAAGTGAAGTGGTGAAGAGACATTC	1080
Qy	361	AsnPheSerGluAspAspValGluAlaValenIleProGluSerLeuProProSerArg	380
Db	1081	AATTTCAGTGAAGAGAGTGAAGAGGAGGAGTGAACATCCCGAGAGGCTCCACCTGCTGT	1140
Qy	381	ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysValAlaAlaLysVal	400
Db	1141	CGTAACACACAGAACCTCTCTGCGCAGGTCTACAGTGAAGAGGCTGTAAGG	1200
Qy	401	IlePheIleIleIlePheSerTyrValLeuSerLeuGlyProTyrCysPheLeuAlaVal	420
Db	1201	ATCTTCATCATCATTTTCTCTCATGTGCTATCCCTGGGGGCTTACTGCTTTTACAGTC	1260
Qy	421	LeuAlaValTrrPValAspValGluThrGlnValProGlnTrrPValIleThrIleIleIle	440
Db	1261	CTGGCCGTTGGGTGATGTCGAACCCAGGTAACCCAGTGGGTATCACCATAATCATTC	1320
Qy	441	TrrLeuPhePheLeuGlnCysCysIleHisProTyrValIleGlyTyrMetHisLysThr	460
Db	1321	TGGCTTTTCTTCTGCAAGTGTGATCCACCCCTATGCTTATGCTTACATGACAAAGAC	1380
Qy	461	IleLysLysGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysPrrProLys	480
Db	1381	ATTAAAGAAAGAAATCAGACATGCTGAAGAGTTCTTCTGCAAGAAAGCCCCGAAA	1440
Qy	481	GluAspSerHisProAspLeuProGlyThrGluGlyIleThrGluGlyLysIleValPro	500
Db	1441	GAAAGATACCCACCCAGACTCTCCCGAACAAGGGTGGAGCTGAAGGCAAGATTGTCCCT	1500
Qy	501	SerTyrAspSerAlaThrPhePro	508
Db	1501	TCTTACGATTCTGCTTCTTCTCT	1524

RESULT 5

ABV74517
 ID ABV74517 standard; cDNA; 1527 BP.

AC ABV74517;
 XX

DT 17-JAN-2003 (first entry)
 XX

DE Human G protein coupled receptor, S0879, coding sequence.
 XX

KW G protein coupled receptor; receptor; anorectic; antiparkinsonian; gene;
 KW hypotensive; hypertensive; tranquilizer; neuroleptic; antidepressant;
 KW nootropic; anticonvulsant; antimigraine; human; S0879; hippocampus;
 KW hypothalamus; brain; obesity; bulimia; anorexia; Parkinson's disease;
 KW hypertension; hyperextension; psychotic disorder; neurological disorder;
 KW anxiety; schizophrenia; manic depression; delirium; dementia; epilepsy;
 KW migraine; insomnia; circadian rhythm disorder; cognitive function; ss.

OS Homo sapiens.
 XX

FN Key Location/Qualifiers
 FT 1..1527
 FT /*tag= a
 FT /product= "G protein coupled receptor"

PD 04-OCT-2002.
 XX

PF 27-MAR-2001; 2001FR-00004074.
 XX

PR 27-MAR-2001; 2001FR-00004074.
 XX

PA (SERV-) LBS LAB SERVER SA.
 XX

PI Galizzi JP, Coge F, Rigue H, Boutin JA;
 XX MPI; 2003-021471/02.
 DR P-PSDB; ABB98721.
 XX

PT New nucleic acid encoding human G protein coupled receptors, useful for
 PT treating e.g. obesity, also derived polypeptides, antibodies and
 PT modulators.
 XX

PS Claim 1: Page 23-24; 44pp; French.

XX The present sequence is the coding sequence for human G protein-coupled
 CC receptor, 50879. The receptor and its coding sequence can be used for
 CC creating diseases associated with abnormal expression of the receptor,
 CC particularly diseases involving the hippocampus or hypothalamus,
 CC particularly obesity, bulimia, anorexia, Parkinson's disease, hypo- or
 CC hyperphrenia, and psychotic or neurological disorders such as anxiety,
 CC schizophrenia, manic depression, delirium, dementia, epilepsy, migraine,
 CC insomnia, circadian rhythm disorders and loss of cognitive function. The
 CC G protein-coupled receptor coding sequence was isolated from human brain
 CC tissue
 XX

SO Sequence 1527 BP; 347 A; 439 C; 419 G; 322 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9.15e-244	Length:	1527
Score:	2644.00	Matches:	508
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-712-615-2 (1-508) X ABV74517 (1-1527)

QY 1 MetThrSerThrCysThrAnserThrArgGluSerAnserSerHisThrCysMetPro 20
 DB 1 ATGACCTCCACCTGCACCAAGCAGCGCGAGATACAGCAGCAGCTGCATGCC 60
 QY 21 LeuSerIleMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
 DB 61 CTCTCCAAATGCCCATACAGCTGCGCCACGGCATATCCGTCACACCGTGTGTATC 120
 QY 41 PheLeuAlaIleSerPheValGlyAsnIleValIleValLeuValLeuGlnArgIlePro 60
 DB 121 TTCCTGCGCGCTCTTTCGTGGCAATAGTCTGCGCTAGTGTGACGCCAAGCGG 180
 QY 61 GlnLeuLeuGlnValThrAnArgPheIlePheAsnLeuLeuValThrAspLeuGln 80
 DB 181 CAGCTGCTCAGGTGACCAACCGTTTATCTTAACTCTCCTCGTCAACGACCTGTCAG 240
 QY 81 IleSerLeuValAlaProThrValValAlaThrSerValProLeuPheThrProLeuAn 100
 DB 241 ATTTGGCTGTGGCCCCCTGGGTGGTGGCCACTGTGCTCTTCTTGGCCCCCTCAAC 300
 QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisIleuPheAlaPheAlaSerValAsn 120
 DB 301 ACCGACTTTCGACGGCCCTGTGTTAGCTTACCCACCTGTGCCCTTCCGCAAGCTCAAC 360
 QY 121 ThrIleValIleuValSerValAspArgIleLeuSerIleIleHisProLeuSerIlePro 140
 DB 361 ACCATGTGTGGTGTCAGTGATCGCTACTGTTCATCATCACCTCTCTCTCCGCG 420
 QY 141 SerIleMetThrGlnArgArgIleIleLeuLeuLeuIleIleThrTrpIleValAlaIle 160
 DB 421 TCCAAAGATACCGAGCGCGGTATCTGCTCTTATGGCACCTGGATGTGGCCATC 480
 QY 161 LeuGlnSerThrProLeuLeuIleIleIleIleIleIleIleIleIleIleIleIleIle 180
 DB 481 CTGCAAGACACTCTCTCACTTACGCGCTGGGCGCAAGGCTGCTTATAGCGCATGCT 540
 QY 181 LeuCysSerMetIleTrpGlyAlaSerProSerIleThrIleLeuSerValIleSerPhe 200
 DB 541 CTCTGCTCATGATCTGGGGGGGCCAGGCCAGCTACATATTCTCAGCGGTGTCTTCT 600

QY 201 IleValIleProLeuIleValMetIleAlaCysIleSerValValPheCysAlaAlaArg 220
 DB 601 ATGCTATTTCCACTGATTTGATGATGCTGCTCTACTCCGTGGTGTCTGTGACGCCGG 660
 QY 221 ArgGlnHisAlaLeuLeuIleThrAnValIleArgHisSerLeuGlnValArgValIleAsp 240
 DB 661 AGCAGACATGCTCTGCTGTACATGTGCAGAGACACAGCTTGGAAGTGCAGTCAAGAC 720
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 QY 261 GluPheArgArgGluHisGluGluGluValIleValAlaIleGluIleValArgMetGluAlaIle 280
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 DB 841 GACGGCAGCTGAAGGCCAAGAGAGAGACACGGGGACCAAGTGAAGTGTGAGAGGCC 900
 QY 301 ArgGlySerGluGluValIleArgIleSerSerThrValAlaSerAspGlySerMetGluGly 320
 DB 901 AGGGCGAGAGAGAGGTCAAGAGACAGCAGCGTGGCCAGCGCAGCATGAGGGT 960
 QY 321 LysGluGlySerThrIleValGluGluAsnSerMetIleAlaAspIleGlyArgThrGlu 340
 DB 961 AAGGAGGCGACACCAAAATTGAGAGAACACAGATGAGGCGACAGAGGCTGCCACAG 1020
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 DB 1021 GTCAACCAATGCAGCATTTGCTGGGTGAAGATGACATGAGTGTGGTGAAGACGACATC 1080
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 DB 1081 AATTTCAGTGAAGATGACCTTCAGGCGAGTGAACATCCCGAGAGCCTCCACCACTGCT 1140
 QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysIleGluCysIleValAlaIleVal 400
 DB 1141 CGTACAGCAGACCAACCTCTCTGCTCCAGAGTGTACAGTGCACAACTGCTAAAGT 1200
 QY 401 IlePheIleIleIlePheSerIleValIleSerLeuGlyProIleCysPheLeuAlaVal 420
 DB 1201 ATCTTCATCATCTTTCTCCATGTCATGCTGCGGGCCGTACGCTTTTATGACAGTC 1260
 QY 421 LeuAlaValIlePheValAspValGluThrGlnValProGlnIleThrIleIleIle 440
 DB 1261 CTGGCCGTGTGGTGTATGCAAAACCCAGTACCCCACTGGGTGATCAACATAATCATC 1320
 QY 441 TrpLeuPhePheLeuGlnCysCysIleHisProIleValIleIleIleIleIleIle 460
 DB 1321 TGGCTTTTCTCTGAGTGTGATCCACCCCTATGTATAGGCTACATGCAAGACCC 1380
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 DB 1381 ATTAAAGAAGAAATCCAGACATGCTGAAGAAGTTCTTTCGCAAGGAAAGCCCGGAA 1440
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 DB 1441 GAAGATAGCACCCAGACCTGCGCGACAGAGGGGTGAGCATGAAGGCAAGATTGCTCT 1500
 QY 501 SerIleAspSerAlaThrPhePro 508
 DB 1501 TCTTACGATTCGTACTTCTCT 1524

RESULT 6
 ID AEA33069 standard; DNA; 1527 BP.
 AC AEA33069;
 DT 11-AUG-2005 (first entry)
 XX

DE Human G-protein coupled receptor HGRPMY8 gene SeqID1.
XX
XX protein purification; cytostatic; neuroprotective; antiparkinsonian;
KM tiranquillizer; hypotension; anti-HIV; virucide; osteoporosis; cancer;
KM asthma; allergy; HIV infection; osteoporosis; Parkinson's disease;
KM anxiety disorder; hypertension; neurological disease; gene; ds; HGRPMY8;
KM G protein coupled receptor.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT CDS 1..1527
FT /tag= a
FT /product= "Human G-protein coupled receptor HGRPMY8
FT protein"
XX
XX WO2005048951-A2.
XX
XX 02-JUN-2005.
XX
XX 12-NOV-2004; 2004MO-US038387.
XX
XX 13-NOV-2003; 2003US-00712615.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Battaglin P, Feder JN, Minter G, Nelson TC, Ramanathan CS;
PI Westphal R, Cacace AM, Barber LE, Hawken DR, Kornacker MG;
XX
XX WPI: 2005-395945/40.
XX
XX P-PSDB; AEA33070.
XX
XX New isolated human G-protein coupled receptor, HGRPMY8, and encoding
PT polynucleotide, useful for diagnosing or treating cancer, asthma,
PT allergies, HIV, osteoporosis, anxiety, hypertension and neurological
PT diseases.
XX
XX Claim 1; SEQ ID NO 1; 261p; English.
XX
XX This invention relates to a novel isolated human G-protein and the DNA
CC sequence which encodes it. The invention may be useful for the
CC development of compounds with a cytostatic, neuroprotective,
CC antiparkinsonian, tranquilizer, hypotension, anti-HIV, virucide or
CC osteopathic activity acting as G-protein antagonists. The methods and
CC compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of the human G-protein coupled receptor,
CC HGRPMY8, such as cancer, asthma, allergies, HIV infections,
CC osteoporosis, Parkinson's disease, anxiety, hypertension and neurological
CC diseases. The present sequence is that of the human HGRPMY8 gene of the
CC invention.
XX
XX Sequence 1527 BP; 347 A; 439 C; 419 G; 322 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 9,156-244 Length: 1527
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-10-712-615-2 (1-508) x AEA33069 (1-1527)
QY 1 MetTtSerTnCyEThAsnSerThrArgGluSerAsnSerSerHisThrCyAmcPro 20
Db 1 ATGAGTCCACCTGCACCAACAGCAGCGCGAGAGTAAACAGCAGCAGCATGCC 60
QY 21 LeuSerLysMetProGluSerLeuAlaHisGlyIleLeuArgSerThrAlaLeuValIle 40
Db 61 CTCCTCAAAATGCCATCATCGCTGGCCCAAGGATCATCCGCTCAACCGTGTGTTATC 120
QY 41 PheLeuAlaAlaSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLysPro 60

Db 121 TTCTCGCCGCGCTTTTGTGTGGCAACATAGTGTGGCTAGTGTCCAGCGCAAGCCG 180
QY 61 GlnLeuLeuGlnVal1ThrAsnArgPhe1IlePheAsnLeuLeuVal1ThrAspLeuLeuGln 80
Db 181 CAGCTGCGCAGGAGTACCAACCGTTTATCTTTAACTTCTCGTCACCGACCTGCTGAG 240
QY 81 IleSerLeuVal1AlaProTyrVal1Val1AlaThrSerVal1ProLeuPheTyrProLeuAsn 100
Db 241 ATTTGCGTGTGGGCCCCGTGGGTGGCCACCTGTGCTCTCTTGTGGCCCTTCAAC 300
QY 101 SerHisPheCyEThrAlaLeuVal1SerLeuThrHisLeuPheAlaPheAlaSerVal1Asn 120
Db 301 AGCCACTTCTCAGCGCCCTGTTAGCCTTCAACCACTGTTGCGCTTGCACGAGCTCAAC 360
QY 121 ThrIleVal1LeuVal1SerVal1AspArgThyLeuSerIle1IleHisProLeuSerTyrPro 140
Db 361 ACCATTGCTTGGGTGTCAGTGAATGCTTACTTGTTCATCATCATCACCTCTCTCTACCG 420
QY 141 SerLysMetThrGlnArgArgGlyTyrIleLeuLeuTyrGlyThrTyrIleVal1AlaIle 160
Db 421 TCCAAGATGACCCAGCGCGCGGTACCTGCTCCTATAGCACCTGATTTGGCCATC 480
QY 161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlnAlaAlaPheAspGluArgAsnAla 180
Db 481 CTGCAGACACTCTCCACTTACGCGTGGGCCAGCGCTGCTTGATGAGCGCAATGCT 540
QY 181 LeuCySerMetIleTyrGlyAlaSerProSerTyrThrIleLeuSerVal1Val1SerPhe 200
Db 541 CTGTCTCATGATCTGGGGGGCCAGCCCAAGCTTACATTAATTCAGGTGGTGTCTTC 600
QY 201 IleVal1IleProLeuIleVal1IleVal1IleVal1IleVal1IleVal1IleVal1IleVal1 220
Db 601 ATTCGATTCATCATGATTTGTATGATGATTCCTGCTACTCCGAGTGTGTGGCAGCCGG 660
QY 221 ArgGlnHisAlaLeuLeuTyrAsnVal1LysArgHisSerLeuGluVal1ArgVal1LysAsp 240
Db 661 AGGCAGCATGCTGCTGCTGTCAATGTCAAGAGACACACTTGGAAGTCCGATCAAGAC 720
QY 241 CysVal1GluAsnGluAspGluGluGluVal1GluLysLysGluGluPheGluAspGluSer 260
Db 721 TGTGTGGAAATGAGATGAGAGAGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 261 GluPheAspArgGlnHisGluGlyGluVal1LysAlaLysGluGlyArgMetGluAlaLys 280
Db 781 GAGTTTCCCGCCGACGATGAG 840
QY 281 AspGlySerLeuLysAlaLysGluGlySerThrGlyThrSerGluSerSerVal1GluAla 300
Db 841 GACGCGACCTGAAAGGCCAAG 900
QY 301 ArgGlySerGluGluVal1ArgGluSerSerThrVal1AlaSerAspGlySerMetGluGly 320
Db 901 AGGGCAGCAGAGAGAGTCAAG 960
QY 321 LysGluGlySerThrLysVal1GluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
Db 961 AAGGAGAGCAGACCAAAAGTTGAGGAGAACAGCATGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 341 ValAsnGlnCySerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
Db 1021 GTCAACCAAGTCAGATTCAGTGGGTGAATGATCATGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 361 AsnPheSerGluAspAspVal1GluAlaVal1AsnIleProGluSerLeuProProSerArg 380
Db 1081 AATTTCACTTGAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCyEThrGlnCyVal1AlaLysVal1 400
Db 1141 GCTAACACAGACAG 1200
QY 401 IlePheIleIleIlePheSerTyrVal1LeuSerLeuGlyProTyrCyPheLeuAlaVal1 420

DB 1201 ATCTTCATCATCTTTTCTTCATATGTCATCCCTGGGGCCCTACTGCTTTTAGCAGTC 1260
QY 421 LeuAlaValTrpValAspValGluThrGlnValProGlnTrpValIleThrIleIle 440
DB 1261 CTGGCGGTGGGTGGATGTCGAACCCAGTACCCAGGGGTGATCCATTATCATC 1320
QY 441 TrpLeuPhePheLeuGlnCysGlyIleHisProTyrValTyrGlyTyrMetHisIleVal 460
DB 1321 TGGCTTTCTTCTCTGAGTGTCTGATTCACCCCTATGTCTATGCTATGATGACAGACC 1380
QY 461 IleValGlyGluIleGlnAspMetLeuValPhePheCysGlyGlyProProIle 480
DB 1381 ATTAAAGAGAAATCCAGACATGCTGAAGAAAGTTCTTCGAAAGAAAGCCCGGAAA 1440
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyIleValPro 500
DB 1441 GAAAGATAGCCACCAAGCTCGCCGGAACAGAGGGTGGACTGAAGCAAGATTGTCCCT 1500
QY 501 SerTyrAspSerAlaThrPhePro 508
DB 1501 TCTACGATTCTGCTACTTTTCT 1524
RESULT 7
ID AAD41170 standard; DNA; 1580 BP.
XX AAD41170;
AC AAD41170;
DT 30-OCT-2002 (first entry)
XX
XX Human HGPBMY8 DNA #1.
DE Human HGPBMY8 DNA #1.
XX
XX Human; G-protein coupled receptor; GPCR; HGPBMY8; drug screening;
KM neurological disorder; brain; immunological; cell growth; cytostatic;
KM neoplastic disease; cAMP; signalling pathway; immune disorder; cancer;
KM gene therapy; tumour; gene; ds.
XX
XX Homo sapiens.
OS
XX
XX MO200240670-A2.
PN 23-MAY-2002.
XX
PF 14-NOV-2001; 2001WO-US043909.
PR 14-NOV-2000; 2000US-0248285P.
PR 14-FEB-2001; 2001US-0268581P.
PR 27-JUL-2001; 2001US-0308285P.
PR 04-SEP-2001; 2001US-0317166P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Battaglini P, Feder J, Mintier G, Nelson T, Ramanathan C;
PI Westphal R, Cacace A, Barber L, Hawken D, Kornacker M;
XX WPI; 2002-519383/55.
XX
PT A substantially purified human G-protein coupled receptor polypeptide,
PT termed HGPBMY8, useful for treating a neurological disorder or brain
PT disorder in a mammal.
XX
XX
PS Disclosure; Page 207; 223pp; English.
XX
XX The invention relates to human G-protein coupled receptor (GPCR), termed
CC HGPBMY8 and its corresponding nucleic acid. HGPBMY8 DNA is useful for
CC screening for candidate compounds which are small molecules, biological
CC agents, therapeutics or drugs. HGPBMY8 or its homologue is useful for
CC treating a neurological disorder or a disease, a disorder or condition
CC related to the brain in a mammal. It is used for treating or preventing
CC neurological disorders, conditions or diseases and for inducing an
CC immunological response in a mammal. HGPBMY8 DNA, protein and its
CC antibody are useful in the diagnosis, treatment or prevention of
CC disorders associated with aberrant or uncontrolled cellular growth and/

CC or function, such as neoplastic diseases e.g., cancers and tumours and
CC diseases or disorders related to the brain, e.g., neurological disorders.
CC HGPBMY8 DNA and protein are useful for modulating intracellular cAMP
CC associated signalling pathways. An expression vector containing HGPBMY8
CC DNA is useful to treat or prevent neoplastic disorders such as cancer or
CC tumours, immune disorders or neurological disorders. HGPBMY8 DNA is used
CC in gene therapy. The present sequence is human HGPBMY8 DNA
XX
SQ Sequence 1580 BP; 357 A; 456 C; 430 G; 337 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 9,62e-244 Length: 1580
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-712-615-2 (1-508) x AAD41170 (1-1580)
QY 1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
DB 32 ATGACGTCACCTGCAACCAAGACAGCGCGAGATGAAGACAGCACAGTGCATGCC 91
QY 21 LeuSerTyrMetProIleSerSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
DB 92 CTCTCCAAATGCGCCATCAGCTCGGCCCAAGGATATCCGTCACCGCGTGGTTATC 151
QY 41 PheLeuAlaIleSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgPro 60
DB 152 TTCCTGCGCGCCCTTCCTGCGCAATAGTGTGCGCTAGTGTGAGCGCAAGCCG 211
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuGln 80
DB 212 CAGCTCTCAGGTGACCAACGTTTATCTTAACTCTCTGACCACTGCTGCAG 271
QY 81 IleSerLeuValAlaProTrpValValAlaThrSerValProLeuPheTrpProLeuAsn 100
DB 272 ATTTGCTGCTGGCCCCCTGGGTGGGACCACTGTGCTCTTCTGGCCCCCTCAAC 331
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
DB 332 AGCCACTTCTGCACGCGCCCTGTTAGCTTACCCACCTGTTCGCCCTTCCGACGCTCAAC 391
QY 121 ThrIleValLeuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
DB 392 ACCATGTCTGTGTCAGTGGATGCTTCTGTCCATATCCACCTCTCTCAACCG 451
QY 141 SerTyrMetThrGlnArgArgGlyTyrLeuLeuLeuTyrGlyThrTrpIleValAlaIle 160
DB 452 TCCAAATGACCCAGGCGCGGCTTACCTGCTCTTATGACCACTCGATTGGGCCATC 511
QY 161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlnAlaAlaPheAspGluArgAsnAla 180
DB 512 CTGCAGAGACATCTCTCACTTACGCTGAGGCGAGGCTGCTTATGAGCGCAATGCT 571
QY 181 LeuCysSerMetIleTrpGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200
DB 572 CTCTGTCCATATATCGGGGGGCGACCCAGCTACATATCTCGCGTGGTGTCTTC 631
QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerValValPheCysAlaAlaArg 220
DB 632 ATCGTATTCACATGATGTGATGATGCTGCTACTCCGTGGTGTCTCTGACGCCGG 691
QY 221 ArgGlnHisAlaLeuLeuTyrAsnValIleArgHisSerLeuGlnValArgValIleAsp 240
DB 692 AGGACACATGCTCTGCTGAACAATGCAAGACACAGCTGGAAATGCGAGTCAAGAC 751
QY 241 CysValGluAsnGluAspGluGlyGlyAlaGlyValGlyValGluGlnPheGlnAspGluSer 260
DB 752 TGTGTGAATAATGAGATGAAGAGGAGACAGAAAGAGAGAGTTCCAGAGTGAAGT 811
QY 261 GluPheArgArgGlnHisGlyGlyValValValAlaValGlyValArgMetGluAlaVal 280

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Db      812 GAGTTTCCCGCCAGCATGAAAGTGAAGTCAAGGCCAAGAGGAGGAGTGAATGGAAGCCAAAG 871
Qy      281 AepgIySerIeuValAlaIySerIeuValIySerThrgIyThrSerGlySerSerValIgluIa 300
Db      872 GACGCGACGCTGTAAGGCCAAGAGAGAGACACGGGACCAAGTGAAGTGTGAAGGCC 931
Qy      301 ArgGlySerGluValIargIySerSerThrvAlaIaSerApGlySerMetGlyGly 320
Db      932 AGGGCGACGAGAGAGTGCAGAGAGACAGACGCTGGCCAGGACGGCAGCATGGAGGGT 991
Qy      321 LysGluGlySerThrvValIgluIuIuIuIuIuIuIuIuIuIuIuIuIuIuIuIuIuIuIu 340
Db      992 AAGGAGGCGACGACAAAGTTTGAAGAGAACACAGCAAGAGGAGGAGGAGGAGGAGGAGG 1051
Qy      341 ValaengIyCySerIleAspIeuGlyIuAspAspMetGluPhgGlyIuAspAspIle 360
Db      1052 GTCAACCGATGCGACATTCGATGGGTGAAGATGACATGAGATTGGTGAAGACGACATC 1111
Qy      351 AsnAspSerGluAspAspValIgluIaValaenIleProGlySerIeuProProSerArg 380
Db      1112 AATTTCAGTGAAGATGACGTGAGGAGGAGTGAACATCCGGAGAGGCTCCACCGAGTGT 1171
Qy      381 ArgAsnSerAsnSerAsnProProIeuProIeuProIeuProIeuProIeuProIeuPro 400
Db      1172 CGTAACACACACAGACACCCCTCTCTGCCAGGTGCTACAGTGCAGAAAGCTCTAAAGTG 1231
Qy      401 IlePheIleIleIlePheSerIyValIleuSerIeuGlyProIyCyAspPheIuValI 420
Db      1232 ATCTTCATCATCATTTTCTCTCTATGTGCTATCTCTGGGGCCCTTACTGCTTTTACGATC 1291
Qy      421 LeuAlaValITrpValIAspValIgluThrgIuValIProGlnITrpValIleThrlleIle 440
Db      1292 CTGGCCGCTGGGTGGATGTCGAAACCCAGTACCCAGTGGGTGATCCATTAATCANTC 1351
Qy      441 TrpIeuPhePheIeuGlnIyCySerIleAspProIyTrpValIyGlyTyrMetIleIyTrp 460
Db      1352 TGGCTTTCTCTCTCAGTGCATCCACCCCTTGTCTAAGGCTACATGCACAGAACCC 1411
Qy      461 IleIyIyIyGluIleGlnAspMetIeuIyIyIyPhePheCyIeuGlyIuAspProProIy 480
Db      1412 ATTAAGAAAGAAATCCAGACATGCTGAAGAAAGTTCTTCTGCAAGAAAGAACCCCGA 1471
Qy      481 GluAspSerIleAspAspIeuProGlyThrgIuGlyIyThrgIuGlyIyIleValIPro 500
Db      1472 GAAGATAGCCACCCAGACCTGCCCGAAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGG 1531
Qy      501 SerIyAspSerAlaIthPhePro 508
Db      1532 TCCTACGATTCGTACTTTCTCT 1555

RESULT 8
AEA33115
ID      AEA33115 standard; DNA; 1580 BP.
XX      AEA33115;
XX      11-AUG-2005 (first entry)
XX      Human GPCR HGRBMW8 gene region SeqId47.
XX      protein purification; cytosolic; neuroprotective; antiparkinsonian;
XX      tranquilizer; hypotension; anti-HIV; virucide; osteopathic; cancer;
XX      asthma; allergy; HIV infection; osteoporosis; Parkinsons disease;
XX      anxiety disorder; hyperemesis; neurological disease; gene; ds; HGRBMW8;
XX      G protein coupled receptor.
XX      Homo sapiens.
XX      OS
XX      PN      WO2005048951-A2.
XX      PD      02-JUN-2005.
XX
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PF      12-NOV-2004; 2004WO-US038387.
XX      13-NOV-2003; 2003US-00712615.
PR      (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX      Batteagline P, Feder JN, Mintier G, Nelson TC, Ramanathan CS;
PI      Westphal R, Cacace AM, Barber LE, Hawken DR, Kornacker MG;
XX      WPI; 2005-395945/40.
XX      New isolated human G-protein coupled receptor, HGRBMW8, and encoding
PT      polynucleotide, useful for diagnosing or treating cancer, asthma,
PT      allergies, HIV, osteoporosis, anxiety, hypertension and neurological
PT      diseases.
XX      Disclosure; SEQ ID NO 47; 261pp; English.
PS      This invention relates to a novel isolated human G-protein and the DNA
XX      sequence which encodes it. The invention may be useful for the
CC      development of compounds with a cytosolic, neuroprotective,
CC      antiparkinsonian, tranquilizer, hypotension, anti-HIV, virucide or
CC      osteopathic activity acting as G-protein antagonists. The methods and
CC      compositions of the present invention are useful for the diagnosis,
CC      prevention and/or treatment of diseases or conditions associated with
CC      aberrant expression or activity of the human G-protein coupled receptor,
CC      HGRBMW8, such as cancer, asthma, allergies, HIV infections,
CC      osteoporosis, Parkinson's disease, anxiety, hypertension and neurological
CC      diseases. The present sequence is that of a region of the human HGRBMW8
CC      gene of the invention.
XX      SQ      Sequence 1580 BP; 357 A; 456 C; 430 G; 337 T; 0 U; 0 Other;
XX      Alignment Scores:
XX      Pred. No.: 9 626-244 Length: 1580
XX      Score: 2644.00 Matches: 508
XX      Percent Similarity: 100.00% Conservative: 0
XX      Best Local Similarity: 100.00% Mismatches: 0
XX      Query Match: 100.00% Indels: 0
XX      DB: 14 Gaps: 0
XX      US-10-712-615-2 (1-508) x AEA33115 (1-1580)
Qy      1 MetTrSerTrhCyThrAsnSerThrvArgIuSerAsnSerSerIeThrCySerPro 20
Db      32 ATGAGTGCACCTGCACCAACAGCAGCGCCAGAGTAAAGAGGACAGCAGTGCATGCC 91
Qy      21 LeuSerIyMetProIleSerIeuAlaIleGlyIleIleArgSerThrvAlaIleValIle 40
Db      92 CTCTCAAAATGCCCATCAGCCTGGCCACGAGCATCATCCGTCMAACGTCGTGTATC 151
Qy      41 PheIeuAlaIaSerPheValIgluValaenIleValaenIleValaenIleValaenIle 60
Db      152 TTCCTGGCCGCTCTTGTGTCGGCAACATAGTGGTGGCTAGAGTTTCAGAGGCAAGCCG 211
Qy      61 GluIeuIeuGlnValIThrAsnArgPheIlePheAsnIeuIeuValIThrAspIeuGln 80
Db      212 CAGCTGCTGCAGGTACCAACCGTTTATCTTTAACCCTCTCGTACCGAGCTGCTGAG 271
Qy      81 IleSerIeuValaIaProITrpValIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 100
Db      272 ATTTGCTCTGAGCCCTCTGGGTGGTGGCCACCTGTGCTCTCTTCTGGCCCTCAAC 331
Qy      101 SerIlePheCyThrvAlaIeuValSerIeuThrvIleIeuPheAlaIaIaIaIaIaIa 120
Db      332 AGCCACTTCTGACGCGCCCTGTGATGCTCACCCAGCTGTGCTTGGCCAGCTCAAC 391
Qy      121 ThrIleValaIeuValaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 140
Db      392 ACCATTGCTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 451
Qy      141 SerIyMetTrhGlnArgArgGlyTyrIleuIeuIeuIyGlyThrvITrpIleValaIle 160
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Db 452 TCCAGATGACCCAGCGCGGCTTACCTGCTCTCTGAGCAGCTTGATGTCCTCANTC 511
Qy 161 LeuGlnSerThrProLeuLeuTyrGlyTyrPglGlyAlaIlePheAspGluArgAsnAla 180
Db 512 CTGCAAGACGCTCTCCATCTACCTGCTGAGGCTGAGGCTGCTTATGAGCCCATGCT 571
Qy 181 LeuGlnSerMetIleTyrGlyAlaSerProSerTyrThrIleLeuSerValValSerPhe 200
Db 572 CTCTGCTCATGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 631
Qy 201 IleValIleProLeuIleValMetIleAlaCysTyrSerValValPheCysAlaAlaArg 220
Db 632 ATGATATTCACATGATGTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 691
Qy 221 ArgGlnIleAlaLeuLeuTyrAsnValIleValArgHisSerLeuGluValArgValIleAsp 240
Db 692 AGGACACATGCTCTGCTGATCATGTCACAGACACACAGCTTGAAGTGCAGCTCAAGAC 751
Qy 241 CysValGluAsnGluAspGluGluGlyAlaGluLysGluGluPheGluAspGluSer 260
Db 752 TGTGTGAGAAATGAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 811
Qy 261 GluPheArgArgGlnHisGluGluGlyValValIleValIleValIleValIleValIle 280
Db 812 GAGTTTCGCGCCAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 871
Qy 281 AspGlySerLeuValAlaValGlyGlySerThrValAlaSerAspGlySerMetGluGly 300
Db 872 GACGCGACCTGAGAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 931
Qy 301 ArgGlySerGluGluValAlaArgIleSerThrValAlaSerAspGlySerMetGluGly 320
Db 932 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 991
Qy 321 LysGluGlySerThrIleValGluGluAsnSerMetLeuAlaAspLysGlyValThrGlu 340
Db 992 AAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1051
Qy 341 ValAsnGlnCysSerIleAspLeuGluGluAspAspMetGluPheGluValAspAla 360
Db 1052 GTCACACAGTGCAGCTTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAAT 1111
Qy 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProProSerArg 380
Db 1112 AATTTACATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1171
Qy 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysLysAlaAlaVal 400
Db 1172 CGTAAACAGAACGCAACCTCTCTGCGCCAGGTCGTCACAGTGCACAAAGCTGCTAAAGTG 1231
Qy 401 IlePheIleIleIlePheSerTyrValIleSerLeuGlyProTyrCysPheLeuAlaVal 420
Db 1232 ATCTTATCATCTATCTTCT 1291
Qy 421 LeuAlaValTyrValAspValGluThrGlnValAlaProGlnTyrValIleThrIleIleIle 440
Db 1292 CTGGCGCTGTGGGTGATGTCGAAACCCAGTACCCAGGCGGTGATACCAATATCATC 1351
Qy 441 TrpLeuPhePheLeuGlnCysCysIleHisProTyrValTyrGlyTyrMetHisLysThr 460
Db 1352 TGGCTTTTCTCTCTGAGTGTCTGATCCACCTCATGTCATGTCATGTCATGTCATGTCAT 1411
Qy 461 IleLysLysGluIleGlnAspMetLeuLysPhePheCysValGluLysProPheLys 480
Db 1412 ATTAAAGAGAAATCCAGGATGTCGAAAGATTTCTTCTGCAAGGAAAGCCCGGAA 1471
Qy 481 GluAspSerHisProAspLeuProGlyTyrGluGlyValTyrThrGluGlyLysIleValPro 500
Db 1472 GAAAGATAGCACCACCACTGCGCCGGAACAGAGGTCGAGCTGAAGCAAGATTGTCCT 1531
Qy 501 SerTyrAspSerAlaThrPhePro 508
Db 1532 TCCTACGATTCGTCTACTTTTCT 1555

RESULT 9
ACF03567
ID ACF03567 standard; cDNA; 1584 BP.
XX
AC F03567;
XX
DT 15-SEP-2003 (first entry)
XX
DE Human NOV14a protein encoding cDNA SEQ ID NO:41.
XX
XX Human; NOVX; cytoskeletal; cardiant; antiinflammatory; immunosuppressive;
KW antiallergic; haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic;
KW anorectic; antiaslathmic; nephrotoxic; antiarthritic; hepatotropic;
KW neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
KW relaxant; anticonvulsant; hypotensive; vasotropic; antiparkinsonian;
KW vulnary; angiogenic; antiangiogenic; gene therapy; vaccine; cancer;
KW cardiomyopathy; atherosclerosis; hypertension; diabetes; inflammation;
KW autoimmune disorder; allergy; blood disorder; AIDS; obesity; asthma;
KW acquired immunodeficiency syndrome; nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; Parkinson's disease; goitre; infection; stroke;
KW muscular dystrophy; epilepsy; wasting disorder; chromosome X; gene; ss.
XX
OS Homo sapiens.
XX
PN MO200294870-A2.
XX
PD 28-NOV-2002.
XX
PE 02-NOV-2001; 2001WO-US051580.
XX
PR 02-NOV-2000; 2000US-0245291P.
XX
PR 02-NOV-2000; 2000US-0245317P.
PR 07-NOV-2000; 2000US-0246562P.
PR 08-NOV-2000; 2000US-0246871P.
PR 26-JAN-2001; 2001US-0264389P.
PR 26-JAN-2001; 2001US-0264423P.
PR 29-JAN-2001; 2001US-0264799P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Grosse WM, MacDougall JR, Smithson G, Millet I, Stone DJ;
PI Gunther E, Ellerman K, Alsobrook JP, Lepley DM, Burgess CE;
PI Spytek KA, Edinger SR, Gangoli EA, Gorman L, Taupier RJ, Li L;
PI Guo X, Fernandes ER, Vernet CAM, Tchernev VT, Casman SJ, Shenoy S;
PI Mishra V, Furtak K, Baumgartner JC, Colman SD;
DR WPI; 2003-140359/13.
DR P-PSDB; ABR57432.
XX
PT New NOVX polypeptide useful for preventing or treating NOVX-associated
PT disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and
PT in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX
XX Claim 8; Page 129; 346pp; English.
XX
ACF03547 to ACF03570 encode the human NOVX proteins (I) given in ABR57412
CC to ABR57435. (I) have cytoskeletal, cardiant, antiinflammatory, nootropic,
CC immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiabetic,
CC antiarteriosclerotic, anorectic, antiaslathmic, nephrotoxic, virucide,
CC antirheumatic, hepatotropic, neuroprotective, antibacterial, relaxant,
CC antiparasitic, anticonvulsant, hypotensive, vasotropic, antiparkinsonian,
CC vulnary, angiogenic and antiangiogenic activities, and can be used in
CC gene therapy and vaccine. The NOVX polypeptides and their antibodies can
CC be used to determine the presence or absence of (I) in a sample. The NOVX
CC polypeptides, polynucleotides encoding them, and antibodies against them,
CC are useful in manufacturing a medicament for treating or preventing a
CC syndrome associated with a NOVX-associated disorder such as hypertension,
CC cardiomyopathy, atherosclerosis, cancer, diabetes, asthma, inflammation,
CC autoimmune disorders, allergies, blood disorders, obesity, acquired
CC immunodeficiency syndrome (AIDS), immunoglobulin (Ig) A nephropathy,
CC cirrhosis, arthritis, Alzheimer's disease, Parkinson's disease, goitre,
CC infections (e.g. bacterial, viral, parasitic), stroke, muscular

← YES, SEQ ID NO:2 is present.

CC dyctrophy, epilepsy, and other wasting disorders associated with chronic
 CC diseases. ACF03571 to ACF03644 represent PCR primers and probes for NOVX
 CC sequence, which are used in an example from the present invention
 XX

SO Sequence 1584 BP; 359 A; 457 C; 430 G; 338 T; 0 U; 0 Other;

Alignment Scores:

Prod. No.: 9,656-244 Length: 1584
 Score: 2644.00 Matches: 508
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-712-615-2 (1-508) x ACF03567 (1-1584)

QY 1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
 DB 31 ATGAGCTCCACTGACCAACAGCAGCGCGAGAGTAAACAGACAGCCACGTCATGCCCC 90
 QY 21 LeuSerLyseMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
 DB 91 CTCCTCAAAATGCCCATACGCTGGCCCGCAGCATCATCCGCTCAACCGCTGCTTATC 150
 QY 41 PheLeuAlaAlaSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLysePro 60
 DB 151 TTCCTCGCGCGCTTTCGTGGGCAACATAGTGTGGCGCTAGTGTGGCGAGCGCAAGCGG 210
 QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuGln 80
 DB 211 CAGCGCTGCGAGGTACCAACCGTTTATCTTAACTCTCGTACCAACCGCTGCGAG 270
 QY 81 IleSerLeuValAlaProTrpValValAlaThrSerValProLeuPheTrpProLeuAsn 100
 DB 271 ATTGGCTCGTGGCCCCCGGGGTGGGCCACCTCTGCTCTCTTCTGGCCCCCTCAAC 330
 QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisAlaLeuPheAlaSerValAsn 120
 DB 331 AGCCACTTCTGCAGCGCCCTGGTTAGCTCACCCACCTGTTGCCCTTGGCCAGCGTCAAC 390
 QY 121 ThrIleValLeuValSerValAsnArgTyrlLeuSerIleIleHisProLeuSerTyrlPro 140
 DB 391 ACCATTGCTTGGTGTGTCAGTGTGCTGCTATCTGTCATCATCACCCCTCTCTCCCAACCG 450
 QY 141 SerLyseMetThrGlyArgArgGlyTyrlLeuLeuLeuTyrlGlyThrTyrlIleValAlaIle 160
 DB 451 TCCAAGATGACCCAGCGCGCGGTTACCTGCTCTCTATGGCACTCGAATTGGCCATC 510
 QY 161 LeuGlnSerThrProProLeuTyrlGlyTyrlGlyGlnAlaAlaPheAspGluArgAsnAla 180
 DB 511 CTGCAAGACACTCTCTCACTTACGGCTGGGGCCAGGCTGCCCTTGTGATGAGCGCATGCT 570
 QY 181 LeuCysSerMetIleTyrlGlyAlaSerProSerTyrlThrIleLeuSerValIleSerPhe 200
 DB 571 CTCTGCTCATGATCTGGGGGGCCAGCCCACTACACATTCCTCAGCGTGTGCTTTC 630
 QY 201 IleValIleProLeuIleValMetIleAlaCysTyrlSerSerValValPheCysAlaAlaArg 220
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 QY 221 ArgGlnHisAlaLeuLeuTyrlAsnValIleArgHisSerLeuGlnValArgValIleAsp 240
 DB 691 AGGCAAGCATGCTCTGCTGTACATGTCAAGAGACACAGCTTGGAGTGGAGTCAAGGAC 750
 QY 241 CysValGluAsnGluAspGluGluGlyAlaGluTyrlValGluGluPheGlnAspGluSer 260
 DB 751 TGTGTGAGAAATGAGAGATGAAAGAGGACGAGAGAGAGAGAGAGTTCAGAGATGAGACT 810
 QY 261 GluPheArgArgGluHisGluGluGluValIleValAlaValGluGluValArgMetGluAlaVal 280
 DB 811 GAGTTTCGGCGCCAGCATGAGGTGAGTGCAGAGGCCAAGAGGCGCAATGGAGGCAAG 870
 QY 281 AspGlySerLeuValAlaValGluGluGluSerThrGlyThrSerGluSerSerValGluAla 300

DB 871 GACGCGACCTCGAAGCGCAAGAAAGAAAGCAACGGGAGCACTGAGATGATGACAGCCC 930
 QY 301 ArgGlySerGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGly 320
 DB 931 AGGGCAGCGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 990
 QY 321 LysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
 DB 991 AAGGAAGCAGACCAAAAGTTGAGGAGAAACAGCATGAAAGGACAGACAGAGGTGACAGAG 1050
 QY 341 ValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
 DB 1051 GTCAACCAAGTGCAGTTCGCTGGGTGAATGACATGAGTGGTGTGGAAGACACATC 1110
 QY 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProSerArg 380
 DB 1111 AATTTCAAGTAGATGAGTGTGAGGAGCATGAAACATCCGAGAGCTCCACCCAGTGTCT 1170
 QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrlGlnCysValAlaAlaLysVal 400
 DB 1171 CGTAAACAGCAACAGCAACCTCTCTGCGCAGGTGCTTACAGTGCAGAGCTGCTTAAAGTG 1230
 QY 401 IlePheIleIleIlePheSerTyrlValLeuSerLeuGlyProTyrlCysPheLeuAlaVal 420
 DB 1231 ATCTTCATCATCATTTTCTCTATGTCTATCCCTGGGCGCCCTACTGCTTTTACAGATC 1290
 QY 421 LeuAlaValTyrPvalAspValGluThrGlnValProGlnTyrPvalIleThrIleIleIle 440
 DB 1291 CTGGCCGTGTGGTGGATGTGCAACCCAGATGCCCGAGTGGGTATATCACTAATATC 1350
 QY 441 TrpLeuPhePheLeuGlnCysCysIleHisProTyrlValTyrlGlyTyrlMetHisLysThr 460
 DB 1351 TGGCTTTCTTCTCTGCAATGCTGCATCCACCCCTATGTCTATGCTATATGACAAAGCC 1410
 QY 461 IleLysLysGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysProLys 480
 DB 1411 ATTAAGAAAGAAATCCAGAGACATGCTGAAGAAATCTTCTGCAAGAAAGCCCGGAAA 1470
 QY 481 GluAspSerHisProAspLeuProGlyThrGluGluGlyThrGluGlyLysIleValPro 500
 DB 1471 GAAGATAGCACCCAGACCTGCCGGAACAGAGGTGGAGTGAAGGCAAGATGTCTCT 1530
 QY 501 SerTyrlAspSerAlaThrPhePro 508
 DB 1531 TCCTAGATTCCTGCTACTTTTCTCT 1554

RESULT 10
 ADF70610
 ID ADF70610 standard; DNA; 2241 BP.
 XX
 AC ADF70610;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Orphan receptor ligand-related human protein gene SegID233.
 XX
 KW ligand: orphan receptor protein; fusion protein; fluorescent protein;
 KW cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
 KW GFPuv; Enhanced GFP; EGFP; human; gene; ds.
 OS Homo sapiens.
 XX
 PN WO2003071272-A1.
 PN
 PD 28-AUG-2003.
 PD
 PF 21-FEB-2003; 2003WO-JP001901.
 PF
 PR 22-FEB-2002; 2002JP-00045728.
 PR
 PR 23-JUL-2002; 2002JP-00213949.
 PR
 PR 11-OCT-2002; 2002JP-00298237.
 XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;

XX MPI: 2003-697654/66.

DR P-PSDB; ADF70508.

XX Transformation of cells with a fusion protein of an orphan receptor
PT protein with a fluorescent protein useful for identification of ligands
PT to the orphan receptor.

PS Example 4; SEQ ID NO 233; 594pp; Japanese.

XX This invention relates to a novel method of identifying ligands to an
CC orphan receptor protein which comprises transforming cells with DNA
CC encoding a fusion protein of the orphan receptor with a fluorescent
CC protein, so that the fusion protein is expressed in the cells (or cell
CC membranes isolated from them) and contacting the cells with the potential
CC ligand to be tested. A suitable fluorescent protein for incorporation in
CC the fusion protein is green fluorescent protein (GFP), for example GFP-1,
CC wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the
CC identification of ligands binding to an orphan receptor protein.

XX Sequence 2241 BP, 578 A, 597 C, 570 G, 496 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	1,6e-243	Length:	2241
Score:	2644.00	Matches:	508
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-712-615-2 (1-508) x ADF70610 (1-2241)

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QY 1 MetThrSerThrCysThrAnsSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
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DB 61 CTCTCCAAATGCGCATCAGCCCTGCGCCACGGCATATCCGCTCAACCGCTGATTATC 120
QY 41 PheLeuAlaIleSerPheValGlyAsnIleValIleuAlaIleuValIleuArgIleuVal 60
DB 121 TTCCTGCGCGCTCTTTCGTCGCAACATGCTGCGCTAGTGTGCGAGCGCAGCGC 180
QY 61 GlnLeuLeuGlnValThrAnsArgPheIlePheAsnLeuLeuValThrAspLeuGln 80
DB 181 CAGCTGCTGCAAGGTGACCAACGCTTTATCTTAACCTCCTGTCACCGACTGCGAG 240
QY 81 IleSerLeuValAlaProTyrValValAlaIleThrSerValProLeuPheTyrProLeu 100
DB 241 ATTTGCGCTGTCGCGCCCTGCGGTGTCGCGCACCCTGTCGCTCTTTCGCGCCCTCAAC 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisIleuPheAlaPheAlaSerVal 120
DB 301 AGCCACTTTCGACGGCCCTGTTAGCTTACACCACCTGTCCTTCGCGCAGCGTCAAC 360
QY 121 ThrIleValIleuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
DB 361 ACCATTGCTGTGGTGTGAGTGATGCTACTTGCATATCATCACCTCTCTCTCAACCG 420
QY 141 SerIleMetThrGlnArgArgGlyTyrLeuLeuLeuTyrGlyThrTrpIleValAlaIle 160
DB 421 TCCAAATATGACCGAGCGCGGTATCGCTCTCTATGCGACCTGGATTTGGGCGATC 480
QY 161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlnAlaIlePheAspGluArgAsnAla 180
DB 481 CTGCAAGACATCTCTCATCTACGCGCTGGGCGCAGGCTCTTTATATGAGCCATGCT 540
QY 181 LeuCysSerMetIleTyrGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200
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DB 541 CTCTGCTCATATCTGCGGGGCGCAGCCCACTACACTATTCTACGCTGCTCTTC 600
QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerValValPheCysAlaIleArg 220
DB 601 ATGTCATTCCACTGATTGTATGATGTGCTGCTACTCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 221 ArgGlnHisAlaLeuLeuTyrAsnValIleValArgHisSerLeuGluValArgValIleAsp 240
DB 661 AGCGACATGCTCTGCTGCAATGTCAGAGACACAGCTTGGAGTGGAGCTCAAGAGAC 720
QY 241 CysValGluAsnGluAspGluGluGlyIleGlyIleValIleValIleValIleValIle 260
DB 721 TGTGTGGAATGAGATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
QY 261 GluPheArgArgGlnHisGluGlyGluValIleValIleValIleValIleValIleValIle 280
DB 781 GAGTTTCCGCGCAGCATTAAGTGTAGGTCAAGGCCAAGAGGCGCAATGAGAGCGCAG 840
QY 281 AspGlySerLeuValAlaValGluGlySerThrGlyThrSerGluSerSerValGluAla 300
DB 841 GACGCGAGCTGAGAGCCCAAGAGAGAGACAGCGGAGCAGAGTAGTGTAGAGGCGC 900
QY 301 ArgGlySerGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGly 320
DB 901 AGGGCGAGGAGAGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 321 LysGluGlySerThrIleValGluGluAsnSerMetIleAspIleValIleValIleValIle 340
DB 961 AAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 341 ValAsnGlnCysSerIleAspLeuGlyIleAspAspMetGluPheGlyGluAspAspIle 360
DB 1021 GTCAACCACTGACAGATTGACTTGGGTGAAATGATGATGAGATTGTGTGAGAGAGCATC 1080
QY 361 AsnPheSerGluAspAspValGluAlaValAlaIleProGluSerLeuProProSerArg 380
DB 1081 AATTTCAGTGAAGATGACCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysIleValAlaIleVal 400
DB 1141 CGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 401 IlePheIleIleIlePheSerTyrValIleSerLeuGlyProTyrCysPheLeuAlaVal 420
DB 1201 ATCTTCATCATCTTTCTCTATGCTATCCCTGCGGCGCTACTGCTTTTATGCAAGTC 1260
QY 421 LeuAlaValIleValAspValGluThrGlnValProGlnTyrValIleThrIleIleIle 440
DB 1261 CTGCGCGTGTGGTGTGATGTCGAAACCCAGTACCCAGTGGGTGATCACCAATTAATCATC 1320
QY 441 TrpLeuPhePheLeuGlnCysGlyIleHisProTyrValIleTyrGlyTyrMetHisIle 460
DB 1321 TGGCTTTTCTTCGAGTGTGATCAACCCCTATGCTATGAGTACATGACAAAGACC 1380
QY 461 IleValIleGluIleGlnAspMetLeuIleValIleValIleValIleValIleValIle 480
DB 1381 ATTAAGAGAGAGATCCAGAGCATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 481 GluAspSerHisProAspLeuProGlyIleThrGluGlyIleThrGluGlyIleValPro 500
DB 1441 GAAAGATAGCACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 501 SerTyrAspSerAlaIlePhePro 508
DB 1501 TCTACGATTCTGCTACTTTTCT 1524
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RESULT 11
ACCS8886
ID ACCS8886 standard; cDNA; 4718 BP.
XX ACCS8886;
AC
XX
DT 22-SBP-2003 (first entry)

XX Human G-protein coupled receptor OM_10 cDNA.
 KW G-protein coupled receptor; GPCR; OM_10; human; receptor; cardiac;
 KW hypersensitive; hypotensive; antianginal; cyostatic; antipruritic;
 KW analgesic; gynaecological; antidepressant; antistatic; osteopathic;
 KW neurologic; cranial; antineoplastic; antitumor; antiallergic;
 KW neurologic; anticonvulsant; neuroprotective; antiparkinsonian;
 KW gene therapy; gene; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 332..1858
 FT /*tag= a
 FT /product= "OM_10"
 XX
 PM MO200304162-A2.
 PD 30-MAY-2003.
 PE 12-NOV-2002; 2002WO-US036204.
 XX
 PR 16-NOV-2001; 2001US-0332110P.
 XX
 PA (AMHP) WYETH.
 PI Blatcher M, Paulsen JE, Bates BG;
 XX
 XX MPI; 2003-449811/42.
 DR P-PSDB; ABR42865.
 XX
 PT New polynucleotides encoding G-protein coupled receptor, i.e. OM-10 and
 PT UP-11 polypeptides, useful for diagnosing, preventing and treating, e.g.
 PT Parkinson's disease, acute heart failure, hypertension, cancer or
 PT osteoporosis.
 XX
 PS Claim 49; Page 174-178; 190pp; English.
 XX
 CC The present sequence is that of cDNA encoding a novel human G-protein
 CC coupled receptor (GPCR) termed OM_10. This orphan GPCR was identified
 CC from a genome database search using the human 5-HT₆ receptor sequence.
 CC Identified regions of genomic DNA were used to predict full-length genes,
 CC and these gene predictions were used to isolate the present sequence from
 CC a cDNA library. OM_10 is predominantly expressed in the putamen and
 CC caudate nucleus. OM_10 and UP_11 polypeptides, polynucleotides, agonists
 CC and antagonists of the invention are useful in drug screening assays,
 CC pharmacogenomics, monitoring of effects during clinical trial, or for
 CC diagnosing, preventing and treating diseases associated with enhanced or
 CC inhibited GPCR activity, e.g. acute heart failure, hypotension,
 CC hypertension, angina pectoris, myocardial infarction, hyperproliferative
 CC diseases such as cancers and psoriasis, apoptotic diseases, pain,
 CC endometriosis, anorexia, bulimia, asthma, osteoporosis, schizophrenia,
 CC delirium, depression, anxiety, urinary retention, ulcers, allergies,
 CC dyskinesias such as Huntington's disorder or Gilles de la Tourette's
 CC syndrome, Alzheimer's disease, or Parkinson's disease
 CC
 SQ Sequence 4718 BP; 1359 A; 1078 C; 1060 G; 1221 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 4 718-243 Length: 4718
 Score: 2644.00 Matches: 508
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0
 US-10-712-615-2 (1-508) x ACCS8886 (1-4718)
 Oy 1 MetThrSerThrCysThrAsnSerThrArgIuserAsnSerSerHisThrCysMetPro 20
 Db 332 ATGAGCTCCACTGCAACCAAGACGCGCGAGAGTAAGACGACCAAGTGCATGCCCC 391

Oy 21 LeuSerIysMetProIleSerLeuAlaHisGlyIleIleIleArgSerThrValLeuValIle 40
 Db 392 CTCTCCAAAAGGCCATCAGCGCTGGCCACGCGCATCATCCGCTCAACCGCTGGTTATTC 451
 Oy 41 PheLeuAlaAlaSerPheValIGLYAsnIleValLeuAlaLeuValLeuGlyArgIysPro 60
 Db 452 TTCTCCGGCGGCTCTTTGCTGGCAACATAGTCTGGGGCTTAGTGTTCAGCGCAAGCCG 511
 Oy 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuGln 80
 Db 512 CAGTGTGTGAGGTGACCAACCGTTTATCTTTAACTCTGTCACCGACCTGTCAG 571
 Oy 81 IleSerLeuValAlaProTyrValAlaAlaThrSerValProLeuPheTyrProLeuAsn 100
 Db 572 ATTTGCTGTGGGCCCCCTGGGTGTGGCCACTCTGCTCTCTTGTGGCCCCCTCAAC 631
 Oy 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
 Db 632 AGCCACTTGTGACGGCCCTGTTAGCTTCAACCCACTGTTGCTTCCGACGCTCAAC 691
 Oy 121 ThrIleValLeuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
 Db 692 ACCATTGTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 751
 Oy 141 SerIysMetThrGlnArgArgGlyTyrIleLeuLeuTyrGlyThrThrIleValAlaIle 160
 Db 752 TCCAAAGATGACCAACGCGCGGTACCTGCTCTCTTATGACACCTGATTTGTGCCATTC 811
 Oy 161 LeuGlnSerThrProProLeuTyrGlyTyrIleGlnAlaAlaPheAspGlyArgAsnAla 180
 Db 812 CTGCAGAGCACTCTCTCACTTACGCGCTGGGGCCAGGCTGCTTTGATGAGCGCATGCT 871
 Oy 181 LeuCysSerMetIleTyrGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200
 Db 872 CTCTGCTCAATGATGTGGGGGGCCAGCCCAAGCTACATATTCTCAGGTGGTGTCTTC 931
 Oy 201 IleValIleProLeuIleValMetIleAlaCysTyrSerSerValValPheCysAlaAlaArg 220
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 Db 992 AGGCGACATGCTCTCTCTTACATGTCGAGACACACACTTGGAGTCCGACTCAAGGAC 1051
 Oy 241 CysValIGLYAsnGlyAspGlyGlyValIleGlyValIleGlyValIleGlyValIleGly 260
 Db 1052 TGTGTGGAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1111
 Oy 261 GluPheArgGlnHisGlyGlyValIleGlyValIleGlyValIleGlyValIleGlyVal 280
 Db 1112 GAGTTTCCCGCCGACATGAAGTGTGAGTCAAGCCCAAGGCGCAGATGCAATGCCAAG 1171
 Oy 281 AspGlySerLeuValAlaIlyGlySerThrGlyThrSerGlySerValIleGlyVal 300
 Db 1172 GACGCGACCTGAAGGCAAGGAGAAAGACGCGGAGACAGAGTAAGTGTAAAGGCC 1231
 Oy 301 ArgGlySerGlyGlyValIlyArgIlySerThrValIleAlaSerAspGlySerMetGly 320
 Db 1232 AGGCGACGAGAGAGTCAAGAGAGACGACGAGTGGCCAGGACGACGACGATGAGAGGT 1291
 Oy 321 IlyGlyGlySerThrIlyValIleGlyValIleGlyValIleGlyValIleGlyValIle 340
 Db 1292 AAGGAAGCAGACCAAGATTGAGAGAAAGACATGAAGAGGACGACAAAGGTCGACAGAG 1351
 Oy 341 ValaGlnCysSerIleAspLeuGlyGlyIlyAspAspMetGlyIlyGlyValAspAsp 360
 Db 1352 GTCAACCAAGTGAAGTGTGGTGAAGATGACATGAGATTGTTGTGAAGACCAATC 1411
 Oy 361 AsnPheSerGlyAspAspValIGLYValIleValIleProGlySerLeuProProSerArg 380
 Db 1412 AATTTCAGTGAAGATGAGTCAAGGACATGAACATCCCGAGAGGCTCCACCCAGTGTGT 1471
 Oy 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysValAlaIlyVal 400

Dd	1472	CGRNACAGCAACAGAACCCCTCCTCTGCGCCAGGTGCATCACGTCCAAAGCTGCTAAAGTG	1531
Oy	401	IlePheIleIleIlePheSerTyrValIeuSerLeuGIlyProTyrCysePheLeuAlaVal	420
Dd	1532	ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGGGCCCTACTGCTTTTAGCAGTC	1591
Oy	421	LeuAlaValTrrpValAspValGIuThnGlnValProGlnTrpValIleThrIleIleIle	440
Dd	1592	CTGGCCCGTGGGGTGAGATGTGAACCACGAGTACCCCGATGGGTGATCACATATATCATC	1651
Oy	441	TrrpLeuPhePheLeuGInCyseCyseIleHisProTyrValTyrGIlyTyrMetHisLysThr	460
Dd	1652	TGGCTTTTCTTCTCCGTGCAGTGCATCCACCCCTATGTCTATGGCTTACATCACAAGACC	1711
Oy	461	IleLysIysGIuIleGInAspMetLeuLysLysPhePheCyseLysGIuLysProProLys	480
Dd	1712	ATTAAAGAAGAAATCCAGACATGCTGANAAGATTTCTTCTGACAAAGAAAAGCCCCGAAA	1771
Oy	481	GIuAspSerHisLspTroAspLeuProGIlyThrGIuGIlyGIlyThrGIuGIlyLysIleValPro	500
Dd	1772	GAAATATGCCCACCCAGACCTGCCCGGAACAGAGGTGGAGCTGAAGGCAMAGATGTGCTCT	1831
Oy	501	SerTyrAspSerAlaThrPhePro 508	
Dd	1832	TCCTACGATCTGCTACTTTTCT 1855	
RESULT 12			
AAL44180	ID	AAL44180 standard; DNA; 1524 BP.	
XX	AC	AAL44180;	
XX	DT	24-OCT-2002 (first entry)	
XX	DE	Human G-protein coupled receptor protein coding sequence #2.	
KW		Human; G-protein coupled receptor protein; TGR34; gene; ds;	
KV		central nervous system disease; Alzheimer's disease; metabolic disease;	
KV		diabetes; cancer; breast cancer; circulatory disease; atherosclerosis;	
KW		inflammatory disease; arthritis; respiratory disease; bronchitis;	
KM		digestive disease; stomach ulcer; immune disorder; autoimmune disease;	
XX		Infection; AIDS.	
XX	OS	Homo sapiens.	
XX	Key	Location/Qualifiers	
FT	CDS	1..1524	
FT		/*tag= a	
FT		/partial	
FT		/product= "Human G-protein coupled receptor protein #2"	
FT		/note= "No stop codon is given"	
XX	WO	200259304-A1.	
XX	PD	01-AUG-2002.	
XX	PE	22-JAN-2002; 2002WO-JP000405.	
XX	PR	23-JAN-2001; 2001JP-00015050.	
XX	PR	30-MAR-2001; 2001JP-00102560.	
XX	PA	(TAKE) TAKEDA CHEM IND LTD.	
XX	PI	Miwa M, Ito T, Shintani Y, Miyajima N,	
XX	DR	WPI; 2002-557949/59.	
XX	DR	P-PSDB; AAO15504.	
XX		Human G-protein coupled receptor protein and DNA encoding it for design	
XX		of drugs and reagents for treatment and diagnosis of cancer or	
XX		respiratory and metabolic diseases.	

PS Claim 7, Page 100-101, 109pp; Japanese.

XX The invention comprises the amino acid and coding sequences of two human
CC G-protein coupled receptor proteins (TG34). The DNA and protein
CC sequences of the invention are useful for the treatment, prevention and
CC diagnosis of: central nervous system diseases (e.g. Alzheimer's disease);
CC metabolic diseases (e.g. diabetes); cancer (e.g. breast cancer);
CC circulatory diseases (e.g. atherosclerosis); inflammatory diseases (e.g.
CC arthritis); respiratory diseases (e.g. bronchitis); digestive diseases
CC (e.g. stomach ulcer); immune disorders (e.g. autoimmune diseases); and
CC infections (e.g. AIDS). The present DNA sequence encodes a human G-
XX protein coupled receptor protein

SO Sequence 1524 BP; 346 A; 439 C; 419 G; 320 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1, 77e-243	Length:	1524
Score:	2641.00	Matches:	507
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.80%	Mismatches:	0
Query Match:	99.8%	Indels:	0
DB:	6	Gaps:	0

US-10-712-615-2 (1-508) x AAL44180 (1-1524)

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Db	1	ATGAGCTGCACCTGCACCAAGACAGCAGCGGAGATACAGACACCAAGCATGATGCC	60
QY	21	LeuSerLyMetProIleSerLeuNah1sGlyIleIleAgserrThraIleuValIle	40
Db	61	CTCTCCAAATGCCCATACGCTGGCCACGCGCATCATCCCTACACCGTGGTATC	120
QY	41	PhleuAlAlaSerPheValAlGlyAenIleValleuAlaLeuValleuGlnArgLyPro	60
Db	121	TTCCTGCGGCTCTTTGTCGCGCAACATAGTCTGGCGCTAGTGTTCAGCGCAAGCCG	180
QY	61	GlnLeuLeuGlnValThraNahRphelIlePheAenLeuValIThraSpLeuLeuGln	80
Db	181	CACGCTGAGAGTGACCAACCGTTTATCTTTAACCTCCGTCACGACCTGCTCAG	240
QY	81	IleSerLeuValAlaProTrpValValAlaThrSerValProLeuPheTrpProLeuAsn	100
Db	241	ATTTCGCTGCTGGCCCCCTGGGTGGTGGCACTCTGGCTCTCTTGGCCCTCAAC	300
QY	101	SerHisPheCysThrAlaLeuValSerLeuThrHisIleuPheAlaPheAlaSerValAsn	120
Db	301	AGCACCTTCGACGGCCCTGGTATGCTCACCCACCTGTGGCTTGCGCCATCGCAGCTAAC	360
QY	121	ThrIleValleuValSerValAspArgLyLeuSerIleIleHisProLeuSerTyPro	140
Db	361	ACCATGTGTGTGTGTGCAATGATGCTTATCTTGCATTCACCAACCTCTCTCTACCG	420
QY	141	SerLyMetThrGlnArgArgLyIleLeuLeuLeuTyGlyThrTrpIleValAlaIle	160
Db	421	TCCAAATATACCAAGCGCGCGGTACCTGCTCTATGACACTGGAATGTGGCCATC	480
QY	161	LeuGlnSerThrProProLeuTyGlyIleTrpGlyGlnAlaAlaPheAspGluArgAsnAla	180
Db	481	CTGCAAGACATCTTCACATTCACGGCGGGGCCAGCGCTGGCTTGTATGAGCGCAAGCT	540
QY	181	LeuCysSerMetIleTrpGlyAlaSerProSerTyThrIleLeuSerValIleSerPhe	200
Db	541	CTGTGCTCATGATCTGGGGGGGCCAGCCCAAGCTACACTATTCACAGCGTGTCTTC	600
QY	201	IleValIleProLeuIleIleValMetIleAlaCysTySerSerValIlePheCysAlaAlaArg	220
Db	601	ATGTGATTCACACTGATGTGTATGATGTGCTGCTACTCCGAGGTCTTGAGCGCCGG	660
QY	221	ArgGlnHisAlaLeuLeuTyTrsValIleArgIleSerLeuGluValArgValIleAsp	240
Db	661	AGGACAGATGCTGTCTGATCAATGTCAAGACACAGCTTGGAAAGTCGAGTCAAGAC	720

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OY 241 CysValIGluAenGluAenGluGluValAGluValylyGluGluPheGluAenGluSer 260
Db 721 TGTGTGGAGAAATGAGATGAAAGAGGACAGAGAAAGAGAGATTCCAGATAGAGT 780
OY 261 GluPheAArgGluNHIGluGluValValLysValLysGluGluArgMetGluLys 280
Db 781 GAGTTTCCGCCGACATGAGGTAGGTCAAGGCCAAGAGGCGCAATGAAAGCCAG 840
OY 281 AepGlySerLeuLysAlaLysGluGlySerThrGlyThrSerGlySerSerValGlu 300
Db 841 GACGCGACGCTGAAGCCAAAGAGAGACACGCGGACACAGTAGAGTAGTAGAGGCC 900
OY 301 ArgGlySerGluGluValArgLysSerThrValAlaSerArgGlySerMetGluGly 320
Db 901 AGGGGACACGAGAGAGTCAAGAGACAGCAGCGTGGCCAGCGGACGCGCATGAGGCT 960
OY 321 LysGluGlySerThrLysValGluGluAenSerMetLysAlaAapLysGlyArgThrGlu 340
Db 961 AAGGAAGGACGACCAAGCTTAGAGAGACATGAAAGGCGACAGAGGCTGCACAGAG 1020
OY 341 ValAenGluCysSerIleAapLysGluGluAapSerMetGluPheGlyGluAapAplle 360
Db 1021 GTCACACGATGACAGATTGACTTTGGGTGAAGATGACATGAGATTGGTGAAGACGACATC 1080
OY 361 AenPheSerGluAapApyValGluValAenIleProGluSerLeuProProSerArg 380
Db 1081 AATTTCAGTAGAGATGACCTCGAGGACAGTAAATCCCGAGAGCCCTCCACCCAGTGGT 1140
OY 381 ArgAenSerAenSerAapProProLeuProArgCysTyrGluCysLysValAlaLysVal 400
Db 1141 CGTAACAGCAACAGCAACCTCTCTGCCAGAGTGTACCAAGTGCMAAGCTCTAAAGTG 1200
OY 401 IlePheIleIleIlePheSerTyrValLysSerLeuGlyProTyrCysPheLeuAlaVal 420
Db 1201 ATCTTCATCATATTTCTCTATGAGTATCCCTGGGGCCCTACGCTTTTATAGAGTC 1260
OY 421 LeuAlaValTyrValAapValGluThrGluValProGluIntTyrValIleThrIleIle 440
Db 1261 CTGGCCGCTGGGTGGATGTCCAAACCCAGGTACCCCACTGGGTGATCCCAATATCATC 1320
OY 441 TrpLeuPhePheLeuGluCysCysIleHisProTyrValTyrGlyTyrMetHisLysThr 460
Db 1321 TGGCTTTTCTTCTCTGACAGTGTGATCCACCCCTATGTATTAGGCTACATGACAGACC 1380
OY 461 IleLysLysGluIleGluAapMetLeuLysLysPhePheCysLysGluLysProProLys 480
Db 1381 ATTAGAAGGAATCCAGACATGCTGAAGAGATTCTTCTGCAAGAGAAAAGCCCCGAAA 1440
OY 481 GluAapSerHisProAapLeuProGlyThrGluGlyValLysIleValPro 500
Db 1441 GAAGATAGCCACCCAGACCTGCCGAAACAGAGGGGTGGACTGAAGGCAAGATTGTCCCT 1500
OY 501 SerTyrAapSerAlaThrPhePro 508
Db 1501 TCCTACGATTCTGCTACTTTTCTT 1524

```

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KM anti-depressant; anorectic; PCR primer; gene therapy.
XX Homo sapiens.
OS WO200162797-A2.
XX
PN 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-US005676.
XX
XX 23-FEB-2000; 2000US-0184247P.
PR 23-FEB-2000; 2000US-0184303P.
PR 23-FEB-2000; 2000US-0184304P.
PR 23-FEB-2000; 2000US-0184305P.
PR 23-FEB-2000; 2000US-0184397P.
PR 02-MAR-2000; 2000US-0186457P.
PR 03-MAR-2000; 2000US-0186810P.
PR 09-MAR-2000; 2000US-0188064P.
PR 13-MAR-2000; 2000US-0188880P.
PR 03-APR-2000; 2000US-0194344P.
PR 23-JUN-2000; 2000US-0213861P.
PR 11-JUL-2000; 2000US-0217369P.
PR 11-JUL-2000; 2000US-0217370P.
PR 14-JUL-2000; 2000US-0218337P.
PR 20-JUL-2000; 2000US-0218492P.
XX
XX (PHNA ) PHARMACIA & UPJOHN CO.
PA
PI Vogeli G, Wood LS, Parodi LA, Lind P;
XX MPI. 2001-570628/64.
XX P-PSDB; AA025605.
DR
PT New isolated nucleic acid encoding a new G-protein coupled receptor
XX polypeptide for detecting receptor modulators that can treat mental
XX disorders, such as schizophrenia, anxiety, depression, or obesity.
XX
XX Claim 4, Page 89-90; 279pp; English.
XX
XX Sequences AAS42806-AAS42926 represent cDNA molecules and PCR primers for
XX cDNA molecules encoding human G-protein coupled receptor (GPCR)
XX polypeptides. The protein and DNA sequences of the invention can be used
XX to identify compounds which bind to GPCR polypeptides and in screening
XX for compounds that modulate GPCR activity. By screening a human subject
XX for the presence of mutations in GPCR DNA, a GPCR-related disorder or a
XX genetic predisposition can be diagnosed. The sequences can also be used
XX for treatment and prevention of mental disorders such as schizophrenia,
XX attention deficit disorder, anxiety, depression, dementia and bipolar
XX disorder, neurological disorders such as Huntington's disease,
XX Parkinson's disease and Tourette's syndrome, metabolic disorders such as
XX obesity, anorexia and type 2 diabetes, cardiovascular disorders such as
XX thrombosis, myocardial infarction, cardiomyopathy and atherosclerosis,
XX viral infections caused by HIV and cancers
XX
SQ Sequence 1527 BP; 347 A; 439 C; 420 G; 321 T; 0 U; 0 Other;

```

Alignment Scores:

```

Pred. No.: 1.78e-243 Length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: Gaps: 0

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US-10-712-615-2 (1-508) x AAS42857 (1-1527)

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OY 1 MetThrSerThrCysThrAenSerThrArgLysSerAenSerSerHisThrCysMetPro 20
Db 1 ATGAGTCACCATCTGCACCAACAGCAGCGCGAGATACAGACGACACGTCATGCC 60
OY 21 LeuSerLysMetProLysSerLeuAlaIleGlyIleIleArgSerThrValLeuValIle 40
Db 61 CTCCTCAAAATGCCATCAGCTGGCCACGAGCATCATCCGCTCAACCGTGTGGTTATC 120

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QY 41 PheLeuAlaIaSerPheValGlyAsnIleValIleuValIleuGlnArgLysPro 60
DB 121 TTCCTCGCGCCCTTTCGTGCGCAACATAGTGTGCGCTAGTGTGCGCGCAAGCCG 180
QY 61 GlnIleuGlnValThrAsnArgPheIlePheAsnIleuValThrAspLeuGln 80
DB 181 CAGCTCTGAGGTGACCAACCGTTTATCTTTAACCTCTCGTCAACCGACTGCGCAG 240
QY 81 IleSerIleValIaIaProTTPValIaIaThrSerValProIleuPheTTPProIleAsn 100
DB 241 ATTTCTGCTGCGCCCTGCGGTGGTGGCCACTGTGCTCTCTTCTGCGCCCTCAAC 300
QY 101 SerHisPheCysThrAlaIleuValSerIleuThrHisIleuPheAlaPheAlaSerValAsn 120
DB 301 AGCCACTTCTGCACGCGCCCTGTTAGCTACCCACCTGTTGCGCTTCCGCAACGTCAC 360
QY 121 ThrIleValIleuValSerValAspArgTyrLeuSerIleIleHisProIleuSerTyrPro 140
DB 361 ACCATTGTGCTGTGTGACGTGATCGCTACTTCTCATCATCCACCTCTCTCTACCCG 420
QY 141 SerIleMetThrGlnArgArgGlyTyrIleuIleuTyrGlyThrTrpIleValAlaIle 160
DB 421 TCCAGATGACCCAGCGCGCGGTACCTGCTCTCATGGCACTGGATTTGGCCATC 480
QY 161 LeuGlnSerThrProProIleuTyrGlyTyrGlyGlnAlaIaPheAspGluArgAsnAla 180
DB 481 CTGCAGACGACTCTCCACTCTACGCGTGGCGCCAGCTGCTTGTATGAGCCCAATGCT 540
QY 181 LeuCysSerMetIleTTPGlyAlaSerProSerTyrThrIleuSerValIaIaSerPhe 200
DB 541 CTCTGCTCATGATGATCGGGGGGCGACGCCAGCTACATCTCTCAGCGTGTGCTCTTC 600
QY 201 IleValIleProIleuIleValMetIleAlaCysTyrSerValIaIaPheCysAlaIaArg 220
DB 601 ATCGTATTCCTCATGTATGATGATGCTGCTACTCCGTGTGTTCTGTGAGCCCGG 660
QY 221 ArgGlnHisAlaIleuIleuTyrAsnValIyAsnValIyAsnArgHisSerLeuGlnValArgValIyAsp 240
DB 661 AGCGACACATGCTCTGCTGTACAAATGTCAGAGACACACAGCTGGAAAGTCAGATCAAGAGAC 720
QY 241 CysValGluAsnGluAspGluGluGlyAlaGluIleValIyAsnGluIleuPheGlnAspGluSer 260
DB 721 TGTGTGAGAAATGAGATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 780
QY 261 GluPheArgArgGlnHisGluGluGlyIleValIyAlaIyAsnGluIyArgMetGluAlaIyAs 280
DB 781 GAGTTTCGCGCCAGCATGAAAGTGAAGTCAAGGCCAAGAGAGAGAGAGAGAGAGAGAG 840
QY 281 AspGlySerIleuIyAsnAlaIyAsnGluIySerThrGlyThrSerGluSerSerValIaIaIa 300
DB 841 GACGCGACCTGAAAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCC 900
QY 301 ArgGlySerGluGluIyAlaIyAsnGluIySerSerThrValIaIaSerAspGlySerMetGluGly 320
DB 901 AGGGGCGAGCGAGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 960
QY 321 LysGluGlySerThrIyAsnValIyGluIleuAsnSerMetIyAlaIyAspIyAsnGlyArgThrGlu 340
DB 961 AAGGAAGGAGAGAGCAAAAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 341 ValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
DB 1021 GTCAACCAAGTCAGCATTTGAGTGGGTGAAGATGACATGAGAGTTTGGTGAAGAGCATC 1080
QY 361 AsnPheSerGluAspAspValIyGluAlaValAsnIleProGluSerIleuProProSerArg 380
DB 1081 AATTTCAGTGAGATGAGTGCAGAGCGATGAACATCCCGAGAGAGCTCCCAACCAAGTCGT 1140
QY 381 ArgAsnSerAsnSerAsnProProIleuProArgCysTyrGlnCysIyAsnAlaIyValIy 400
DB 1141 CGTAACAGCAAGCAACCTCTCTGCGCAAGGTGTCTACAGTCAAGCAAAAGCTGCTAAAGTG 1200

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QY 401 IlePheIleIlePheSerTyrValIleuSerIleuGlyProTyrCysPheIleuAlaVal 420
DB 1201 AFTTCATCATCATTTTCTCTATGATGCTATCCCTGCGGCCCTTACTGCTTTTATGAGATC 1260
QY 421 LeuAlaValTTPValAspValGluThrGlnValProGlnTTPValIleThrIleIleIle 440
DB 1261 CTGGCCGTGTGGGTGATGTGCAAAACCCAGGATCCCACTGGGTGATCAACATATCATC 1320
QY 441 TrpLeuPhePheIleuGlnCysIleHisProTyrValTyrGlyTyrMetHisLysThr 460
DB 1321 TGCTTTTCTTCTCTGAGAGTGTGATCATCAACCCCTATGTCTATGCTACATGCAAGAGCC 1380
QY 461 IleLysLysGluIleGlnAspMetIleuLysPhePheCysLysGluLysProLys 480
DB 1381 ATTAAGAGGAATCCAGAGCATGCTGAAGAGAGTTCTTCTGCAAGGAAAAGCCCCGAAA 1440
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyIleValIPro 500
DB 1441 GAAGATAGCCACCCCAACCTGCGCGAGACAGAGGGTGGACTGAAGCAAGATTTGCCCT 1500
QY 501 SerTyrAspSerAlaThrPhePro 508
DB 1501 TCTTACGATTTGCTACTTTTCT 1524

```

RESULT 14

AA507942 ID AA507942 standard; cDNA; 1527 BP.

AA507942; AC

23-OCT-2001 (first entry) XX

Human cDNA encoding G-protein coupled receptor, hrup15. DE

Human; G-protein coupled receptor; GPCR; hrup15; agonist; KW

inverse agonist; lung cancer; ss. XX

Homo sapiens. OS

Key Location/Qualifiers FH

CDS 1..1527 FT

FT /*tag= a /product= "hrup15" XX

MO200136471-A2. PN

16-NOV-2000; 2000WC-US031509. PF

17-NOV-1999; 99US-0166088P. PR

17-NOV-1999; 99US-0166099P. PR

23-DEC-1999; 99US-0171900P. PR

23-DEC-1999; 99US-0171901P. PR

11-FEB-2000; 2000US-0181749P. PR

14-MAR-2000; 2000US-0189258P. PR

14-MAR-2000; 2000US-0189259P. PR

10-APR-2000; 2000US-0195898P. PR

10-APR-2000; 2000US-0195899P. PR

28-APR-2000; 2000US-0200419P. PR

12-MAY-2000; 2000US-0203630P. PR

12-JUN-2000; 2000US-0210741P. PR

12-JUN-2000; 2000US-0210982P. PR

21-AUG-2000; 2000US-0226760P. PR

26-SEP-2000; 2000US-0235418P. PR

20-OCT-2000; 2000US-0242332P. PR

20-OCT-2000; 2000US-0242343P. PR

24-OCT-2000; 2000US-0243019P. XX

PA (AREN-) ARENA PHARM INC.

XX Chen R, Dang HT, Lowitz KP;

XX WPI: 2001-355616/37.

DR P-PSDB: AA004369.

XX Endogenous and non-endogenous versions of human G-protein coupled
PT receptors for direct identification of candidate compounds as agonists,
PT inverse agonists or partial agonists for use as therapeutic agents.

XX Claim 31, Page 102; 160pp; English.

XX The sequence encodes a human G-protein coupled receptor (GPCR), hRUP15.
CC The endogenous and non-endogenous, constitutively activated versions of
CC human G-protein coupled receptors (GPCR), are useful for direct
CC identification of candidate compounds as receptor agonists, inverse
CC agonists or partial agonists having applicability as therapeutic agents
CC for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous
CC version of human GPCRs are also utilized in research settings and in
CC vitro and in vivo system, incorporating GPCRs can be utilized to
CC elucidate and understand the roles these receptors play in the human
CC condition, both normal and diseased

XX Sequence 1527 BP; 347 A; 439 C; 420 G; 321 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,78e-243	Length:	1527
Score:	2641.00	Matches:	507
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.80%	Mismatches:	0
Query Match:	99.89%	Indels:	0
	5	Gaps:	0

US-10-712-615-2 (1-508) x AAS07942 (1-1527)

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DB	1	ATGAGCTCCACCTGCACCAACAGCAGCGCGAGATTAACAGACGACGATGCCCC	60
QY	21	LeuSerIleMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle	40
DB	61	CTCTCCAAATGCGCATTCAGCCTGGCCACGGGATATCGGCTCAACCGTGGTTATC	120
QY	41	PheLeuAlaIleSerPheValGlyAsnIleValLeuAlaLeuValIleArgIlePro	60
DB	121	TTCCTGGCGGCTCTTTCGTGGCAACATAGTGTGGCGCTAGTGTGAGGCGAAGCGG	180
QY	61	GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuGln	80
DB	181	CAGCTGCTGCAGGTGACCAACCGTTTATCTTAACTCTCTGTCACCGACTGTCGACG	240
QY	81	IleSerLeuValAlaProThrValValAlaThrSerValProLeuPheThrProLeuAsn	100
DB	241	ATTGCTCTGTGGCCCCCTGGGTGGTGCCACTCTGTCTCTTCTTGGCCCCCTCAAC	300
QY	101	SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn	120
DB	301	AGCATTCTGCACGGCCCTGTTAGCTCACCCACCTTGGCCCTTCCGACGCGCAAC	360
QY	121	ThrIleValLeuValSerValAspArgIleLeuSerIleIleHisProLeuSerTyPro	140
DB	361	ACCATTGTCTGTGTGTCAGTGCCTACTTGTCCATCATCACCTCTCTCTCAACCGG	420
QY	141	SerIleMetThrGlnArgArgIleTyIleLeuLeuLeuTyIleThrTrpIleValAlaIle	160
DB	421	TCCAAAGATGACCCAGGCGCGGTTACCTGCTCTCTATAGGACCTGGATTGTGGCATC	480
QY	161	LeuGlnSerThrProProLeuTyArgIleTyPglGlnAlaAlaPheAspGluArgAsnAla	180
DB	481	CTGCAGAGACTCTCTCACTTAAGGCTGGGGCGAGGCTCTTTGATATAGGCAATGCT	540
QY	181	LeuCysSerMetIleTrpGlyAlaSerProSerTyThrIleLeuSerValIleSerPhe	200

DB	541	CTGTCTCCATGATCTGGGGGCGCCAGCCAGCTACACTATTCTCAGGTGTCTTC	600
QY	201	IleValIleProLeuIleValMetIleAlaCysTyIleSerValIlePheCysAlaIleArg	220
DB	601	ATCGTCAATTCACATGATGTGATGATTCCTGCTACTCTCCGTGTCTTCTGTGACCGG	660
QY	221	ArgGlnHisAlaLeuLeuTyIleAsnValIleAspArgHisSerLeuGlnValArgValIleAsp	240
DB	661	AGGCGACATGCTCTGCTGTACATGTCAATGTCAAGACACACACTTGGAAGTCCGAGTCAAGAC	720
QY	241	CysValGlyAsnGlnAspGlnGluGlyValGluValGlyValGluValPheGlnAspGlnSer	260
DB	721	TGTGTGAGAAATGAGATGAAGAGGAGCAGAGAGAGAGAGAGATTCAGGATGAGAT	780
QY	261	GluPheAspArgGlnHisGlyGlyValIleValIleValIleValIleValIleValIleVal	280
DB	781	GAGTTTCCCGCCGACATGAAAGTGAAGTCAAGGCCAAGAGGAGGAGAGAGAGAGAGAG	840
QY	281	AspGlySerLeuValIleGlyGlyIleSerThrGlyThrSerGluSerSerValGluAla	300
DB	841	GACGGCAGCTGAAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCC	900
QY	301	ArgGlySerGlnGluValArgGluSerSerThrValAlaSerAspGlySerMetClnGly	320
DB	901	AGGGGACCGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGT	960
QY	321	IleGlyGlySerThrIleValGluGluAsnSerMetCysAlaAspGlyValArgThrGlu	340
DB	961	AAGAGAGCAGACCAAAAGTTGAGAGAAACAGCATGAAGGAGAGAGAGAGAGAGAGAG	1020
QY	341	ValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle	360
DB	1021	GTCACCAAGTGCAGCATTCGTTGGGTGAAGTACATGATGTTGTGAAGACAGCATC	1080
QY	361	AsnPheSerGluAspAspValGluAlaValAsnIleProGlnSerLeuProProSerArg	380
DB	1081	AATTTCACTGAGAGAGAGTGAAGGAGTGAACATCCCGAGAGAGCTCCACCGAGTGT	1140
QY	381	ArgAsnSerAsnSerAsnProProLeuProArgCysTyIleGlnCysAlaIleAlaIleVal	400
DB	1141	CGTAACAGACAGACAGACCTCTCTGCGCAGGTCTACAGTGCAGAGCTCTAAAGTG	1200
QY	401	IlePheIleIleIlePheSerTyValLeuSerLeuGlyProTyIleCysPheLeuAlaVal	420
DB	1201	ATCTTCATCATCTTTCTCTCATGTGCTATCCCTGGGGCCCTACTGCTTTTACAGATC	1260
QY	421	LeuAlaValTrpValAspValGluThrGlnValProGlnTrpValIleThrIleIleIle	440
DB	1261	CTGGCCGCTGTGGTGAATGTGAAACCCAGGTACCCAGTGGTGAATACCACTAATATCATC	1320
QY	441	TrpLeuPhePheLeuGlnCysCysIleHisProTyIleValTyIleGlyIleMetHisIleThr	460
DB	1321	TGGCTTTCTTCTCTCAAGTGTGATCCACCCCTATGTCTATGCTTAACATGACAAAGCC	1380
QY	461	IleIleValGlyIleGlnAspMetLeuIleValIleValIleValIleValIleValIleVal	480
DB	1381	ATTAAAGAAAGAAATCCAGAGACATGCTGAAGAAAGTTCTTCTGAAGAAAGAAAGCCGAAA	1440
QY	481	GluAspSerHisProAspLeuProGlyIleThrGlyGlyIleThrGlyGlyIleValIlePro	500
DB	1441	GAAAGTACCAACCCAGACTGCGGAGAACAGAGGTGTGAGATGAAGGAGCAAGATTGTCCCT	1500
QY	501	SerTyIleAspSerAlaThrPhePro	508
DB	1501	TCTTAGATTCGTACTTTTCTT	1524

RESULT 15

AAS18899
ID AAS18899 standard, cDNA, 1527 BP.

XX AAS18899;
AC
XX

DT 26-MAR-2002 (first entry)
XX Human cDNA encoding alpha1a adrenenergic receptor-like GPCR.
XX
XX
XX Human; ss: alpha1a adrenenergic receptor; G protein-coupled receptor; GPCR;
XX peripheral nervous system disease; central nervous system disease;
XX urinary incontinence; benign prostatic hypertrophy; infection;
XX HIV infection; human immunodeficiency virus; pain; cancer; anorexia;
XX bulimia; asthma; Parkinson's disease; obesity; acute heart failure;
XX hypotension; hypertension; urinary retention; osteoporosis;
XX angina pectoris; myocardial infarction; ulcer; allergy; psychosis;
XX neurological disorder; anxiety; schizophrenia; manic depression;
XX delirium; dementia; severe mental retardation; dyskinesia;
XX Huntington's disease; Tourette's syndrome.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX CDS 1..1527
XX /tag= a
XX /product= "Alpha1a adrenenergic receptor"
XX
XX MO200189126-A2.
XX
XX 22-NOV-2001.
XX
XX 11-MAY-2001; 2001MO-EP005383.
XX
XX 15-MAY-2000; 2000US-0204145P.
XX 04-DEC-2000; 2000US-0250505P.
XX
XX (FARB) BAYER AG.
XX
XX Ramakrishnan S;
XX
XX MPI; 2002-106124/14.
XX P-PSDB; AAU011764.
XX
XX New polynucleotide, useful for treating pain, cancer, Parkinson's
XX diseases, obesity, hypertension, asthma, schizophrenia, encodes an alpha
XX (1a) adrenenergic receptor-like G-protein coupled receptor (GPCR).
XX
XX Claim 1; Fig 2; 123pp; English.
XX
XX The invention relates to an isolated polynucleotide encoding an alpha1a
XX adrenenergic receptor-like G-protein coupled receptor (GPCR) polypeptide,
XX the encoded polypeptide, fragments, derivatives and allelic variants.
XX Also include are an expression vector comprising the polynucleotide, a
XX host cell containing the vector, screening for therapeutic agents which
XX decrease or increase the activity of the receptor by binding a test agent
XX to the protein and determining whether the activity is decreased or
XX increased. A modulator of the receptor is useful for treating alpha1a
XX adrenenergic receptor-like GPCR disorder such as peripheral or central
XX nervous system disease, urinary incontinence or benign prostatic
XX hypertrophy. The receptor, polynucleotide or modulator is useful for
XX treating disorders such as bacterial, fungal, protozoan, and viral
XX infections, particularly those caused by HIV (human immunodeficiency
XX virus), pain, cancer, anorexia, bulimia, asthma, Parkinson's diseases,
XX obesity, acute heart failure, hypotension, hypertension, urinary
XX retention, osteoporosis, angina pectoris, myocardial infarction, ulcer,
XX allergy, benign prostatic hypertrophy, and psychotic and neurological
XX disorders, including anxiety, schizophrenia, manic depression, delirium,
XX dementia, severe mental retardation, and dyskinesias, such as
XX Huntington's disease and Tourette's syndrome. The polynucleotide is
XX useful in diagnostic assays for detecting diseases and abnormalities or
XX susceptibility to disease and abnormalities related to the presence of
XX mutations in the gene. The protein is useful to identify test compounds
XX which may act as agonists or antagonists, and for raising antibodies
XX which can block the receptor and effectively prevent ligand binding. The
XX present sequence is the cDNA encoding the alpha1a adrenenergic receptor-
XX like GPCR
XX
XX Sequence 1527 BP; 347 A; 439 C; 420 G; 321 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,786-243 Length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: Gaps: 0
US-10-712-615-2 (1-508) x AAS18899 (1-1527)
QY 1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
DB 1 ATGACCTCCACCTGCACCAACAGCAGCGCCGAGAGTAACAGCAGCAGCTGCATGCC 60
QY 21 LeuSerIleMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuVal111e 40
DB 61 CTCTCCAAATGCGCCATCAGCCCTGGGCCCGCATCATCTCCGTCACCGCTGCTTATC 120
QY 41 PheLeuAlaIleSerPheValGlyAsnIleValIleAlaLeuValLeuGlnArgIlePro 60
DB 121 TTCCTGCGCGCTCTTCTTCTGCGCAACATATGCTGCGCTTGTGTCAGCGCAGCGG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuGln 80
DB 181 CAGCTGCTCAGGTGACCAACCGTTTATCTTTAACTCTCCTCGTCAACCGCTGTCGAG 240
QY 81 IleSerLeuValAlaProTTPValValAlaIleThrSerValProLeuPheTrpProLeuAn 100
DB 241 ATTTGCTGTGTGGCCCCCTGGGTGGTGGCCACTGTGCTCTCTTCTGGCCCCCTCAAC 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisIlePheAlaPheAlaSerVal1aAn 120
DB 301 AGCCACTTCTGCACGCGCTTGTACCTTACCTCACCTCTGTGCTTGCCTTGCACGCTCAAC 360
QY 121 ThrIleValIleuValSerValAspArgIleuSerIleIleHisProLeuSerIlePro 140
DB 361 ACCATTGCTGTGGTGCATGTGATGCTTACCTTGTCTCATCATCACCTCTCTCTACCGG 420
QY 141 SerIleMetThrGlnArgArgIleuLeuLeuLeuIleuValIleValIleVal1a11e 160
DB 421 TCCAAATGACCAAGCGCGCGGTACCTGCTCTTACGAGCAGCTGGATTTGTGGCCATC 480
QY 161 LeuGlnSerThrProProLeuTrpGlyTrpGlyGlnAlaIlePheAspGluArgAsn1a 180
DB 481 CTGCAGAGACTCTCTCACTTACGCTGCGGCGCAGGCTTGTGATAGCGCAATGCT 540
QY 181 IleuCysSerMetIleTrpGlyIleAspProSerIleThrIleLeuSerValIleSerPhe 200
DB 541 CTCTGCTCATGATCTGGGGGGCGCAGCCCACTACATATTCTCAGCGTGGTCTTC 600
QY 201 IleValIleProLeuIleValMetIleAlaCysIleSerValIlePheCysAla1a1aArg 220
DB 601 ATGTCATTCCACTGATTTGTCATGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
QY 221 ArgGlnHisAlaLeuLeuTrpAsnValIleAspHisSerLeuGluValArgValIleAsp 240
DB 661 AGCCAGCATGCTCTGTGTGACATGTCAGAGACACAGCTTGAAGTGGAGTCAAGAC 720
QY 241 CysValGluAsnGluAspGluGluGluValIleGluIleValIleValIleValIleVal 260
DB 721 TGTGTGAGAAATGAGAGTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTAC 780
QY 261 GluPheAsnArgGlnHisGluGluValIleValIleValIleValIleValIleValIle 280
DB 781 GAGTTTGGCGCGCACCATCAAGTGAAGTCAAGGCGCAAGGAGGAGGAGGAGGAGGAG 840
QY 281 AspGlySerLeuValAlaValGluIleSerThrGlyThrSerValIleSerValGlu1a 300
DB 841 GACGGCAGCTTAAGGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 301 ArgGlySerGluGluValArgGluSerThrValAlaSerAspGlySerMetGluIle 320

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Db 901 AGGGCAGCGAGAGGTGAGAGAGCAGCAGCGTGCCAGCGACGCGACATGAGGGT 960
Qy 321 LysGluGlySerThrLysValGluLysSerMetLysAlaAspLysGlyArgThrGlu 340
Db 961 AAGGAAGGACAGCAAGATTGAGGAAACAGCATGAAGGACAGAGGTGCGACAGAG 1020
Qy 341 ValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
Db 1021 GTCAACCGAGTGACATTGACTTGGGTGAAATGACATGAGAGTTGGTGAAACGACATC 1080
Qy 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProPheSerArg 380
Db 1081 AATTTCAGTGAAGATGACGTCCAGGACAGATCCGAGAGCCTCCACCCAGTCGT 1140
Qy 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysLysAlaLysVal 400
Db 1141 CGTACACAGCAACGACCCCTCTGCGCCAGGTGCTACAGTGCACAAAGCTCTAAAGTG 1200
Qy 401 IlePheIleIleIlePheSerTyrValLeuSerLeuGlyProTyrCysPheLeuAlaVal 420
Db 1201 ATCTTCATCATCATTTTCTCTATGTGTATCCTGCGGGCCCTACTGCTTTTTCAGAGTC 1260
Qy 421 LeuAlaValTyrPValAspValGluThrGlnValProGluTyrPValIleThrIleIleIle 440
Db 1261 CTGGCCGTGTGGGTGATGTCCAAACCCAGTACCAGTGGGTGATCACCAATATCATC 1320
Qy 441 TrpLeuPhePheLeuGlnCysCysIleHisProTyrValTyrGlyTyrMetHisLysThr 460
Db 1321 TGGCTTTTCTTCTCTGACGTGCAATCCACCCTATGTCTATGGCTACATGCACAAAGACC 1380
Qy 461 IleLysLysGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysProPheLys 480
Db 1381 ATTAAAGAGGAATCCAGGACATGCTGAAGAAATTCTTCTGCAGAGAAAAGCCCCGAAA 1440
Qy 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyLysIleValPro 500
Db 1441 GAAATAGCCACCCAGACCTGCCCCGGAACAGAGGTGGAGCTGAAGGCAAGATTGTCCCT 1500
Qy 501 SerTyrAspSerAlaThrPhePro 508
Db 1501 TCCTACGATTCTGCTACTTTTCTT 1524
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Search completed: December 10, 2005, 05:16:32
Job time : 634 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:31:47 ; Search time 133.35 seconds
(without alignments)
1591.731 Million cell updates/sec

Title: US-10-712-615-2

Perfect score: 2644
Sequence: 1 MTSTCTNSTRESNSHTCMP.....GTGGTGKIVPSYDSTAFP 508Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

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- 2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
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- 6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2644	100.0	508	3	US-09-992-238-2
2	2644	100.0	508	4	US-10-993-983-9
3	2644	100.0	508	4	US-10-712-615-2
4	2644	100.0	746	5	US-10-505-486-131
5	2641	99.9	508	3	US-09-791-932-112
6	2641	99.9	508	4	US-10-094-417-6
7	2641	99.9	508	4	US-10-345-332-2
8	2641	99.9	508	4	US-10-088-726-21
9	2641	99.9	508	4	US-10-321-807-16
10	2641	99.9	508	4	US-10-276-243-3
11	2641	99.9	508	4	US-10-436-715-14
12	2641	99.9	508	4	US-10-343-650A-90
13	2641	99.9	508	4	US-10-321-807-16
14	2641	99.9	508	4	US-10-314-048A-16
15	2641	99.9	508	5	US-10-897-815-16
16	2641	99.9	508	5	US-10-930-662-16
17	2641	99.9	508	6	US-11-086-846-6
18	2641	99.9	604	4	US-10-017-161-1088
19	2641	99.9	926	4	US-10-321-807-104
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23	2641	99.9	926	5	US-10-930-662-104
24	2637	99.7	508	4	US-10-225-567A-583
25	2637	99.7	508	4	US-10-608-990-2
26	2636	99.7	508	4	US-10-321-807-92
27	2636	99.7	508	4	US-10-321-807-92

28	2636	99.7	508	4	US-10-314-048A-92	Sequence 92, Appl
29	2636	99.7	508	5	US-10-897-815-92	Sequence 92, Appl
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31	2628	99.4	508	3	US-09-992-238-49	Sequence 49, Appl
32	2628	99.4	508	4	US-10-712-615-49	Sequence 49, Appl
33	2619	99.1	508	3	US-09-971-269-2	Sequence 2, Appl1
34	2518	95.2	485	4	US-10-219-834-21	Sequence 21, Appl
35	2518	95.2	485	4	US-10-292-798-926	Sequence 926, Appl
36	2518	95.2	485	4	US-10-311-671-12	Sequence 12, Appl
37	2518	95.2	485	6	US-11-100-583-12	Sequence 12, Appl
38	2258	85.4	448	3	US-09-992-238-43	Sequence 43, Appl
39	2258	85.4	448	3	US-10-712-615-43	Sequence 43, Appl
40	2257	85.4	448	3	US-09-992-238-41	Sequence 41, Appl
41	2257	85.4	448	3	US-09-992-238-42	Sequence 42, Appl
42	2257	85.4	448	4	US-10-712-615-41	Sequence 41, Appl
43	2257	85.4	448	4	US-10-712-615-42	Sequence 42, Appl
44	2021	76.4	398	3	US-09-841-741-2	Sequence 2, Appl1
45	2021	76.4	398	4	US-10-343-332-5	Sequence 5, Appl1

ALIGNMENTS

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RESULT 1
US-09-992-238-2
; Sequence 2, Application US/09992238
; Publication No. US2003005444A1
GENERAL INFORMATION:
; APPLICANT: BATTAGLINO, PETER
; APPLICANT: FEDER, JOHN N
; APPLICANT: MINTIER, GABE
; APPLICANT: NELSON, THOMAS C
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: WESTPHAL, RYAN
; APPLICANT: CACACE, ANGELA
; APPLICANT: BARBER, DONALD R
; APPLICANT: HAWKEN, LAUREN
; APPLICANT: KORACKER, MICHAEL G
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMYG,
; TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN
; FILE REFERENCE: D0047ND
; CURRENT APPLICATION NUMBER: US/09/992,238
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/317166
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/308285
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/268581
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/248285
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 508
; ORGANISM: Homo sapiens
US-09-992-238-2
Query Match      100.0%; Score 2644; DB 3; Length 508;
Best Local Similarity 100.0%; Pred. No. 3e-182;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1  MTSTCTNSTRESNSHTCMPLSKMTISLAHGIRSTVVIFFLAASFVGVIVATLVQRKP 60
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DB      1  MTSTCTNSTRESNSHTCMPLSKMPISLAHGIRSTVVIFFLAASFVGVIVATLVQRKP 60
QY      61  QLLQVTRRFIPULVTDLQISLVAPMVVATSVPLFWPLNSHFTALVSLTHLPAFASVN 120
      |||||||
DB      61  QLLQVTRRFIPULVTDLQISLVAPMVVATSVPLFWPLNSHFTALVSLTHLPAFASVN 120
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QY     121  TIVLVSVDRYLSIIPLSYPSIMTORRGVLLYGTWIVAIIGSTPLPYGMGQAADFERN 180
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Db 121 TIVLVSVDRYLSIIHPLSPSKMTQRGVLIIYGTWIVAILOSTPPLVYGMQAAFDERNA 180
Qy 181 LCSMWGASPSYTIISVSVFIVIPLIWIMACYSVFCAARQHALLVNKRSLSEVRVD 240
Db 181 LCSMWGASPSYTIISVSVFIVIPLIWIMACYSVFCAARQHALLVNKRSLSEVRVD 240
Qy 241 CVENDEBGAKEKEEFODESEFRROHEGEVAKAEGMEAKDGLAKEGSTGTSESSVEA 300
Db 241 CVENDEBGAKEKEEFODESEFRROHEGEVAKAEGMEAKDGLAKEGSTGTSESSVEA 300
Qy 301 RGESEVRRESSSTVASGSMGEGSTKVEENSMKADKGRTEVNQCSIDIGEDDMEFGEDI 360
Db 301 RGESEVRRESSSTVASGSMGEGSTKVEENSMKADKGRTEVNQCSIDIGEDDMEFGEDI 360
Qy 361 NFESEDDVAVNIPESLPSPRRNSNPNPLPCYCKCAKAVFIIFSVYLSLGPYCFILAV 420
Db 361 NFESEDDVAVNIPESLPSPRRNSNPNPLPCYCKCAKAVFIIFSVYLSLGPYCFILAV 420
Qy 421 LAVWVDETQVPOWVITIIIMLFLOCCIHPPYVGYMKTIKKEIQDMLKKFCEKEPPK 480
Db 421 LAVWVDETQVPOWVITIIIMLFLOCCIHPPYVGYMKTIKKEIQDMLKKFCEKEPPK 480
Qy 481 EDSHBDLPGTGTEGTEGKIIVPSYDSATFP 508
Db 481 EDSHBDLPGTGTEGTEGKIIVPSYDSATFP 508

RESULT 2

US-10-293-983-9

; Sequence 9, Application US/10293983
; Publication No. US20030149998A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Blatcher, Maria

; APPLICANT: Paulsen, Janet

; APPLICANT: Bates, Brian G

; TITLE OF INVENTION: Genes Encoding G Protein Coupled Receptors and Uses Therefor

; FILE REFERENCE: AM100476

; CURRENT APPLICATION NUMBER: US/10/293,983

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 508

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-293-983-9

Query Match 100.0%; Score 2644; DB 4; Length 508;

Best Local Similarity 100.0%; Pred. No. 3e-182;

Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVIVIFLAASFVGNIVLALVLOKRP 60
Db 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVIVIFLAASFVGNIVLALVLOKRP 60
Qy 61 QLLQVTFNFIENLVTDLQISLVAPWVAVTSVPLFMPLNHFCTALVSLTHLFAFASVN 120
Db 61 QLLQVTFNFIENLVTDLQISLVAPWVAVTSVPLFMPLNHFCTALVSLTHLFAFASVN 120
Qy 121 TIVLVSVDRYLSIIHPLSPSKMTQRGVLIIYGTWIVAILOSTPPLVYGMQAAFDERNA 180
Db 121 TIVLVSVDRYLSIIHPLSPSKMTQRGVLIIYGTWIVAILOSTPPLVYGMQAAFDERNA 180
Qy 181 LCSMWGASPSYTIISVSVFIVIPLIWIMACYSVFCAARQHALLVNKRSLSEVRVD 240
Db 181 LCSMWGASPSYTIISVSVFIVIPLIWIMACYSVFCAARQHALLVNKRSLSEVRVD 240
Qy 241 CVENDEBGAKEKEEFODESEFRROHEGEVAKAEGMEAKDGLAKEGSTGTSESSVEA 300
Db 241 CVENDEBGAKEKEEFODESEFRROHEGEVAKAEGMEAKDGLAKEGSTGTSESSVEA 300
Qy 301 RGESEVRRESSSTVASGSMGEGSTKVEENSMKADKGRTEVNQCSIDIGEDDMEFGEDI 360
Db 301 RGESEVRRESSSTVASGSMGEGSTKVEENSMKADKGRTEVNQCSIDIGEDDMEFGEDI 360

Db 301 RGESEVRRESSSTVASGSMGEGSTKVEENSMKADKGRTEVNQCSIDIGEDDMEFGEDI 360
Qy 361 NFESEDDVAVNIPESLPSPRRNSNPNPLPCYCKCAKAVFIIFSVYLSLGPYCFILAV 420
Db 361 NFESEDDVAVNIPESLPSPRRNSNPNPLPCYCKCAKAVFIIFSVYLSLGPYCFILAV 420
Qy 421 LAVWVDETQVPOWVITIIIMLFLOCCIHPPYVGYMKTIKKEIQDMLKKFCEKEPPK 480
Db 421 LAVWVDETQVPOWVITIIIMLFLOCCIHPPYVGYMKTIKKEIQDMLKKFCEKEPPK 480
Qy 481 EDSHBDLPGTGTEGTEGKIIVPSYDSATFP 508
Db 481 EDSHBDLPGTGTEGTEGKIIVPSYDSATFP 508

RESULT 3

US-10-712-615-2

; Sequence 2, Application US/10712615

; Publication No. US20040214317A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMRY8, EXPRESSED

; FILE REFERENCE: D0047A-CIP

; CURRENT APPLICATION NUMBER: US/10/712,615

; PRIOR FILING DATE: 2003-11-13

; PRIOR APPLICATION NUMBER: U.S. 09/992,238

; PRIOR FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: U.S. 60/248,285

; PRIOR FILING DATE: 2000-11-14

; PRIOR APPLICATION NUMBER: U.S. 60/268,581

; PRIOR FILING DATE: 2001-02-14

; PRIOR APPLICATION NUMBER: U.S. 60/308,285

; PRIOR FILING DATE: 2001-07-27

; PRIOR APPLICATION NUMBER: U.S. 60/317,166

; PRIOR FILING DATE: 2001-09-04

; NUMBER OF SEQ ID NOS: 134

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 508

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-712-615-2

Query Match 100.0%; Score 2644; DB 4; Length 508;

Best Local Similarity 100.0%; Pred. No. 3e-182;

Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVIVIFLAASFVGNIVLALVLOKRP 60
Db 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVIVIFLAASFVGNIVLALVLOKRP 60
Qy 61 QLLQVTFNFIENLVTDLQISLVAPWVAVTSVPLFMPLNHFCTALVSLTHLFAFASVN 120
Db 61 QLLQVTFNFIENLVTDLQISLVAPWVAVTSVPLFMPLNHFCTALVSLTHLFAFASVN 120
Qy 121 TIVLVSVDRYLSIIHPLSPSKMTQRGVLIIYGTWIVAILOSTPPLVYGMQAAFDERNA 180
Db 121 TIVLVSVDRYLSIIHPLSPSKMTQRGVLIIYGTWIVAILOSTPPLVYGMQAAFDERNA 180
Qy 181 LCSMWGASPSYTIISVSVFIVIPLIWIMACYSVFCAARQHALLVNKRSLSEVRVD 240
Db 181 LCSMWGASPSYTIISVSVFIVIPLIWIMACYSVFCAARQHALLVNKRSLSEVRVD 240
Qy 241 CVENDEBGAKEKEEFODESEFRROHEGEVAKAEGMEAKDGLAKEGSTGTSESSVEA 300
Db 241 CVENDEBGAKEKEEFODESEFRROHEGEVAKAEGMEAKDGLAKEGSTGTSESSVEA 300
Qy 301 RGESEVRRESSSTVASGSMGEGSTKVEENSMKADKGRTEVNQCSIDIGEDDMEFGEDI 360
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Qy 361 NSESDVEAVNIPESIPSRNSNSNPPLPCYQCAAAVPIIIFSYLISGPIYCFNAV 420
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Db 361 NSESDVEAVNIPESIPSRNSNSNPPLPCYQCAAAVPIIIFSYLISGPIYCFNAV 420
Qy 421 LAWVWDEVEQVQWVTTIIIMLFLOCCIHPIYVGYMHTTIKEIODMLKFFCECKEPK 480
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Db 421 LAWVWDEVEQVQWVTTIIIMLFLOCCIHPIYVGYMHTTIKEIODMLKFFCECKEPK 480
Qy 481 EDSHPDLPETEGTEGKIVPSYDSATFP 508
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Db 481 EDSHPDLPETEGTEGKIVPSYDSATFP 508

RESULT 4
US-10-505-486-131
; Sequence 131, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Determination of a ligand
; FILE REFERENCE: P03-0006PCT
; CURRENT APPLICATION NUMBER: US/10/505,486
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: JP 2002-45728
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: JP 2002-298237
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 131
; LENGTH: 746
; TYPE: PRT
; ORGANISM: Human
US-10-505-486-131

Query Match 100.0%; Score 2644; DB 5; Length 746;
Best Local Similarity 100.0%; Pred. No. 4,9e-182;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSTCTNSTRESNSSHCTCPLSKMPSISLAHGIIIRSTVVIPIAASFVGNIVLALVLRKP 60
Qy 61 QLLQVYTNRFIFNLVLTDLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTHLFAFASVN 120
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Db 61 QLLQVYTNRFIFNLVLTDLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTHLFAFASVN 120
Qy 121 TIVLVSVDRYLSIIHPLSYPSKMTQRGYLLLYGTWIVAILOSTPPLYGWMGAAPDERNA 180
| | | | |
Db 121 TIVLVSVDRYLSIIHPLSYPSKMTQRGYLLLYGTWIVAILOSTPPLYGWMGAAPDERNA 180
Qy 181 LCSMTWGSAPSTYIISVVSFIYIPLIVMIACYSVVFCAARRQHALINYNKRSLEVRVXD 240
| | | | |
Db 181 LCSMTWGSAPSTYIISVVSFIYIPLIVMIACYSVVFCAARRQHALINYNKRSLEVRVXD 240
Qy 241 CVENDEDEGAKEKEEFRODESEFRROHEGKVAKEGMEAKDGLKXKEGSTGTSSSSVVA 300
| | | | |
Db 241 CVENDEDEGAKEKEEFRODESEFRROHEGKVAKEGMEAKDGLKXKEGSTGTSSSSVVA 300
Qy 301 ROSEVEBRESSTVADSGMEKSGSTKVEENSMKADKGRTEVNAQSIDLGEDDMFEGEDI 360
| | | | |
Db 301 ROSEVEBRESSTVADSGMEKSGSTKVEENSMKADKGRTEVNAQSIDLGEDDMFEGEDI 360
Qy 361 NSESDVEAVNIPESIPSRNSNSNPPLPCYQCAAAVPIIIFSYLISGPIYCFNAV 420
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Db 361 NSESDVEAVNIPESIPSRNSNSNPPLPCYQCAAAVPIIIFSYLISGPIYCFNAV 420
Qy 421 LAWVWDEVEQVQWVTTIIIMLFLOCCIHPIYVGYMHTTIKEIODMLKFFCECKEPK 480
| | | | |
Db 421 LAWVWDEVEQVQWVTTIIIMLFLOCCIHPIYVGYMHTTIKEIODMLKFFCECKEPK 480
Qy 481 EDSHPDLPETEGTEGKIVPSYDSATFP 508
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Db 481 EDSHPDLPETEGTEGKIVPSYDSATFP 508
| | | | |

RESULT 5
US-09-791-932-112
; Sequence 112, Application US/09791932
; Publication No. US20030003451A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayles, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030003451A1el G Protein-Coupled Receptors Cross-Referen
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,980
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/186,810
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/188,064
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/186,457
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/213,861
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/194,344
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/218,337
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 112
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-932-112

Query Match 99.9%; Score 2641; DB 3; Length 508;
Best Local Similarity 99.8%; Pred. No. 5e-182;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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| | | | |
Db 1 MSTCTNSTRESNSSHCTCPLSKMPSISLAHGIIIRSTVVIPIAASFVGNIVLALVLRKP 60
Qy 61 QLLQVYTNRFIFNLVLTDLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTHLFAFASVN 120
| | | | |
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Qy 121 TIVLVSVDRYLSIIHPLSYPSKMTQRGYLLLYGTWIVAILOSTPPLYGWMGAAPDERNA 180
| | | | |

Db 121 TIVVSVDRYLSIIHPLSPSKMQRGVLIIYGTWIVAILQSTPPLVYGMGOAFAEDRNA 180
Qy 181 LCSMWGASPSYTIISVSVFIVIPLIIVMIACYSVVFCAARRQHALLVNKRHSLVRYKD 240
Db 181 LCSMWGASPSYTIISVSVFIVIPLIIVMIACYSVVFCAARRQHALLVNKRHSLVRYKD 240
Qy 241 CVENDEBGAKEKEEFODESEFRQHEGEVAKEGRMADKGRTEVNOCSIDLGEDMFEGBDDI 360
Db 241 CVENDEBGAKEKEEFODESEFRQHEGEVAKEGRMADKGRTEVNOCSIDLGEDMFEGBDDI 360
Qy 301 RGSSEVBSSTVADSGMEGEGSTKYBENSMDKGRTEVNOCSIDLGEDMFEGBDDI 360
Db 301 RGSSEVBSSTVADSGMEGEGSTKYBENSMDKGRTEVNOCSIDLGEDMFEGBDDI 360
Qy 361 NFSDEDDVAVNIPESLPPSRNSNSNPPLPRCYCKAAKVIIFIIIFSIVLSLGPYCLAV 420
Db 361 NFSDEDDVAVNIPESLPPSRNSNSNPPLPRCYCKAAKVIIFIIIFSIVLSLGPYCLAV 420
Qy 421 LAVWVDETQVQVWVITIIIMLFLOCCIHPIYVGYMKTIKKSIQDMLKKFCEKRPK 480
Db 421 LAVWVDETQVQVWVITIIIMLFLOCCIHPIYVGYMKTIKKSIQDMLKKFCEKRPK 480
Qy 481 EDSHDLPGTEGTEGKIIVPSYDSATFP 508
Db 481 EDSHDLPGTEGTEGKIIVPSYDSATFP 508

RESULT 6
US-10-094-417-6
; Sequence 6, Application US/10094417
; Publication No. US20030045685A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiayang
; APPLICANT: Chen, Jin-long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: NO. US20030045685A1e1 Receptors
; FILE REFERENCE: 016781-008100S
; CURRENT APPLICATION NUMBER: US/10/094,417
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/802,803
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 60/276,649
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR36
US-10-094-417-6

Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 5e-182;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTSTCTNSTRESNSHTCMPISKMPISLAHGIIIRSTVIVIFLAASFVGNITVALVLRKP 60
Db 1 MTSTCTNSTRESNSHTCMPISKMPISLAHGIIIRSTVIVIFLAASFVGNITVALVLRKP 60
Qy 61 QLLQVTRNFIFNLVTDLQISLVAPWVAVTSVPLFWPLNSHFTALVSLTHLPAFASVN 120
Db 61 QLLQVTRNFIFNLVTDLQISLVAPWVAVTSVPLFWPLNSHFTALVSLTHLPAFASVN 120
Qy 121 TIVVSVDRYLSIIHPLSPSKMQRGVLIIYGTWIVAILQSTPPLVYGMGOAFAEDRNA 180
Db 121 TIVVSVDRYLSIIHPLSPSKMQRGVLIIYGTWIVAILQSTPPLVYGMGOAFAEDRNA 180
Qy 181 LCSMWGASPSYTIISVSVFIVIPLIIVMIACYSVVFCAARRQHALLVNKRHSLVRYKD 240
Db 181 LCSMWGASPSYTIISVSVFIVIPLIIVMIACYSVVFCAARRQHALLVNKRHSLVRYKD 240

Db 181 LCSMWGASPSYTIISVSVFIVIPLIIVMIACYSVVFCAARRQHALLVNKRHSLVRYKD 240
Qy 241 CVENDEBGAKEKEEFODESEFRQHEGEVAKEGRMADKGRTEVNOCSIDLGEDMFEGBDDI 360
Db 241 CVENDEBGAKEKEEFODESEFRQHEGEVAKEGRMADKGRTEVNOCSIDLGEDMFEGBDDI 360
Qy 301 RGSSEVBSSTVADSGMEGEGSTKYBENSMDKGRTEVNOCSIDLGEDMFEGBDDI 360
Db 301 RGSSEVBSSTVADSGMEGEGSTKYBENSMDKGRTEVNOCSIDLGEDMFEGBDDI 360
Qy 361 NFSDEDDVAVNIPESLPPSRNSNSNPPLPRCYCKAAKVIIFIIIFSIVLSLGPYCLAV 420
Db 361 NFSDEDDVAVNIPESLPPSRNSNSNPPLPRCYCKAAKVIIFIIIFSIVLSLGPYCLAV 420
Qy 421 LAVWVDETQVQVWVITIIIMLFLOCCIHPIYVGYMKTIKKSIQDMLKKFCEKRPK 480
Db 421 LAVWVDETQVQVWVITIIIMLFLOCCIHPIYVGYMKTIKKSIQDMLKKFCEKRPK 480
Qy 481 EDSHDLPGTEGTEGKIIVPSYDSATFP 508
Db 481 EDSHDLPGTEGTEGKIIVPSYDSATFP 508

RESULT 7
US-10-345-332-2
; Sequence 2, Application US/10345332
; Publication No. US20030129705A1
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: CL000754CON
; CURRENT APPLICATION NUMBER: US/10/345,332
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/769,741
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/205,166
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/638,018
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-345-332-2

Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 5e-182;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTSTCTNSTRESNSHTCMPISKMPISLAHGIIIRSTVIVIFLAASFVGNITVALVLRKP 60
Db 1 MTSTCTNSTRESNSHTCMPISKMPISLAHGIIIRSTVIVIFLAASFVGNITVALVLRKP 60
Qy 61 QLLQVTRNFIFNLVTDLQISLVAPWVAVTSVPLFWPLNSHFTALVSLTHLPAFASVN 120
Db 61 QLLQVTRNFIFNLVTDLQISLVAPWVAVTSVPLFWPLNSHFTALVSLTHLPAFASVN 120
Qy 121 TIVVSVDRYLSIIHPLSPSKMQRGVLIIYGTWIVAILQSTPPLVYGMGOAFAEDRNA 180
Db 121 TIVVSVDRYLSIIHPLSPSKMQRGVLIIYGTWIVAILQSTPPLVYGMGOAFAEDRNA 180
Qy 181 LCSMWGASPSYTIISVSVFIVIPLIIVMIACYSVVFCAARRQHALLVNKRHSLVRYKD 240
Db 181 LCSMWGASPSYTIISVSVFIVIPLIIVMIACYSVVFCAARRQHALLVNKRHSLVRYKD 240
Qy 241 CVENDEBGAKEKEEFODESEFRQHEGEVAKEGRMADKGRTEVNOCSIDLGEDMFEGBDDI 360
Db 241 CVENDEBGAKEKEEFODESEFRQHEGEVAKEGRMADKGRTEVNOCSIDLGEDMFEGBDDI 360

QY 301 RSEEEVRESSTVASDGSMEGKSTVEENSMKADGRTEVNOCSIDLGEDDMEFGEDDI 360
DB 301 RSEEEVRESSTVASDGSMEGKSTVEENSMKADGRTEVNOCSIDLGEDDMEFGEDDI 360
QY 361 NFESEDVEAVNIPESLPPSRNSNSNPPLPRCYQCAAKVIFIIISYVLSLGPYCFLLAV 420
DB 361 NFESEDVEAVNIPESLPPSRNSNSNPPLPRCYQCAAKVIFIIISYVLSLGPYCFLLAV 420
QY 421 LAWVVDVETQVQWVITIIIMLFLOCCIHPPYVGYMHTIKKEIODMLKKEFKCKEPPK 480
DB 421 LAWVVDVETQVQWVITIIIMLFLOCCIHPPYVGYMHTIKKEIODMLKKEFKCKEPPK 480
QY 481 EDSHPDLPGTEGTEGKIIVSYDSATFP 508
DB 481 EDSHPDLPGTEGTEGKIIVSYDSATFP 508

RESULT 8
US-10-088-726-21
; Sequence 21, Application US/10088726
; Publication No. US20030157558A1
; GENERAL INFORMATION:
; APPLICANT: Matsunoto et al.
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE-BINDING PROTEIN-COUPLED RECEPTORS AND
; FILE REFERENCE: 62514
; CURRENT APPLICATION NUMBER: US/10/088,726
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: PCT/JP00/09408
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 1999-375152
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: JP 2000-101339
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-088-726-21

Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 5e-182;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSSHCTCPLSKMPSISLAHGIIIRSTVLVIFLAASFVGNIVLALVQRKP 60
DB 1 MTSTCTNSTRESNSSHCTCPLSKMPSISLAHGIIIRSTVLVIFLAASFVGNIVLALVQRKP 60
QY 61 QLLQVTRNRFIPLNLTVDLQISLVAPWVATSVPLFWPLNSHFTALVSLTHLFAFASVN 120
DB 61 QLLQVTRNRFIPLNLTVDLQISLVAPWVATSVPLFWPLNSHFTALVSLTHLFAFASVN 120
QY 121 TIVVSVVDRLSIHPLSYPSKMTQRGYLLYGTVIAIILQSTPPLYGGMQAADDERNA 180
DB 121 TIVVSVVDRLSIHPLSYPSKMTQRGYLLYGTVIAIILQSTPPLYGGMQAADDERNA 180
QY 181 LGSMTWGAASPSYITLISVSVFIVPLIWMACYSVVFCAARQHALLYNKRSLLEVAVD 240
DB 181 LGSMTWGAASPSYITLISVSVFIVPLIWMACYSVVFCAARQHALLYNKRSLLEVAVD 240
QY 241 CVENEDDEGABKEKEEFQDSEFRRQHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVYA 300
DB 241 CVENEDDEGABKEKEEFQDSEFRRQHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVYA 300
QY 301 RGSSEVRESSTVASDGSMEGKSTVEENSMKADGRTEVNOCSIDLGEDDMEFGEDDI 360
DB 301 RGSSEVRESSTVASDGSMEGKSTVEENSMKADGRTEVNOCSIDLGEDDMEFGEDDI 360
QY 361 NFESEDVEAVNIPESLPPSRNSNSNPPLPRCYQCAAKVIFIIISYVLSLGPYCFLLAV 420
DB 361 NFESEDVEAVNIPESLPPSRNSNSNPPLPRCYQCAAKVIFIIISYVLSLGPYCFLLAV 420

QY 421 LAWVVDVETQVQWVITIIIMLFLOCCIHPPYVGYMHTIKKEIODMLKKEFKCKEPPK 480
DB 421 LAWVVDVETQVQWVITIIIMLFLOCCIHPPYVGYMHTIKKEIODMLKKEFKCKEPPK 480
QY 481 EDSHPDLPGTEGTEGKIIVSYDSATFP 508
DB 481 EDSHPDLPGTEGTEGKIIVSYDSATFP 508

RESULT 9
US-10-321-807-16
; Sequence 16, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Rupong
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: NO. US20030166148A1-Endogenous, Constitutively Activated Human G
; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/09/714,008
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-807-16

Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 5e-182;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSSHCTCPLSKMPSISLAHGIIIRSTVLVIFLAASFVGNIVLALVQRKP 60
DB 1 MTSTCTNSTRESNSSHCTCPLSKMPSISLAHGIIIRSTVLVIFLAASFVGNIVLALVQRKP 60
QY 61 QLLQVTRNRFIPLNLTVDLQISLVAPWVATSVPLFWPLNSHFTALVSLTHLFAFASVN 120
DB 61 QLLQVTRNRFIPLNLTVDLQISLVAPWVATSVPLFWPLNSHFTALVSLTHLFAFASVN 120
QY 121 TIVVSVVDRLSIHPLSYPSKMTQRGYLLYGTVIAIILQSTPPLYGGMQAADDERNA 180
DB 121 TIVVSVVDRLSIHPLSYPSKMTQRGYLLYGTVIAIILQSTPPLYGGMQAADDERNA 180
QY 181 LGSMTWGAASPSYITLISVSVFIVPLIWMACYSVVFCAARQHALLYNKRSLLEVAVD 240
DB 181 LGSMTWGAASPSYITLISVSVFIVPLIWMACYSVVFCAARQHALLYNKRSLLEVAVD 240
QY 241 CVENEDDEGABKEKEEFQDSEFRRQHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVYA 300
DB 241 CVENEDDEGABKEKEEFQDSEFRRQHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVYA 300

Db 241 CVENDEGAKEKEFEODESEFRQHEGEVAKKEGRMEAKDGSILAKKSGTGTSSSEVEA 300
Qy 301 RGSSEVRSSSTVAASDGSMEGKSGTKVEENSMKADKRGTEVNOCSIDLGEDDMEFGEDI 360
Db 301 RGSSEVRSSSTVAASDGSMEGKSGTKVEENSMKADKRGTEVNOCSIDLGEDDMEFGEDI 360
Qy 361 NFSEDDVEAVNIPESLPPSRNNSNPPLPRCYCKAKAKVFIIFISYVLSLGPYCFIAY 420
Db 361 NFSEDDVEAVNIPESLPPSRNNSNPPLPRCYCKAKAKVFIIFISYVLSLGPYCFIAY 420
Qy 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPRVYGVNMHTIKKEIQDMLKKFCKEKRPK 480
Db 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPRVYGVNMHTIKKEIQDMLKKFCKEKRPK 480
Qy 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508
Db 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508

RESULT 10
US-10-276-243-3
; Sequence 3, Application US/10276243
; Publication No. US20030187219A1

; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: REGULATION OF HUMAN alphaA ADRENERGIC RECEPTOR-LIKE G
; FILE REFERENCE: PROTEIN-COUPLED RECEPTOR
; CURRENT FILING DATE: 2002-11-14
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/250,505
; PRIOR FILING DATE: 2000-12-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-243-3

Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 5e-182;

Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60
Db 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60
Qy 61 QLLQVTRNFIFNLVTDLQISLVAAPWVATSVPLFMPNLNHFCTALVSLTHLPAFASVN 120
Db 61 QLLQVTRNFIFNLVTDLQISLVAAPWVATSVPLFMPNLNHFCTALVSLTHLPAFASVN 120
Qy 121 TIVVSVDRYLSIIHPLSYPSKMTQRGTYLLYGTWIVAILQSTPPLVGMGQAAFDERNA 180
Db 121 TIVVSVDRYLSIIHPLSYPSKMTQRGTYLLYGTWIVAILQSTPPLVGMGQAAFDERNA 180
Qy 181 LCSMWGASPSYTIILSVSFIVPLIWMACYSVFCAARRQHALLVNKRHSLSEVRKYD 240
Db 181 LCSMWGASPSYTIILSVSFIVPLIWMACYSVFCAARRQHALLVNKRHSLSEVRKYD 240
Qy 241 CVENDEGAKEKEFEODESEFRQHEGEVAKKEGRMEAKDGSILAKKSGTGTSSSEVEA 300
Db 241 CVENDEGAKEKEFEODESEFRQHEGEVAKKEGRMEAKDGSILAKKSGTGTSSSEVEA 300
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Db 301 RGSSEVRSSSTVAASDGSMEGKSGTKVEENSMKADKRGTEVNOCSIDLGEDDMEFGEDI 360
Qy 361 NFSEDDVEAVNIPESLPPSRNNSNPPLPRCYCKAKAKVFIIFISYVLSLGPYCFIAY 420
Db 361 NFSEDDVEAVNIPESLPPSRNNSNPPLPRCYCKAKAKVFIIFISYVLSLGPYCFIAY 420

Db 361 NFSEDDVEAVNIPESLPPSRNNSNPPLPRCYCKAKAKVFIIFISYVLSLGPYCFIAY 420
Qy 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPRVYGVNMHTIKKEIQDMLKKFCKEKRPK 480
Db 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPRVYGVNMHTIKKEIQDMLKKFCKEKRPK 480
Qy 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508
Db 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508

RESULT 11
US-10-436-715-14
; Sequence 14, Application US/10436715
; Publication No. US20040018976A1

; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,
; FILE REFERENCE: D0262 NP
; CURRENT FILING DATE: 2003-05-13
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-436-715-14

Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 5e-182;

Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60
Db 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60
Qy 61 QLLQVTRNFIFNLVTDLQISLVAAPWVATSVPLFMPNLNHFCTALVSLTHLPAFASVN 120
Db 61 QLLQVTRNFIFNLVTDLQISLVAAPWVATSVPLFMPNLNHFCTALVSLTHLPAFASVN 120
Qy 121 TIVVSVDRYLSIIHPLSYPSKMTQRGTYLLYGTWIVAILQSTPPLVGMGQAAFDERNA 180
Db 121 TIVVSVDRYLSIIHPLSYPSKMTQRGTYLLYGTWIVAILQSTPPLVGMGQAAFDERNA 180
Qy 181 LCSMWGASPSYTIILSVSFIVPLIWMACYSVFCAARRQHALLVNKRHSLSEVRKYD 240
Db 181 LCSMWGASPSYTIILSVSFIVPLIWMACYSVFCAARRQHALLVNKRHSLSEVRKYD 240
Qy 241 CVENDEGAKEKEFEODESEFRQHEGEVAKKEGRMEAKDGSILAKKSGTGTSSSEVEA 300
Db 241 CVENDEGAKEKEFEODESEFRQHEGEVAKKEGRMEAKDGSILAKKSGTGTSSSEVEA 300
Qy 301 RGSSEVRSSSTVAASDGSMEGKSGTKVEENSMKADKRGTEVNOCSIDLGEDDMEFGEDI 360
Db 301 RGSSEVRSSSTVAASDGSMEGKSGTKVEENSMKADKRGTEVNOCSIDLGEDDMEFGEDI 360
Qy 361 NFSEDDVEAVNIPESLPPSRNNSNPPLPRCYCKAKAKVFIIFISYVLSLGPYCFIAY 420
Db 361 NFSEDDVEAVNIPESLPPSRNNSNPPLPRCYCKAKAKVFIIFISYVLSLGPYCFIAY 420
Qy 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPRVYGVNMHTIKKEIQDMLKKFCKEKRPK 480
Db 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPRVYGVNMHTIKKEIQDMLKKFCKEKRPK 480
Qy 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508
Db 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508

Db	241	CVENEDBEGAEKKEEFQDESEFRQHEGEVKAKEGMEAKDGLAKEGSGTGTSSSVYA	300
Qy	301	RGSEEVRESSITVADSGMEKEGSTYVENSMKADKGRTEVNQCSIDLGEDMEFGEDDI	360
Db	301	RGSEEVRESSITVADSGMEKEGSTYVENSMKADKGRTEVNQCSIDLGEDMEFGEDDI	360
Qy	361	NFSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYQCKAKVIFIIIPSYVLSLGPYCFIAY	420
Db	361	NFSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYQCKAKVIFIIIPSYVLSLGPYCFIAY	420
Qy	421	LAVWYDVETQVPQWITIIIMLFLOCCIHPPYVGYMHTIKKEIODMLKEFCCKEPPK	480
Db	421	LAVWYDVETQVPQWITIIIMLFLOCCIHPPYVGYMHTIKKEIODMLKEFCCKEPPK	480
Qy	481	EDSHPDLPSTEGTSGKIIVPSYDSATFP	508
Db	481	EDSHPDLPSTEGTSGKIIVPSYDSATFP	508

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Job time : 136.35 secs

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Qy 121 TIVVSVDRYLSIIHPLSYPSKMTQRGYYLLYGTWIVAILQSTPPLYGWQAAFDERNA 180
Db 121 TIVVSVDRYLSIIHPLSYPSKMTQRGYYLLYGTWIVAILQSTPPLYGWQAAFDERNA 180
Qy 181 LCSMWGASPSYTIISVSVFIVPIVIMACYVVFCAARQHALLVNKRHSLERVKD 240
Db 181 LCSMWGASPSYTIISVSVFIVPIVIMACYVVFCAARQHALLVNKRHSLERVKD 240
Qy 241 CVENDEEGAEEKEEFQDESEFRQHEGEVYAKEGRMAKDGSLKAKEGSTGTSSESVYA 300
Db 241 CVENDEEGAEEKEEFQDESEFRQHEGEVYAKEGRMAKDGSLKAKEGSTGTSSESVYA 300
Qy 301 RGSSEVRSSSTVYASDGSMEGEGSTKYBENSMAKDKRTEVNOCSIDLGEDMFEGBDDI 360
Db 301 RGSSEVRSSSTVYASDGSMEGEGSTKYBENSMAKDKRTEVNOCSIDLGEDMFEGBDDI 360
Qy 361 NFSEDDVEAVNIPESLPSRRNSNSNPPLPRCYCKAKAVFIITIFSIVLSLGPYCFIAY 420
Db 361 NFSEDDVEAVNIPESLPSRRNSNSNPPLPRCYCKAKAVFIITIFSIVLSLGPYCFIAY 420
Qy 421 LAVWVDETQVQWVITITIIWLFLQCCIHBYVGYMHTIKKEIQDMLKKFCKEKRPK 480
Db 421 LAVWVDETQVQWVITITIIWLFLQCCIHBYVGYMHTIKKEIQDMLKKFCKEKRPK 480
Qy 481 EDSHPDLPGTEGTEGKIYPSYDSATFP 508
Db 481 EDSHPDLPGTEGTEGKIYPSYDSATFP 508
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RESULT 2
US-10-314-048A-104
; Sequence 104, Application US/10314048A
; Patent No. 6902902
; GENERAL INFORMATION:
; APPLICANT: Unet, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Huang T.
; APPLICANT: Choi, Bryan
; APPLICANT: Leonard, James
; APPLICANT: Hakak, Yaron
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lerner, Michael
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
; FILE REFERENCE: 22, US6, CIP
; CURRENT APPLICATION NUMBER: US/10/314,048A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/096,511
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/995,543
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/399,917
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/404,761
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/410,747
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 926
; TYPE: PRT
; ORGANISM: Homo sapiens and Rat
US-10-314-048A-104
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Query Match 99.9%; Score 2641; DB 2; Length 926;
Best Local Similarity 99.8%; Pred. No. 5,56-205;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 1 MTCTCTNSTRESNSHTCMPLSKMPISLANGIIRSTVLVIFLASPVGNIVLAVLORPK 60
Qy 1 MTCTCTNSTRESNSHTCMPLSKMPISLANGIIRSTVLVIFLASPVGNIVLAVLORPK 60
Db 1 MTCTCTNSTRESNSHTCMPLSKMPISLANGIIRSTVLVIFLASPVGNIVLAVLORPK 60
Qy 61 QLVQVTRFIFNLVTDLQISLVAPWVATSVLPFPLNSHFTALVSLTHLFAFASVN 120
Db 61 QLVQVTRFIFNLVTDLQISLVAPWVATSVLPFPLNSHFTALVSLTHLFAFASVN 120
Qy 121 TIVVSVDRYLSIIHPLSYPSKMTQRGYYLLYGTWIVAILQSTPPLYGWQAAFDERNA 180
Db 121 TIVVSVDRYLSIIHPLSYPSKMTQRGYYLLYGTWIVAILQSTPPLYGWQAAFDERNA 180
Qy 181 LCSMWGASPSYTIISVSVFIVPIVIMACYVVFCAARQHALLVNKRHSLERVKD 240
Db 181 LCSMWGASPSYTIISVSVFIVPIVIMACYVVFCAARQHALLVNKRHSLERVKD 240
Qy 241 CVENDEEGAEEKEEFQDESEFRQHEGEVYAKEGRMAKDGSLKAKEGSTGTSSESVYA 300
Db 241 CVENDEEGAEEKEEFQDESEFRQHEGEVYAKEGRMAKDGSLKAKEGSTGTSSESVYA 300
Qy 301 RGSSEVRSSSTVYASDGSMEGEGSTKYBENSMAKDKRTEVNOCSIDLGEDMFEGBDDI 360
Db 301 RGSSEVRSSSTVYASDGSMEGEGSTKYBENSMAKDKRTEVNOCSIDLGEDMFEGBDDI 360
Qy 361 NFSEDDVEAVNIPESLPSRRNSNSNPPLPRCYCKAKAVFIITIFSIVLSLGPYCFIAY 420
Db 361 NFSEDDVEAVNIPESLPSRRNSNSNPPLPRCYCKAKAVFIITIFSIVLSLGPYCFIAY 420
Qy 421 LAVWVDETQVQWVITITIIWLFLQCCIHBYVGYMHTIKKEIQDMLKKFCKEKRPK 480
Db 421 LAVWVDETQVQWVITITIIWLFLQCCIHBYVGYMHTIKKEIQDMLKKFCKEKRPK 480
Qy 481 EDSHPDLPGTEGTEGKIYPSYDSATFP 508
Db 481 EDSHPDLPGTEGTEGKIYPSYDSATFP 508
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```
RESULT 3
US-10-314-048A-92
; Sequence 92, Application US/10314048A
; Patent No. 6902902
; GENERAL INFORMATION:
; APPLICANT: Unet, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Huang T.
; APPLICANT: Choi, Bryan
; APPLICANT: Leonard, James
; APPLICANT: Hakak, Yaron
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lerner, Michael
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
; FILE REFERENCE: 22, US6, CIP
; CURRENT APPLICATION NUMBER: US/10/314,048A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/096,511
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/995,543
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/399,917
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/404,761
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/410,747
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/ PRIOR FILING DATE: 2002-09-13
/ NUMBER OF SEQ ID NOS: 161
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 92
/ LENGTH: 508
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-314-048A-92

Query Match 99.7%; Score 2636; DB 2; Length 508;
Best Local Similarity 99.6%; Pred. No. 6.5e-205;
Matches 506; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSTCNSTRESNNSHTCMPLSKMPLSLAGIIRSTVLVIPLAASFGNIVLALVQRP 60
DB 1 MTSTCNSTRESNNSHTCMPLSKMPLSLAGIIRSTVLVIPLAASFGNIVLALVQRP 60
QY 61 QLLQVTNRIFNLVLTDLQISLVAWVAVTSVPLFWPLNSHFTALVSLTHLFAFASVN 120
DB 61 QLLQVTNRIFNLVLTDLQISLVAWVAVTSVPLFWPLNSHFTALVSLTHLFAFASVN 120
QY 121 TIVVSVVDYLSIHPILSPKMTORRGYLLXGTVIVALILOSPPLYGMOGAAPDERNA 180
DB 121 TIVVSVVDYLSIHPILSPKMTORRGYLLXGTVIVALILOSPPLYGMOGAAPDERNA 180
QY 181 LCSMIGASPSYTIISVGFIVPLIVMIACYSVFCARROHALLYNKRSLERVRD 240
DB 181 LCSMIGASPSYTIISVGFIVPLIVMIACYSVFCARROHALLYNKRSLERVRD 240
QY 241 CVENEDBGAKEKEEFODESEFRROHEGEVKAKEGMEAKDGLKAKEGSTGTSSSVA 300
DB 241 CVENEDBGAKEKEEFODESEFRROHEGEVKAKEGMEAKDGLKAKEGSTGTSSSVA 300
QY 301 RSESEPRESTYASDGMGKSGSTVEENSMKADGRTEVNOCSIDLGEDMEFEDDI 360
DB 301 RSESEPRESTYASDGMGKSGSTVEENSMKADGRTEVNOCSIDLGEDMEFEDDI 360
QY 361 NSEDDVEAVNIPELPPSRNNSNPPLPRCYQCAKAVIFIIISYVLSIGPYCEFLAV 420
DB 361 NSEDDVEAVNIPELPPSRNNSNPPLPRCYQCAKAVIFIIISYVLSIGPYCEFLAV 420
QY 421 LAWVAVDETQVQWVITIIIMLFLOCCIHPPYVGYMKTIKKEIQDMLKKEFCCKEPRK 480
DB 421 LAWVAVDETQVQWVITIIIMLFLOCCIHPPYVGYMKTIKKEIQDMLKKEFCCKEPRK 480
QY 481 EDSHPDLPTGEGTEGKIYPSYDATFP 508
DB 481 EDSHPDLPTGEGTEGKIYPSYDATFP 508

RESULT 4
US-09-364-425B-23
/ Sequence 23, Application US/09364425B
/ Patent No. 6653086
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lin, I-Lin
/ APPLICANT: Lowitz, Kevin P.
/ APPLICANT: Chen, Roping
/ TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Receptor
/ FILE REFERENCE: Apend047
/ CURRENT APPLICATION NUMBER: US/09/364,425B
/ PRIOR FILING DATE: 2001-12-18
/ PRIOR APPLICATION NUMBER: 60/094,879
/ PRIOR FILING DATE: 1998-07-31
/ PRIOR APPLICATION NUMBER: 60/106,300
/ PRIOR FILING DATE: 1998-10-30
/ PRIOR APPLICATION NUMBER: 60/110,906
/ PRIOR FILING DATE: 1998-12-04
/ PRIOR APPLICATION NUMBER: 60/121,851
/ PRIOR FILING DATE: 1999-02-26

/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 23
/ LENGTH: 407
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-364-425B-23

Query Match 14.8%; Score 391; DB 2; Length 407;
Best Local Similarity 23.6%; Pred. No. 1.5e-23;
Matches 106; Conservative 67; Mismatches 130; Indels 146; Gaps 11;

QY 31 GIIRSTVLVIPLAASFGV--GNIVLALVQRPQLQVTNRIFNLVLTDLQISLVAWV 88
DB 25 GVIIIOFALIVITIFVCLGNLVIWTLTKSKYLLTNSKFEVSLTNSFLSLVLPV 84
QY 89 VATSVPPLWPLNSHFTALVSLTHLFAFASVTVTVLSVDRSLSIHPILSPKMTORRG 148
DB 85 VTSSIRREWIFGVWNCFSALLYLLISSASMLTIGVIAIDRYAVALYPMVYPMKTGNRA 144
QY 149 YLLXGTVIVALILOSPPLYGMOGAAPDERNALCSMIGASPSYTIISVGFIVPLIVM 208
DB 145 VVALVYIMLSLIGCLPLFGMSVVEFDFKMMCVAAHREGYTAFMQIWALFPFLVM 204
QY 209 IACYSVFCARROHALLYNKRSLERVRDQVENEDEBGAKEKEEFODESEFRROHEG 268
DB 205 LVCYGFIRVAR-----VKARKHCGTVIYE-EDAQ----- 235
QY 269 EVKAKEGMEAKDGLKAKEGSTGTSSSVEARGSEBRESSTVASDGMGKSGTKVE 328
DB 236 ---RTGR-----KNSSTSTSSSG----- 250
QY 329 ENSMKADGRTEVNOCSIDLGEDMEFEDDIINSEDDVEAVNIPELPPSRNS----- 383
DB 251 -----SRNAFQGV 260
QY 384 -NSNPPLPRCYQCAKAVIFIIISYVLSIGPY-CFLAVLAWV--VDVETQVQWVITII 439
DB 261 YSAN-----QCKALITLVLVGLAFMTWGWYVVIASEALMGSSVSPSLETA----- 309
QY 440 IMLFLOCCIHPPYVGYMKTIKKEIQDMLKKEFCCKEPRK 468
DB 310 TWLSFSAVACHPLIYGLWMTKVRKELGLM 338

RESULT 5
US-08-748-485-1
/ Sequence 1, Application US/08748485
/ Patent No. 5817480
/ GENERAL INFORMATION:
/ APPLICANT: Au-Young, Janice
/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Goli, Surya K.
/ APPLICANT: Murty, Lorna E.
/ TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: US
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/748,485
/ FILING DATE: Herewith
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0159 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: 1722180
;
US-08-748-485-1
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Query Match      14.7%; Score 388.5; DB 1; Length 454;
Best Local Similarity 22.9%; Pred. No. 2.8e-23;
Matches 103; Conservative 72; Mismatches 129; Indels 145; Gaps 10;
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QY 31 GIIRSTVLVIFLAASFV--GNIVLALVLRKPOLQVTRFENLVTDLQISLVAPMV 88
DB 25 GVIIIFQIAIIVITTFVCLGNLVIVTLYKSKYLLTSLNKFVFSITLSNFIISVLVLPFV 84
QY 89 VATSVLPMPNLNHSHTLVSLTHLPFASVNTIVLVSDRYLSTIIHPLSPSKMTORRG 148
DB 85 VTSSIRREWIFGVVWNCNFSALYLLIISASMLTGLVIALDRYVAALVPMVYPMKLTGNRA 144
QY 149 YLLVGTWIVALLQSTPPLYGWGOAFDERNALCSMIGWASPSTYLLSVSFIVLPLVM 208
DB 145 VMALVYIWLHSLIGCLPFLFGWSVPEDFEKKMCAAMHREBGYAFQWICWALPFLVM 204
QY 209 IACISVVFCAARQHALLVNKRHSLERVKDCVENEDEGAKEKEEFQDESEFRROHEG 268
DB 205 LVCTGFIFRVAR----- 216
QY 269 EYKAEKGMKADGSLKAKEGSTGTSESVEARGSEVRESESTVASDGSMEKSGSTKYE 328
DB 217 -VKAR-----KVNCGTVVVEEDAQGTG---VKNSSTSTSS----- 250
QY 329 ENSMKADKRTVENQCSIDLGEDMEFGEDINFSEDDVEAVNIPESLPPSRNS----- 383
DB 251 -----GSRNNAFGVV 261
QY 384 -NSNPPLPRCYOCKAKAVIFIIIFSYVLSLGPY-CFLAVLAVM--VDVETQVPOWVITTI 439
DB 262 YSAN-----QCKALITILVLVGLAFMVTWGPYMWVIASEALMGKSVSPSLETWA----- 310
QY 440 IWLFLQCCIHPIYVYGVYMKTIKKEIDQM 468
DB 311 TWLSFASAVCHPLIYGLMKNKTIVKELGM 339
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```

RESULT 6
US-08-467-568-2
; Sequence 2, Application US/08467568
; Patent No. 5817477
; GENERAL INFORMATION:
; APPLICANT: SOPPET, DANIEL R
; TITLE OF INVENTION: ADRENERGIC RECEPTOR
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Giffillan, Cecchi,
; ADDRESS: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
;
```

```

; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,568
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-324
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 529 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-467-568-2
```

```

Query Match      14.0%; Score 371; DB 1; Length 529;
Best Local Similarity 23.1%; Pred. No. 8.9e-22;
Matches 110; Conservative 69; Mismatches 132; Indels 166; Gaps 14;
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QY 6 TNSRPE-----SNSHTCMPISKMPISLHAGIISTVIVITFLASFVGNIVLALVLRKP 60
DB 14 SNLTREEEGEGASSPSSPSLSP-----FLSA--WGNLVIVTLYKKS 56
QY 61 QLVQVTRFENLVTDLQISLVAPMVVATSVLPFLPMLNHFCTALVSLTHLPFASVN 120
DB 57 YLITLSNKFVSLTSLNLTSLVLPFVYTSIRREWIFGVVWNCNFSALYLLIISASML 116
QY 121 TIVLVSDRYLSTIIHPLSPSKMTORRGYLLLYGTWIVALLQSTPPLYGWGOAFDERNA 180
DB 117 TLGVIALDRYVAALVPMVYPMKLTGNRAVMALVYIWLHSLIGCLPFLFGWSVPEGEKMW 176
QY 181 LCSMIGWASPSTYLLSVSFIVPLIWLACISVVFCAARQHALLVNKRHSLERVKD 240
DB 177 MCVAAHREPYTAFQWICWALPFLVWLVCYGFIFRVAR-----VKARKVCGTV 228
QY 241 CVENEDEGAKKEEFQDESEFRROHEGEVAKKGMKADGSLKAKEGSTGTSESVYA 300
DB 229 IVE-EDAQ-----RTGR-----KNSSISTSS----- 249
QY 301 RGSSEVRESESTVASDGSMEKSGSTKVENSMKADKRTVENQCSIDLGEDMEFGEDDI 360
DB 250 -----GR----- 251
QY 361 NPSDDVEAVNIPESLPPSRNS-----NSNPPLPRCYOCKAKAVIFIIIFSYVLSLGP 414
DB 252 -----RNNAFGVVYSAN-----QCKALITILVLVGLAFMVTWGP 285
QY 415 Y-CFLAVLAVM--VDVETQVPOWVITTIIMFLPQCCIHPIYVYGVYMKTIKKEIDQM 468
DB 286 YMWVIASEALMGKSVSPSLETWA-----TWLSFASAVCHPLIYGLMKNKTIVKELGM 338
```

```

RESULT 7
US-09-030-582-2
; Sequence 2, Application US/09030582
; Patent No. 5994506
; GENERAL INFORMATION:
; APPLICANT: SOPPET, DANIEL R
; TITLE OF INVENTION: ADRENERGIC RECEPTOR
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Giffillan, Cecchi,
; ADDRESS: Stewart & Olstein
;
```

STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,582
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,568
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-324
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 529 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-030-582-2

Query Match 14.0%; Score 371; DB 1; Length 529;
Best Local Similarity 23.1%; Pred. No. 8.9e-22;
Matches 110; Conservative 69; Mismatches 132; Indels 166; Gaps 14;
QY 6 TNSTRE-----SNSHTCMPLSKMPISLAHGIRSTVLVIFLAASFGNIVLALVLRKP 60
DB 14 SNLTEEGBEGASSPSSPSLSP-----FLSA--KGNLVIVTLVLYKKS 56
QY 61 QLLQVTRNRIENLVTDLQISLVAPWVYATSVPLFWPLNHFCTALVSLTHLFAFASV 120
DB 57 YLLTISNKFVFLTSLNFLSLVLPVVTSSIRREWIFGVWCMFSLYLLISSASWL 116
QY 121 TIVLVSVDRIYLIHPLSPSKMTORRGYLLYGTVIAIILSTPPLYGMOGAAPDERNA 180
DB 117 TLGVIAIDRYAVLIPMYTPMKITGNRAVMALVYIWLHSLIGCLPPLFGWSSVEYGENKM 176
QY 181 LCSMTWGAASPSYTIISVSVFIVPLIWMACYSVFCARQHALLYNKRHSLEVRVD 240
DB 177 MCVAAWHREPGYTAAFWQICALFPLVMLVCYGFIFRVAR-----VKARKVHCITV 228
QY 241 CVENDEBGAKEKEFODESEFRROHGBGVKAKEGMEAKDGLKAKESGTSTSSSVEA 300
DB 229 IVE-BDAQ-----RTGR-----KNSSTSSS----- 249
QY 301 RGSSEVRSSSTVASDGSMEGKSGTKVEENSKAKDKGRTEVNOCSIDLGEDMEGGEEDI 360
DB 230 -----GR----- 251
QY 361 NFESEDDVEAVNIPESLPSRRNS-----NSNPPLPRCYOCKAKAVIPIIFSVYLSGP 414
DB 252 -----RNAFGGVYTSAN-----QCKALLITILVLAGAFMTWGP 285
QY 415 Y-CFLAVLAVW--VDVETQVPQWVITIIWLFLOCCIHPIVYGYMHTIKKEIDM 468
DB 286 YWVIASEALMGKSSVSPSLSTWA-----TWLSFASAVCHPLIYGLMKNKTIVRKELGM 338

RESULT 8
PCT-US94-09051-2
; Sequence 2, Application PC/TUS9409051
; GENERAL INFORMATION:

APPLICANT: LI, ET AL.
TITLE OF INVENTION: Adrenergic Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CITY: ROSELAND
STREET: 6 BECKER FARM ROAD
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09051
FILING DATE: Submitted herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 529 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US94-09051-2

Query Match 14.0%; Score 371; DB 4; Length 529;
Best Local Similarity 23.1%; Pred. No. 8.9e-22;
Matches 110; Conservative 69; Mismatches 132; Indels 166; Gaps 14;
QY 6 TNSTRE-----SNSHTCMPLSKMPISLAHGIRSTVLVIFLAASFGNIVLALVLRKP 60
DB 14 SNLTEEGBEGASSPSSPSLSP-----FLSA--KGNLVIVTLVLYKKS 56
QY 61 QLLQVTRNRIENLVTDLQISLVAPWVYATSVPLFWPLNHFCTALVSLTHLFAFASV 120
DB 57 YLLTISNKFVFLTSLNFLSLVLPVVTSSIRREWIFGVWCMFSLYLLISSASWL 116
QY 121 TIVLVSVDRIYLIHPLSPSKMTORRGYLLYGTVIAIILSTPPLYGMOGAAPDERNA 180
DB 117 TLGVIAIDRYAVLIPMYTPMKITGNRAVMALVYIWLHSLIGCLPPLFGWSSVEYGENKM 176
QY 181 LCSMTWGAASPSYTIISVSVFIVPLIWMACYSVFCARQHALLYNKRHSLEVRVD 240
DB 177 MCVAAWHREPGYTAAFWQICALFPLVMLVCYGFIFRVAR-----VKARKVHCITV 228
QY 241 CVENDEBGAKEKEFODESEFRROHGBGVKAKEGMEAKDGLKAKESGTSTSSSVEA 300
DB 229 IVE-BDAQ-----RTGR-----KNSSTSSS----- 249
QY 301 RGSSEVRSSSTVASDGSMEGKSGTKVEENSKAKDKGRTEVNOCSIDLGEDMEGGEEDI 360
DB 230 -----GR----- 251
QY 361 NFESEDDVEAVNIPESLPSRRNS-----NSNPPLPRCYOCKAKAVIPIIFSVYLSGP 414
DB 252 -----RNAFGGVYTSAN-----QCKALLITILVLAGAFMTWGP 285
QY 415 Y-CFLAVLAVW--VDVETQVPQWVITIIWLFLOCCIHPIVYGYMHTIKKEIDM 468


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Db      31 VVTSYQVITSLTGLTIFCAVGNACVVAIALER--SLQNVANYLIGSLAVTDLWVYL 88
      84 VAPMWAVTSVPLFPWLNHFTALVSLTLPAPASVNTVLVSVDRLYSIIHPLSPSKM 143
      89 VLPMAALYQVNLKMTLGQVTCDFIALDVLCTCTSSILHCAIALDRYWAITPIDYVNR 148
Qy      144 TORRGVLLYGTWIVAILOSTPPLYGWGOAFDERNALCSMIMGASPSYTIISVVSFIYI 203
      149 TPRRAAALISLTWILGFLISIPMLGMRTP--EDRSDPACTISKDHGTYITSTGAFYI 206
Db      204 PLIWIACSVVFCARQGHALLVYKRSLEVRVDCVENEDEBGAEKKEPFODESEPR 263
      207 PLLMLLVLYGRIFRAR-----FRIKTYKVKYKGTGADTRHGASPAPOPK 251
Qy      264 RQHEGEVAKKEGRM--EAKDGL-----KAKGSGTSSSEVARGSEVRSSITYASDG 316
      252 KSVNGESGSRNRLVGVESKAGALCANGAVRQDDGALAEVIEVH----- 296
Db      317 SMEKGSGTKVEENSKADKGRTEVNOCSIDLGEDMERGEDDINFSEDDVEAVNIPESL 376
      297 ----RVGNSK-BHLPLPSAGPTPCAPASFE----- 322
Qy      377 PPSRRNSNPNPLPRCYOQAKAVIIFIISVYLSLGPYCFIPLAVLWVDTQVPOWYI 436
      323 RGRERNAEKRMALAREKTYKTIGIINGTFLICWLPFFIYALVLPFCSSCHMPTLLG 382
Db      437 TIIIMFLQCCIHPIVYVGYMKTIKKEIOMLKKPFCKE 476
      383 AIINWLGYSNLSLNPVIYAFVFNKDFONAFKIIKCLFCRQ 422

```

RESULT 11

```

US-08-117-006-3
; Sequence 3, Application US/08117006
; Patent No. 5639652
; GENERAL INFORMATION:
; APPLICANT: Weinshank, Richard L.
; APPLICANT: Branchek, Theresa
; APPLICANT: Hartig, Paul R.
; TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1F RECEPTOR AND
; TITLE OF INVENTION: US8 THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: WordPerfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,006
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1795/39318
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear

```

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; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; IMMEDIATE SOURCE:
; CLONING: 5-HT1A
US-08-117-006-3

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Query Match      13.0%; Score 343.5; DB 1; Length 422;
Best Local Similarity 22.0%; Pred. No. 1.1e-19;
Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

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Qy      26 ISLAGIIRSTVLVIFLASFVGN--IVLAVLQKRPOLLQVTRNPIENLVTLQISL 83
      31 VVTSYQVITSLTGLTIFCAVGNACVVAIALER--SLQNVANYLIGSLAVTDLWVYL 88
Db      84 VAPMWAVTSVPLFPWLNHFTALVSLTLPAPASVNTVLVSVDRLYSIIHPLSPSKM 143
      89 VLPMAALYQVNLKMTLGQVTCDFIALDVLCTCTSSILHCAIALDRYWAITPIDYVNR 148
Qy      144 TORRGVLLYGTWIVAILOSTPPLYGWGOAFDERNALCSMIMGASPSYTIISVVSFIYI 203
      149 TPRRAAALISLTWILGFLISIPMLGMRTP--EDRSDPACTISKDHGTYITSTGAFYI 206
Db      204 PLIWIACSVVFCARQGHALLVYKRSLEVRVDCVENEDEBGAEKKEPFODESEPR 263
      207 PLLMLLVLYGRIFRAR-----FRIKTYKVKYKGTGADTRHGASPAPOPK 251
Qy      264 RQHEGEVAKKEGRM--EAKDGL-----KAKGSGTSSSEVARGSEVRSSITYASDG 316
      252 KSVNGESGSRNRLVGVESKAGALCANGAVRQDDGALAEVIEVH----- 296
Db      317 SMEKGSGTKVEENSKADKGRTEVNOCSIDLGEDMERGEDDINFSEDDVEAVNIPESL 376
      297 ----RVGNSK-BHLPLPSAGPTPCAPASFE----- 322
Qy      377 PPSRRNSNPNPLPRCYOQAKAVIIFIISVYLSLGPYCFIPLAVLWVDTQVPOWYI 436
      323 RGRERNAEKRMALAREKTYKTIGIINGTFLICWLPFFIYALVLPFCSSCHMPTLLG 382
Db      437 TIIIMFLQCCIHPIVYVGYMKTIKKEIOMLKKPFCKE 476
      383 AIINWLGYSNLSLNPVIYAFVFNKDFONAFKIIKCLFCRQ 422

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RESULT 12

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US-08-216-594-3
; Sequence 3, Application US/08216594
; Patent No. 5652113
; GENERAL INFORMATION:
; APPLICANT: Weinshank, Richard L.
; APPLICANT: Branchek, Theresa
; APPLICANT: Hartig, Paul R.
; TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1F RECEPTOR
; TITLE OF INVENTION: AND US8 THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/216,594
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/39318
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP UT
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
IMMEDIATE SOURCE:
CLONE: 5-HT1A
US-08-216-594-3

Query Match 13.0%; Score 343.5; DB 1; Length 422;
Best Local Similarity 22.0%; Pred. No. 1,1e-19;
Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

QY 26 ISLAGIIRSTVLVIFLAASFVGN--IVLALVLRKPOLQVTRFIFNLVTLDTLQISL 83
DB 31 VTSVQVITSLILGLTIFCAVGNACVVAIALER--SLQNVANYLIGSLAVTDLMSVL 88
QY 84 VAPWVAVSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVLVSVDRYLSIHPSPSKM 143
DB 89 VLPMAALYQVNLKMTLGGVTCDFIALDLVLCCTSSILHLCAIALDRYVALTDPIDYVNR 148
QY 144 TORRGYLLLYGTWVAIIQSTPRLYWGQAAFDERNALCSMIWGASPSYTLISVSVFIY 203
DB 149 TPRRAAALISLTWILGLFISIPMLGWRTP--EDRSDPACTISKDHGTIYSTFGAFYI 206
QY 204 PLIWIACYSVFCARQHALLVNKRHSLEVRVKDCVENEDGAEKKEEFQDESEPR 263
DB 207 PLLMLLVLYGRIFRAAR-----FRIRKTVKVEKGTGADTRHGASAPQPK 251
QY 264 ROHEGEVAKEGRM--EAKDGL-----KAKGSTGTSSSEVARGSEVRRESSSTVADG 316
DB 252 KSVNDESSGRMRLVESKAGALCANGAVRGDDGALVEVH----- 296
QY 317 SMEKEGSTKYVENSMKADKGRTEVNOCSIDLGEDDMEGEDDINFSEDDVAVNIPBSL 376
DB 297 ---RVGNSK-EHLPLSEAGTPCAPASF----- 322
QY 377 PPSRRNSNPNPLPRCYQCKAKAVIFIIIFSVLSLGPYCFILAVLAVWDETQVQWVI 436
DB 323 RKNERNAAKRMALARRKTVKTGIIMGTIFILCMLPFFIVALVLPFCSSCHMPTLLG 382
QY 437 TIIWLFLOCCIHPPYVGYMHTIKKEIQDMLKKFPCKE 476
DB 383 AIINWLGYSNLNPLVIAVFNKDFQNAFKKIICLFCRQ 422

RESULT 13
US-08-542-358-3
Sequence 3, Application US/08542358
Patent No. 5786155
GENERAL INFORMATION:
APPLICANT: Weinshank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1E RECEPTOR AND USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,358
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/39317-2Z/JPW/MAT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-542-358-3

Query Match 13.0%; Score 343.5; DB 1; Length 422;
Best Local Similarity 22.0%; Pred. No. 1,1e-19;
Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

QY 26 ISLAGIIRSTVLVIFLAASFVGN--IVLALVLRKPOLQVTRFIFNLVTLDTLQISL 83
DB 31 VTSVQVITSLILGLTIFCAVGNACVVAIALER--SLQNVANYLIGSLAVTDLMSVL 88
QY 84 VAPWVAVSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVLVSVDRYLSIHPSPSKM 143
DB 89 VLPMAALYQVNLKMTLGGVTCDFIALDLVLCCTSSILHLCAIALDRYVALTDPIDYVNR 148
QY 144 TORRGYLLLYGTWVAIIQSTPRLYWGQAAFDERNALCSMIWGASPSYTLISVSVFIY 203
DB 149 TPRRAAALISLTWILGLFISIPMLGWRTP--EDRSDPACTISKDHGTIYSTFGAFYI 206
QY 204 PLIWIACYSVFCARQHALLVNKRHSLEVRVKDCVENEDGAEKKEEFQDESEPR 263
DB 207 PLLMLLVLYGRIFRAAR-----FRIRKTVKVEKGTGADTRHGASAPQPK 251
QY 264 ROHEGEVAKEGRM--EAKDGL-----KAKGSTGTSSSEVARGSEVRRESSSTVADG 316
DB 252 KSVNDESSGRMRLVESKAGALCANGAVRGDDGALVEVH----- 296
QY 317 SMEKEGSTKYVENSMKADKGRTEVNOCSIDLGEDDMEGEDDINFSEDDVAVNIPBSL 376
DB 297 ---RVGNSK-EHLPLSEAGTPCAPASF----- 322
QY 377 PPSRRNSNPNPLPRCYQCKAKAVIFIIIFSVLSLGPYCFILAVLAVWDETQVQWVI 436
DB 323 RKNERNAAKRMALARRKTVKTGIIMGTIFILCMLPFFIVALVLPFCSSCHMPTLLG 382
QY 437 TIIWLFLOCCIHPPYVGYMHTIKKEIQDMLKKFPCKE 476
DB 383 AIINWLGYSNLNPLVIAVFNKDFQNAFKKIICLFCRQ 422

RESULT 14
US-08-157-185-13
Sequence 13, Application US/08157185
Patent No. 5985585
GENERAL INFORMATION:
APPLICANT: Bard A. Jonathan

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? APPLICANT: Branchek A. Theresa
? APPLICANT: Weinsthank L. Richard
? TITLE OF INVENTION: DNA ENCODING A HUMAN SEROTONIN
? TITLE OF INVENTION: RECEPTOR (5-HT4B) AND USES THEREOF
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Cooper & Dunham LLP
? STREET: 1185 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: U.S.A.
? ZIP: 10036
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.24
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/157,185
? FILING DATE: 15-JUN-1995
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: White P., John
? REGISTRATION NUMBER: 28,678
? REFERENCE/DOCKET NUMBER: 41908-A-PCT-US/JPW/MAT
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 278-0400
? TELEFAX: (212) 391-0525
? INFORMATION FOR SEQ ID NO: 13:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 422 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
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? US-08-157-185-13
?
? Query Match      13.0%; Score 343.5; DB 1; Length 422;
? Best Local Similarity 22.0%; Pred. No. 1.1e-19;
? Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;
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QY 26 ISLNGIIRSTVLVFLAASPVGN--IVLATVLQRRPOLQVTRNFIMLVTDLIQISL 83
DB 31 VVVSQVITSLTGLTIFCAVLGNACVVAIALER--SIQNVANVLIGSLAVTDLMVSVL 88
QY 84 VAPMVAVTSVPLFWPLNSHFTALVSLTHLFAPASVNTIVLSVDRYLSIIHPLSYPSKM 143
DB 89 VLPMAALYQVLNKMWTIGQVTCDFIALDVLCTSSILHLCAIALDRYMAITPIDVYVNR 148
QY 144 TORRGYLLYGTWIVAIILQSTPPLYGQGAARDEENALCSMTWGSPTSILSVSFYI 203
DB 149 TFRRAAALISLTWILGFLISIPMLGWRTP--EDRSDPDACTISKDHGTTIYSTGAFYI 206
QY 204 PLIVMIACYSVVFCAARQHALLVNKRHSLEVRKDCVENDEGAKEKEFEODESEFR 263
DB 207 PLLMLVLVYGRIFRAAR-----FRIRKTVKVEKGTGADTRHGASAPAPQK 251
QY 264 RQHEBEVAKKEGRM--EAKDGSL-----KAKEGSTSTSSSVEARGSEVRSSSTVASDG 316
DB 252 KSVNKGSGSRNMRNLGVESKAGALCANGAVRQGDGAALVEIVH----- 296
QY 317 SMEKGEGSTKVEENMKADKGRTEVNQCSIDLGEDMEFGEDDINFSDDVEAVNIPESL 376
DB 297 ----RVGNK-BHPLPSEAGPTPCAPASFE----- 322
QY 377 PPSRRNSNPNPLPRCYOCKAKAVIFIIIFSIVLSIGPYCFPLAVLAVWVDETQVPQWVI 436
DB 323 RKNERAAEKAKRKAALARKERTVLTIGITGTFILCLPFIIVLAVLPFCSSSCHMPTLLG 382
QY 437 TIIIMFLFQCCIHPRVYGYMKTIKKEIQDMLKRFCKE 476
DB 383 AIIIMLGYSNLINPLVIAVFNKDFONAFKTIKCLFCFQ 422
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? RESULT 15
? US-08-281-526B-13
? Sequence 13, Application US/08281526B
? Patent No. 6083749
?
? GENERAL INFORMATION:
? APPLICANT: Bard A. Jonathan
? APPLICANT: Branchek A. Theresa
? APPLICANT: Weinsthank L. Richard
? TITLE OF INVENTION: DNA ENCODING A HUMAN SEROTONIN
? TITLE OF INVENTION: RECEPTOR (5-HT4B) AND USES THEREOF
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Cooper & Dunham LLP
? STREET: 1185 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: U.S.A.
? ZIP: 10036
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.24
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/281,526B
? FILING DATE: 27-JUL-1994
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: White P., John
? REGISTRATION NUMBER: 28,678
? REFERENCE/DOCKET NUMBER: 41908-1/JPW
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 278-0400
? TELEFAX: (212) 391-0525
? INFORMATION FOR SEQ ID NO: 13:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 422 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
? US-08-281-526B-13
?
? Query Match      13.0%; Score 343.5; DB 2; Length 422;
? Best Local Similarity 22.0%; Pred. No. 1.1e-19;
? Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;
?
QY 26 ISLNGIIRSTVLVFLAASPVGN--IVLATVLQRRPOLQVTRNFIMLVTDLIQISL 83
DB 31 VVVSQVITSLTGLTIFCAVLGNACVVAIALER--SIQNVANVLIGSLAVTDLMVSVL 88
QY 84 VAPMVAVTSVPLFWPLNSHFTALVSLTHLFAPASVNTIVLSVDRYLSIIHPLSYPSKM 143
DB 89 VLPMAALYQVLNKMWTIGQVTCDFIALDVLCTSSILHLCAIALDRYMAITPIDVYVNR 148
QY 144 TORRGYLLYGTWIVAIILQSTPPLYGQGAARDEENALCSMTWGSPTSILSVSFYI 203
DB 149 TFRRAAALISLTWILGFLISIPMLGWRTP--EDRSDPDACTISKDHGTTIYSTGAFYI 206
QY 204 PLIVMIACYSVVFCAARQHALLVNKRHSLEVRKDCVENDEGAKEKEFEODESEFR 263
DB 207 PLLMLVLVYGRIFRAAR-----FRIRKTVKVEKGTGADTRHGASAPAPQK 251
QY 264 RQHEBEVAKKEGRM--EAKDGSL-----KAKEGSTSTSSSVEARGSEVRSSSTVASDG 316
DB 252 KSVNKGSGSRNMRNLGVESKAGALCANGAVRQGDGAALVEIVH----- 296
QY 317 SMEKGEGSTKVEENMKADKGRTEVNQCSIDLGEDMEFGEDDINFSDDVEAVNIPESL 376
DB 297 ----RVGNK-BHPLPSEAGPTPCAPASFE----- 322
QY 377 PPSRRNSNPNPLPRCYOCKAKAVIFIIIFSIVLSIGPYCFPLAVLAVWVDETQVPQWVI 436
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Db 323 RKNERNAEAKRRKMALAREKTVKTLGIMGTFILCMLPPFIVALVLPCESSCHMPTLLG 382
Qy 437 TIIIMLFPLQCCIHPEYVYGYMHKTIKEIODMLKKFCKE 476
Db 383 AIINWLGYSNSILNPVIYAFNKFQNAFKKIKCLFCRQ 422

Search completed: December 3, 2005, 06:37:51
Job time : 41.1 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:36:57 ; Search time 6.92727 Seconds
(without alignments)
351.144 Million cell updates/sec

Title: US-10-712-615-2

Perfect score: 2644
Sequence: 1 MISTCTNSTRESNHSHTCMP.....GTEGTEKIVPSYDSTRFP 508

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:*
1: /cgn2_6/prodata/1/pubppaa/US09_NEW_PUB.pep:*
2: /cgn2_6/prodata/1/pubppaa/US06_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubppaa/US07_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubppaa/US08_NEW_PUB.pep:*
5: /cgn2_6/prodata/1/pubppaa/PCT_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubppaa/US10_NEW_PUB.pep:*
7: /cgn2_6/prodata/1/pubppaa/US11_NEW_PUB.pep:*
8: /cgn2_6/prodata/1/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2641	99.9	508	6	US-10-980-388-112 Sequence 112, App
2	791	29.9	204	6	US-10-980-388-68 Sequence 68, App1
3	204.5	7.7	352	7	US-11-068-686-20 Sequence 20, App1
4	198	7.5	417	6	US-10-992-577-44 Sequence 44, App1
5	197.5	7.5	419	7	US-11-067-884-8 Sequence 8, App11
6	194.5	7.4	352	7	US-11-068-686-2 Sequence 2, App11
7	191.5	7.2	432	6	US-10-992-577-2 Sequence 2, App11
8	186.5	7.1	355	7	US-11-068-686-4 Sequence 4, App11
9	184.5	7.0	440	6	US-10-502-893-2 Sequence 2, App11
10	175.5	6.6	430	6	US-10-992-577-8 Sequence 8, App11
11	174.5	6.6	420	6	US-10-992-577-6 Sequence 6, App11
12	174.5	6.6	522	6	US-10-510-018-2 Sequence 2, App11
13	171.5	6.5	409	6	US-10-627-633-4 Sequence 4, App11
14	166	6.3	415	6	US-10-627-633-2 Sequence 2, App11
15	164.5	6.2	352	6	US-10-627-633-6 Sequence 6, App11
16	164	6.2	340	6	US-10-980-388-117 Sequence 117, App
17	163.5	6.2	342	6	US-10-980-388-118 Sequence 118, App
18	144	5.4	360	6	US-10-851-667A-26 Sequence 26, App
19	137.5	5.2	181	6	US-10-980-388-100 Sequence 100, App
20	137	5.2	485	6	US-10-821-234-934 Sequence 934, App
21	131.5	5.0	358	6	US-10-980-388-96 Sequence 96, App1
22	131.5	5.0	389	6	US-10-980-388-116 Sequence 116, App
23	128.5	4.9	271	6	US-10-980-388-67 Sequence 67, App1
24	125.5	4.7	347	6	US-10-131-826A-18 Sequence 18, App1
25	120.5	4.6	350	6	US-10-502-145-1 Sequence 1, App1

26	114	4.3	337	6	US-10-980-388-115 Sequence 115, App
27	114	4.3	353	7	US-11-067-884-6 Sequence 6, App11
28	111.5	4.2	351	7	US-11-067-884-4 Sequence 4, App11
29	111	4.2	349	6	US-10-131-826A-424 Sequence 424, App
30	106	4.0	313	7	US-11-095-093-2 Sequence 2, App11
31	106	4.0	364	7	US-11-067-884-2 Sequence 2, App11
32	100	3.8	313	6	US-10-980-388-63 Sequence 63, App1
33	99	3.7	1388	6	US-10-821-234-1143 Sequence 1143, App
34	96	3.6	793	7	US-11-060-914-2 Sequence 2, App11
35	95	3.6	287	6	US-10-980-388-66 Sequence 66, App1
36	94.5	3.6	356	6	US-10-980-388-70 Sequence 70, App1
37	93	3.5	543	6	US-10-689-742-78 Sequence 78, App1
38	93	3.5	858	6	US-10-645-441-18 Sequence 18, App1
39	92	3.5	432	7	US-11-055-822-1096 Sequence 1096, App
40	91.5	3.5	431	7	US-11-092-140-6 Sequence 6, App11
41	91.5	3.5	790	6	US-10-131-826A-204 Sequence 204, App
42	91	3.4	312	6	US-10-858-730-122 Sequence 122, App
43	91	3.4	782	6	US-10-793-626-2352 Sequence 2352, App
44	91	3.4	858	6	US-10-645-441-23 Sequence 23, App1
45	90.5	3.4	615	6	US-10-982-545-14 Sequence 14, App1

ALIGNMENTS

RESULT 1
US-10-980-388-112
; Sequence 112, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayes, Paul S.
; APPLICANT: Huff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325 US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 112
; TYPE: PRT
; LENGTH: 508
; ORGANISM: Homo sapiens
; US-10-980-388-112
Query Match 99.9%; Score 2641; DB 6; Length 508;
Best local Similarity 99.8%; Pred. No. 4,4e-198;

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Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 121 TIVVSVDRYLSIHPLEPSKMTQRGYLELGYTWIYVLIQSTPPLVGMGQAAEDENA 180
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Db 181 LCSMIMGASPSYTIISVSVFIVIPLIWIAVCSVFCARQHALLVNWKSHLEVRVYD 240
Qy 241 CVENEDDEGAKEKEFEQDESEFRQHEGEVYAKEGRMAKQSLKAKGSGTSTSSVEA 300
Db 241 CVENEDDEGAKEKEFEQDESEFRQHEGEVYAKEGRMAKQSLKAKGSGTSTSSVEA 300
Qy 301 RGSSEVRSSSTVYASDGSMEKSGSTKVENSMKADKGRTEVNOCSIDLGEDDMERGEDDI 360
Db 301 RGSSEVRSSSTVYASDGSMEKSGSTKVENSMKADKGRTEVNOCSIDLGEDDMERGEDDI 360
Qy 361 NFSEDDVAVNIPESLPPSRNSNSNPPLPRCYCKAKAVIFIIISVYLSLGPYCFPLAV 420
Db 361 NFSEDDVAVNIPESLPPSRNSNSNPPLPRCYCKAKAVIFIIISVYLSLGPYCFPLAV 420
Qy 421 LAWVVDVETQVQWVITIIIMFLQCCIHPRVYGYMKTIKKEIQDMLKRFCEKRPK 480
Db 421 LAWVVDVETQVQWVITIIIMFLQCCIHPRVYGYMKTIKKEIQDMLKRFCEKRPK 480
Qy 481 EDSHDPDPTGEGTEGKIIVPSYDSATFP 508
Db 481 EDSHDPDPTGEGTEGKIIVPSYDSATFP 508

RESULT 2
US-10-980-388-68
; Sequence 68, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayles, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325-US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
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; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 68
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-68

Query Match 29.9%; Score 791; DB 6; Length 204;
Best Local Similarity 98.7%; Pred. No. 4,46-55;
Matches 156; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIRSTVLVIFLASFVGNIVLALVLRKP 60
Db 47 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIRSTVLVIFLASFVGNIVLALVLRKP 106
Qy 61 QLLQVTRNFIFNLVTDLQISLVAPWVAVTSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
Db 107 QLLQVTRNFIFNLVTDLQISLVAPWVAVTSVPLFWPLNSHFCTALVSLTHLFAFASVN 166
Qy 121 TIVVSVDRYLSIHPLEPSKMTQRGYLELGYTWIY 158
Db 167 TIVVSVDRYLSIHPLEPSKMTQRGYLELGYTWIY 204

RESULT 3
US-11-068-686-20
; Sequence 20, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicki L.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6100 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068,686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Grete E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6500
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-11-068-686-20

Query Match 7.7%; Score 204.5; DB 7; Length 352;
Best Local Similarity 26.3%; Pred. No. 2,7e-09;
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Matches 61, Conservative 49, Mismatches 103, Indels 19, Gaps 7
Oy 16 HTCHPPLSMPI-SLAHGIRSTVAVIFLAASVGVIVLALVYQRKPOLQVNRETLNL 74
Db 15 YTSEPCQIKVVKQIAARLLPPLYSLVF-FGVGVILVLLINCKRLKSMTDIYLLNIA 73
Oy 75 VTDLQISLVA.PMWAVATVPLFWPLNSHFCATLSLTHLPAFASVNTVLVSVDRLYSII 134
Db 74 ISDLLEFLTVPPW--AHYAAAMQDFGNTWCQLLTGLYFIFGFSGLFTIILLTIDRLAIIV 131
Oy 135 HPLSPSKMTRORRGVILLTGTIVVILLOSTPPLYGMOAAPERNAALCS-----MIW 186
Db 132 HAVFALKARITYFGVGVTSVITMVAVAPSLPEII-FTRSQRGHAYTSCSHPEYQYQFW 190
Oy 187 GASPEYITLSVSGFVIVPLIYMIACYSVVFCAARQHALINVKHSLSEVRV 238
Db 191 --KNFQTKMIVLGLVLLPLLVVICYSGILTKTLR----CRNEKKRHAVRL 236

RESULT 4
US-10-992-577-44
; Sequence 44, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P. G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FP (NPFF) Receptors
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 57155-D/UPW
; CURRENT APPLICATION NUMBER: US/10/992,577
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-992-577-44

```

Query Match	7.5%	Score 198;	DB 6;	Length 417;
Best Local Similarity	17.4%	Pred. No. 1e-08;		
Matches	82;	Conservative	69;	Mismatches 141; Indels 180; Gaps 12;
Qy	33	IRSTVTVFLTAAPGNYIVLALVLRKKQLQYTRFFNLVTDLLQSLVAAPVAVTS	92	
Db	49	ISSYFLIFLC--MGNTVVCQVVRNRMYHTVTFLENAISDLLGVICFMPPTLLDN	106	
Qy	93	VPLEWPLSHFCTALVSLTHLFAFASVNTIVLVSVDRLSIILHPSYFSKMTORRGYLL	152	
Db	107	IAGPFPSSMCKISGLVGISVVASVFLVALVADRRCVYF--FPRKLTVKAFPMI	164	
Qy	153	YGTIVVALLOSTPRPY-----GNGQAFFDERNALCGMINGAS--PS-----YTIISV	197	
Db	165	VIIMGLATTIMTPSAIMLHVQEKYRVRLLSHNTSTVYVWREDWPMQEMRIITVYLF	224	
Qy	198	VSFIYPIVLIMVACSVVFCARROHALLVYNRKSLSEVRVQDVENEDBEAGKEEFQ	257	
Db	225	ATVIAPLSLIVMYA-----RIGASLFTKSAMS-----TGKQLBQM-	262	
Qy	258	DESEFRQHEGVAKKEGRMEAKDGLAKKSGSTGTSSSVEARSGEVRBESVTYASGS	317	
Db	263	-----HVSKKKQ-----	269	

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Qy 318 MECKESTVEENSKKADKGRTEVNOGSDJGDDMDMEGDDINFSEDDVEAVNIPESLP 31777
Db 270 -----2659-----
Qy 378 PSRRNSNSNPPLBRCYQCKAKAVIFIIIESVYLSGPFCLAVLVAVWDVETQVQWVIT 4337
Db 270 -----KVIRMLLTVALMLTILSLMLPLMTLMTMSDYADISPNKLR-VIN 310
Qy 438 III-----WLFPQCCIHPPYVYGVYMKIKKEIODMLKPFCKEKEKPEKEDSH 484
Db 311 IIVYPAHMLAFONSSVNPPIITYGFEENEPFRSGQDAPQ--FCQKXKVPQEXY 360

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RESULT 5
US-11-067-884-8
; Sequence 8, Application US/11067884
; Publication No. US20050261252A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Duane D.
; APPLICANT: TigyI, Gabor
; APPLICANT: Dalton, James T.
; APPLICANT: Sarder, Vineet M.
; APPLICANT: Elrod, Don B.
; APPLICANT: Xu, Huidong
; APPLICANT: Baker, Daniel L.
; APPLICANT: Wang, Dean
; APPLICANT: Lilliom, Karoly
; APPLICANT: Fischer, David J.
; APPLICANT: Virag, Tamas
; APPLICANT: Nusser, Nora
; TITLE OF INVENTION: LPS RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
; TITLE OF INVENTION: LPS
; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/611,838
; PRIOR FILING DATE: 2001-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 419
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-067-884-8

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	Query Match	7.5%;	Score 197.5;	DB 7.5;	Length 419;
	Best Local Similarity	17.4%;	Pred. No. 1.2e-08;		
	Matches	90;	Conservative 78;	Mismatches 168;	Indels 181; Gaps 15;
Qy	1	MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVLVIFLAAFPVGNIVALVLRKP	60		
	:	:::	:	:	:
	:	:::	:	:	:
Dd	56	LSLUTLVNSTAVPT-----PAAFSLNLPIDITLSAIMIFLPVSPFGNLVCLMAYYKA	110		
	:	:	:	:	:
	:	:	:	:	:
Qy	61	QLDLOVNRFEINLLVTDLQISLVAENVVATSVPLEFMLENSHFTALVSLTHLFASFVN	120		
	:	:	:	:	:
	:	:	:	:	:
Dd	111	AMRSAINILLASLAPADMLLAVLNMPALVTILTTTRWTFGKFCFRVSAMPFLVEIEGVA	170		
	:	:	:	:	:
	:	:	:	:	:
Qy	121	TIVLVSDRYLSTIHPLSYPSKMTQRGRGYLLXGTGWIVALLQSTPPLYGMQQAADFENNA	180		
	:	:	:	:	:
	:	:	:	:	:
Dd	171	ILLIISIDRFILTV--ORODKLMPYRKYAKVLIIVASMTATSCFAEFLAVGNPDLOIPSPAP	227		
	:	:	:	:	:
	:	:	:	:	:
Qy	181	LCSMIWGASPEY----TILSVSFEFVLPDYIMACYSVFCABAROHALLYNVRKHSLEV	236		
	:	:	:	:	:
	:	:	:	:	:
Dd	228	QCVCVGYTNPFQYQAVILISLISFF-IPLVYL--YSTMG-----LIANTLRHN---	272		
	:	:	:	:	:
	:	:	:	:	:
Qy	237	RVKDCVENEDEGAEKKKEEPQDESEFRROHEGEVAKAGEGRMEAKDGLIKAKEGSTGTSES	296		
	:	:	:	:	:
	:	:	:	:	:
Dd	273	-----ALRHISYPEGICLDS	286		
	:	:	:	:	:
	:	:	:	:	:
Qy	297	SVEARGSEEVRESSTVASDGSMCKEGESTKYKENSMTAKDKRTREVNOCSDLDGEDDMFEG	356		

Db 287 QASKGLMSLOPP-----QMSIDMG----- 307
Qy 357 EDDINFSEDDVEAVNIPESLPSPRRNSNPNPLPRCYOAKAVIFIIIFSYLSLGPYC 416
Db 308 -----FKTRAFITLLILEFAVIVCMALFT 331
Qy 417 FLAVLAV-----WVDVETQVPQVVTITIIWLFPLQCCIPHPYGVGMKTIKKEIQ 466
Db 332 TYSLVATSKHPHYOHNFEIST-----W-----LMLWCYLKSLNPLIYWM----- 373
Qy 467 DMLKKEF--CKEKPKEDSHPLPGTEGTEGKIYPS 501
Db 374 -RIKKEFDACIDMPK--SFKEFLPOLPGHTKRIRPS 407

RESULT 6

US-11-068-686-2
Sequence 2, Application US/11068686
Publication No. US20050260565A1
GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
Schweickart, Vicky L.
Report, Carol J.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/068,686
FILING DATE: 28-Feb-2005
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33670
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: /= "88C amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-11-068-686-2

Query Match 7.4%; Score 194.5; DB 7; Length 352;
Best Local Similarity 25.0%; Pred. No. 1.6e-08;
Matches 58; Conservative 51; Mismatches 104; Indels 19; Gaps 7;
Qy 16 HTCMPLSKMPT-SLAHGIIIRSTVIVIFLAAGFVGNIVLALVQKRPQLQVNNRIIFNL 74
Db 15 YTSECCQKINVKQIARLLPLXSLVFI-FGFVGMLVTLILINCKRLKSMIDIVLNL 73
Qy 75 VTDLQISLVAPWVATSVPLFWPLNSHFCIALVSLTHLFAFASVNTIVLVSDRYLSII 134
Db 74 ISDLFFLLVPPW--AHYAAAGMDFGNTMQLLTGLYIFGFSGLFIITLLIDRIYLV 131

Qy 135 HPLSPSKMTORRGVLLYGTVIVAILOSTPPLYGMGAADERNALCS-----MIW 186
Db 132 HAVFALKARTYTFGVNYSVITWVAVFASLPGII-FTRSQEGAHYTCSSHPFSQYQFW 190
Qy 187 GASPSYTLISVSVFVPLIYMIACYSVFCFAARQHALYVNRKHSLEVY 238
Db 191 --KNFQIKIVILGLVLPVLVWVICYSIGILKTLR---CNEKKRRAVYL 236

RESULT 7

US-10-992-577-2
Sequence 2, Application US/10992577
Publication No. US20050260687A1
GENERAL INFORMATION:
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Jones, Kenneth A.
APPLICANT: Bonini, James A.
APPLICANT: Borowsky, Beth E.
APPLICANT: Craig, Douglas A.
TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
FILE REFERENCE: 57155-D/JPW
CURRENT APPLICATION NUMBER: US/10/992,577
PRIOR FILING DATE: 2004-11-18
PRIOR APPLICATION NUMBER: US/09/538,036
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/405,558
PRIOR FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: 09/255,368
PRIOR FILING DATE: 1999-02-22
PRIOR APPLICATION NUMBER: 09/161,113
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 2
LENGTH: 432
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-992-577-2

Query Match 7.2%; Score 191.5; DB 6; Length 432;
Best Local Similarity 16.6%; Pred. No. 3.6e-08;
Matches 94; Conservative 64; Mismatches 144; Indels 265; Gaps 17;
Qy 2 TSTCTNSSTRSNSHTCMPLSKMPTSLAHGIIIRSTVIVIFLAAGFVGNIVLALVQKRPQ 61
Db 24 TSMATSLTFSSYYQHS-SPVAM-----FLAIVLIFLCC--MVGNTLVCFVLKRRH 73
Qy 62 LIQVTNRIFNLVTDLQISLVAPWVATSVPLFWPLNSHFCIALVSLTHLFAFASVNT 121
Db 74 KRTVTNMFILNLAVSDLLVGIFCMFTTLVDMLITGMFPDNTCKMSGILVQGMVSASVFT 133
Qy 122 IVLVSVDRYLSIIHPLSPSKMTORRGVLLYGTVIVAILQSTP----- 165
Db 134 LVAILVERFCIVHD--FREKTLTKALFTTAVIWMALLMCSAVTLTYTRESHHML 191
Qy 166 -----PLYGMGAADERNALCSMIW---GASPSYTLISVSVFVPLIYMIACYSV 215
Db 192 DARRNSYPLYS-----CWEAWPEKGMKRVYAVFAHYLVPLALIVMY--- 236
Qy 216 FCAARRQHALYVNRKHSLEVRYKDCVENDEBGAKEKEEFQDSSEFRRQHEGVAKEG 275
Db 237 -----VRIARKLC----- 244
Qy 276 RMEAKDSLKAKESGTSTSESVARSGSEVRESSTVASDSMGEKSGSTVKEENSMKAD 335
Db 245 -----QAPGRARDEEA-----VAE 259
Qy 336 KGRTEVNCOSIDLGEDMFEDEDINFSEDDVEAVNIPESLPSPRRNSNPNPLPRCYQC 395
Db 260 GGR-----SRR-----RA 268
Qy 396 KAAKVIITIIIFSYLSLGPYCFLLAVLAVWVDVETQVPQWVITITII----- 440

Db 269 RVVHMLVWALFETLS-----W-----LPLWVLLLLIDYGBLSLQHLHLSV 310
Qy 441 -----WLFLOCCIHPIVYGYMHTIKKEIDMLKKEFC-----KEKP----- 478
Db 311 VAFPLAHMLAFHSSANPIIYGFNFGRFOALRAQLCWPMAAHKQAYSERPNRL 370
Qy 479 -----PKEDSHDLPDTEGTEG 496
Db 371 RRRVVVDVQPSDGLPSESGLSPG 397

RESULT 8
US-11-068-686-4
; Sequence 4, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; Schmeickart, Vicky L.
; Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068,686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88-2B amino acid sequence"
; US-11-068-686-4

Query Match 7.1%; Score 186.5; DB 7; Length 355;
Best Local Similarity 24.0%; Pred. No. 6.9e-08;
Matches 47; Conservative 48; Mismatches 86; Indels 15; Gaps 5;

Qy 40 IFLAASFVGNIVLALVQRRPOLQVTRNPFILVLTDLQISLVAIPWVAVSPLEW 99
Db 43 LVFTVGLLGNVVMMLIKRRIRMTNTIYLNLAISDLFLVTLFVFWIHYVR-GNNWF 101
Qy 100 NSHFTALVSLTHLFAFASVNTIVLVSDRYLSIHPLSYPSKMTGRGYLLYGTWIVA 159
Db 102 GGGMCCLLSGFGYHTGYSFIIFLLITIDRYLAIVAVPALRARTVTFGVITSIVTWGLA 161
Qy 160 ILSSTFP-LYMGQAFAFDERNALCSMIMGASPSY-----TILSVSFIVIPYIYVIA 212
Db 162 VLAALPEFIYETEELEER--TLCALVYRBDIVYSWRHHTYLMITFCLVPLVLAICY 219

Qy 213 SVVF-----CAARRQH 223
Db 220 TGIKTLRCPSKKY 235

RESULT 9
US-10-502-893-2
; Sequence 2, Application US/10502893
; Publication No. US20050255529A1
; GENERAL INFORMATION:
; APPLICANT: Bayer HealthCare AG
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Geerts, Andreas
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with a New
; FILE REFERENCE: Ica 35 827
; CURRENT APPLICATION NUMBER: US/10/502,893
; PRIOR FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: PCT/EP03/000479
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: EP 02001942.8
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent version 3.2
; SEQ ID NO 2
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-502-893-2

Query Match 7.0%; Score 184.5; DB 6; Length 440;
Best Local Similarity 26.7%; Pred. No. 1.3e-07;
Matches 56; Conservative 35; Mismatches 76; Indels 43; Gaps 7;

Qy 35 STVLVIFLAASFVGNIVLALVQRRPOLQVTRNPFILVLTDLQISLVAIP----- 86
Db 30 AALCVIALTPAANSILIALICTOPALNTSNFVLSFTSDLMGLVMPAMLNALY 89
Qy 87 --MVVATSVPLFWPILNSHCTALVSLTHLFAFASVNTIVLVSDRYLSIHPLSYSKMT 144
Db 90 GHWLARGCLMTAPDVNCS-----ASILNCLISLDRYLLTILSPURYLRMT 139
Qy 145 QRRGYLLVGTWIVAILQS--TPPLYGW-----GOAFAFDERNALCSMIMGASPSY 192
Db 140 PLRALALVIGANSLAALASFLPLILGHEHGHARPPVVGQ-----CRLL-ASLPV 189
Qy 193 TILSVSFIVIPYIYVIAICYSVFCAARRQ 222
Db 190 LVASGLTFE-LPSGALCFYCRILLAAARQ 218

RESULT 10
US-10-992-577-8
; Sequence 8, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerold, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; FILE REFERENCE: 57155-D/JFM
; CURRENT APPLICATION NUMBER: US/10/992,577
; PRIOR FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22

```
;; PRIOR APPLICATION NUMBER: 09/161,113
;; PRIOR FILING DATE: 1998-09-25
;; NUMBER OF SEQ ID NOS: 71
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 8
;; LENGTH: 430
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-992-577-8

Query Match      6.6%; Score 175.5; DB 6; Length 430;
Best Local Similarity 25.1%; Pred. No. 6.3e-07;
Matches 61; Conservative 39; Mismatches 90; Indels 53; Gaps 9;

QY 6 TNSRRESNSHTCMPLSKMPISLHAGIRSTVLVIFLAASFVGNITVALVQKPKQLQY 65
DB 28 TNLFFSSYYOHT-SPVAAMFI-VAAYAL-----IFLLC-MVGNLTVCFIVLKNHMTV 77
QY 66 TNRFTFNLVLDLQISLVAAPVAVTSVPLFWPLNSHCTALVSLTHFAPASVNTIVLV 125
DB 78 TMMFLMLNLAVDLVLGIFCMPTTLVDNLITGMPFDNATCKMSGVLQGMSVASVETLVAI 137
QY 126 SVDRYLSIHPISYPSKMTORRGVLLVGTWIVALTQSTP----- 165
DB 138 AVERRCIVHP--FRKLTIRKALVTIATVATMALIMCPASVTLTTRREHHPVDAKN 195
QY 166 ---PLYGWGOAFADEBNALCSMW---GASPSYTLISVSVFIVLIVMIACYSVY---F 216
DB 196 RSYPLYS-----CMEAWPEKGMRRVYTTVLFSHYLADLALIVVAVARIARKL 243
QY 217 CAA 219
DB 244 CQA 246

RESULT 11
US-10-992-577-6
; Sequence 6, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; FILE REFERENCE: 57155-D/JPM
; CURRENT APPLICATION NUMBER: US/10/992,577
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-992-577-6

Query Match      6.6%; Score 174.5; DB 6; Length 420;
Best Local Similarity 18.7%; Pred. No. 7.3e-07;
Matches 84; Conservative 74; Mismatches 145; Indels 147; Gaps 14;

QY 33 IRSTVLVIFLAASFVGNITVALVQKPKQLQVTRNRFNLVLDLQISLVAAPVAVTS 92
DB 49 IISYFLIFLC--MMGNVVCFTIVRNKRMHTVTNLFIINLAISDLVLGIFCMPTTLDN 106
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QY 93 VPLFWPLNSHCTALVSLTHFAPASVNTIVLVSDRYLSIHPISYPSKMTORRGVLL 152
DB 107 IIAGMFGNTMCKISGLVQGISVAASVETLVAIVDFQCQVYP--FRPKLTITATAVII 164
QY 153 YGTWIVALTQSTPPLYGWGOAFADEBNALCSMWGASPSYTLISVSVFIVPLVIAC 212
DB 165 MIWVLAI-----TIMS-----PSAVML--- 182
QY 213 SVFECAARRQHALLYNVRKHSLEVRVKDVENEDBEAGKEEFPQDESEFRROHEGEVKA 272
DB 183 -----HYGEKXYRRLNS-----QNKTSPLYWCGEDBP----- 211
QY 273 KEGMEAKDGLKAKEGSTGSTSESSVEARSGSEVRESSTYVADSQSMCKEGSTVEENSM 332
DB 212 -----NOEMRKXYT-----TVLFANIT 228
QY 333 KADGRTEVNCSIDLGEDDMEFGEDDINFEDEDDVEAVNIPESLPSPRRNSNPPLPRC 392
DB 229 LA-----PLSLIYIMYGRIGISLFR---AAVPHT---GRKQDEQHHVYSRK 268
QY 393 YQCAKAVIFIIISYVLSLGPYCFVLAVAVVDETQVPQWVTITII-----WLFPLQC 447
DB 269 KQ-KIKMLLIVALLFILSMPLMTLMLSDYADLSNBLQ-INIYIYPRAHMLAFGNS 326
QY 448 CIHPYVYGYMAKTIKSIQDMKKPFCEK 477
DB 327 SVNPIIYGFENENFRGRFOEAFQLOLCOKR 356

RESULT 12
US-10-510-018-2
; Sequence 2, Application US/10510018
; Publication No. US20050244896A1
; GENERAL INFORMATION:
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Golz, Stefan
; APPLICANT: Weingarten, Bernhard
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
; FILE REFERENCE: Le A 35 945
; CURRENT APPLICATION NUMBER: US/10/510,018
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: PCT/EP2003/002962
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: EP 02007270.8
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 2
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-018-2

Query Match      6.6%; Score 174.5; DB 6; Length 522;
Best Local Similarity 18.7%; Pred. No. 9.6e-07;
Matches 84; Conservative 74; Mismatches 145; Indels 147; Gaps 14;

QY 33 IRSTVLVIFLAASFVGNITVALVQKPKQLQVTRNRFNLVLDLQISLVAAPVAVTS 92
DB 151 IISYFLIFLC--MMGNVVCFTIVRNKRMHTVTNLFIINLAISDLVLGIFCMPTTLDN 208
QY 93 VPLFWPLNSHCTALVSLTHFAPASVNTIVLVSDRYLSIHPISYPSKMTORRGVLL 152
DB 209 IIAGMFGNTMCKISGLVQGISVAASVETLVAIVADRCQCVYP--FRPKLTITATAVII 266
QY 153 YGTWIVALTQSTPPLYGWGOAFADEBNALCSMWGASPSYTLISVSVFIVPLVIAC 212
DB 267 MIWVLAI-----TIMS-----PSAVML--- 284
QY 213 SVFECAARRQHALLYNVRKHSLEVRVKDVENEDBEAGKEEFPQDESEFRROHEGEVKA 272
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Db 285 -----HVQEEKYRVRVRLNS-----QNKTSFVYWCREDWP----- 313
Qy 273 KEGREAKDGLKAKEGSTGTSSESVBARGSEVEBESSTVASDGSMEKGSTKVEBENM 332
Db 314 -----NOEMRKITYT-----TULFANITY 330
Qy 333 KADKRETEVNOCSIDLGEDDMEFEGEDDINFSEDDVEAVNIPESLPPSRNSNSNPPLPRC 392
Db 331 LA-----PLSLIVMYGRIGISLFR-----AAVPHPT---GRKNGQOMHVSRK 370
Qy 339 YCCAKAVFIIFISFVLSLGPYCFALAVAVNDVETQVPQWVITITII-----WLFELQC 447
Db 371 KQ-KIIMLLIYALLFIISMLPLMTLMLSDYADLSPNELQ-IINITYIPFAHWLAFGNS 428
Qy 448 CIHPYVGYVMHKTIKKEIDMLKKFPCXEX 477
Db 429 SVNPITIIYGFENFRGRFOEAFQLOLCQKR 458

RESULT 13
US-10-627-633-4
; Sequence 4, Application US/10627633
; Publication No. US20050250720A1
; GENERAL INFORMATION:
; APPLICANT: Charles, Andrew David
; APPLICANT: Brenmand, John Charles
; APPLICANT: Hart, Kevin Anthony
; TITLE OF INVENTION: Novel Compound
; FILE REFERENCE: 1991-221
; CURRENT APPLICATION NUMBER: US/10/627,633
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 09/722,342
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/172,146
; PRIOR FILING DATE: 1999-12-17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-627-633-4

Query Match 6.5%; Score 171.5; DB 6; Length 409;
Best Local Similarity 25.6%; Pred. No. 1.2e-06;
Matches 46; Conservative 37; Mismatches 90; Indels 7; Gaps 3;

Qy 40 IFLAA-----SFVGNIVLALVLRKPQLQVTRRFENLLVTDLQISLVAWVAVTSVPL 95
Db 64 IFFGALMLFSIFGNSLVCLVHRSRRTOSTNYFVVMACADLLISVASTPFLVLOFTTG 123
Qy 96 FWPJNSHFCIALVSLTHLFAFASVNTIVLVSDRYLSIIHPLSYPSKMTQRRGYLLLYGT 155
Db 124 RWTLSAMCKVRYRQYVLPQVIVLISICIDRFYTIYPLSF--KVSREKAKKMIAS 181
Qy 156 WIVALLQSTPPLYGQGAADFERNALCSIMWGPSPTLTSVSVFIVPLIYMIACYSV 215
Db 182 WILDAFVTPVFFFGSNMDSHCNIFLPSPWEGT-AYVIHFLVGVFVLSIILFYQKV 240

RESULT 14
US-10-627-633-2
; Sequence 2, Application US/10627633
; Publication No. US20050250720A1
; GENERAL INFORMATION:
; APPLICANT: Charles, Andrew David
; APPLICANT: Brenmand, John Charles
; APPLICANT: Hart, Kevin Anthony
; TITLE OF INVENTION: Novel Compound
; FILE REFERENCE: 1991-221
; CURRENT APPLICATION NUMBER: US/10/627,633
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 09/722,342
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; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/172,146
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-627-633-2

Query Match 6.3%; Score 166; DB 6; Length 415;
Best Local Similarity 24.3%; Pred. No. 3.3e-06;
Matches 49; Conservative 43; Mismatches 104; Indels 6; Gaps 3;

Qy 14 SHTCMPSKMPISLAHGISTVIVIFLAASFVNITLALVLRKPQLQVTRRFIRLU 73
Db 51 SNQTDLHYVLKGEVATASIFPGILMLF--SIFGNSLVCLVHRSRRTOSTNYFVVM 107
Qy 74 LVTDLQISLVAWVAVTSVPLFWPJNSHFCIALVSLTHLFAFASVNTIVLVSDRYLSI 133
Db 108 ACADLLISVASTPFLVLOFTTGRTGRTLSATCNVRYRQYVLPQVIVLISICIDRFYTI 167
Qy 134 IHPISYPSKMTQRRGYLLLYGTIVALLQSTPPLYGQGAADFERNALCSIMWGPSPT 193
Db 168 VYPLSF--KVSREKAKKMIASWIFDAGFVTPVLFYGSNMDSHCNIFLPSPWEGT-AYT 224
Qy 194 ILSVSVFIVPLIYMIACYSV 215
Db 225 VIHFLVGVFVLSIILFYQKV 246

RESULT 15
US-10-627-633-6
; Sequence 6, Application US/10627633
; Publication No. US20050250720A1
; GENERAL INFORMATION:
; APPLICANT: Charles, Andrew David
; APPLICANT: Brenmand, John Charles
; APPLICANT: Hart, Kevin Anthony
; TITLE OF INVENTION: Novel Compound
; FILE REFERENCE: 1991-221
; CURRENT APPLICATION NUMBER: US/10/627,633
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 09/722,342
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/172,146
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-627-633-6

Query Match 6.2%; Score 164.5; DB 6; Length 352;
Best Local Similarity 24.4%; Pred. No. 3.5e-06;
Matches 44; Conservative 38; Mismatches 91; Indels 7; Gaps 3;

Qy 40 IFLAA-----SFVGNIVLALVLRKPQLQVTRRFENLLVTDLQISLVAWVAVTSVPL 95
Db 29 IFFGALMLFSIFGNSLVCLVHRSRRTOSTNYFVVMACADLLISVASTPFLVLOFTTG 88
Qy 96 FWPJNSHFCIALVSLTHLFAFASVNTIVLVSDRYLSIIHPLSYPSKMTQRRGYLLLYGT 155
Db 89 RWTLSAMCKVRYRQYVLPQVIVLISICIDRFYTIYPLSF--KVSREKAKKMIAS 146
Qy 156 WIVALLQSTPPLYGQGAADFERNALCSIMWGPSPTLTSVSVFIVPLIYMIACYSV 215
Db 147 WILDAFVTPVFFFGSNMDSHCNIFLPSPWEGT-AYVIHFLVGVFVLSIILFYQKV 205
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Search completed: December 3, 2005, 06:55:54
Job time : 8.92727 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:22:45 ; Search time 28.8636 Seconds
(without alignments)
1693.415 Million cell updates/sec

Title: US-10-712-615-2

Perfect score: 2644
Sequence: 1 MTSTCTNSTRESNSHTCMP.....GTEGTEKIVPSYDSTRPP 508

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	343.5	13.0	490	2 A35546	muscarinic acetylch
2	340.5	12.9	422	2 I38209	serotonin receptor
3	340	12.9	477	2 S71323	alpha-1A adrenergic
4	336	12.7	466	2 I57959	alpha-1C adrenergic
5	335.5	12.7	421	2 I49375	serotonin receptor
6	333.5	12.6	429	2 S65656	alpha-1C-adrenergic
7	333.5	12.6	466	2 J07065	alpha-1C-adrenergic
8	333.5	12.6	499	2 S65657	alpha-1C-adrenergic
9	331.5	12.5	422	2 JH0315	serotonin receptor
10	325.5	12.3	466	2 A35375	alpha-1-adrenergic
11	319	12.1	509	2 A47174	serotonin receptor
12	314.5	11.9	501	2 JH0447	alpha-1A-adrenergic
13	314.5	11.8	572	2 I39369	alpha-1A-adrenergic
14	312.5	11.8	484	2 S48657	muscarinic acetylch
15	306.5	11.6	560	2 A38731	alpha-1A adrenergic
16	304.5	11.5	601	2 JH0170	octopamine receptor
17	296.5	11.2	601	2 S12004	tyramine receptor
18	294	11.1	466	2 S10856	muscarinic acetylch
19	291	11.0	466	2 JH0197	muscarinic acetylch
20	291	11.0	479	2 S10327	muscarinic acetylch
21	289	10.9	466	2 A27386	muscarinic acetylch
22	288	10.9	488	2 T15941	hypothetical prote
23	288	10.9	515	2 S10125	alpha-1B-adrenergic
24	287	10.8	466	2 S10126	muscarinic acetylch
25	285	10.8	610	2 T32917	hypothetical prote
26	283	10.7	515	2 A40491	alpha-1B-adrenergic
27	283	10.7	517	2 A45121	alpha-1B adrenergic
28	282.5	10.7	478	2 C29514	muscarinic acetylch
29	282	10.7	479	2 S33776	muscarinic acetylch

30	280	10.6	466	2 A40972	muscarinic acetylch
31	279.5	10.6	476	2 JCS042	G protein-coupled
32	277.5	10.5	531	2 JTO531	muscarinic acetylch
33	276	10.4	564	2 A38271	serotonin receptor
34	275.5	10.4	484	2 S58668	G protein-coupled
35	275.5	10.4	532	2 JTO530	muscarinic acetylch
36	273	10.3	443	1 DTHUD2	dopamine receptor
37	273	10.3	445	2 A48881	serotonin receptor
38	270	10.2	448	2 A47519	serotonin receptor
39	268	10.1	448	2 S36402	serotonin receptor
40	267.5	10.1	442	1 DTHUD2	dopamine receptor
41	265	10.0	501	2 T18863	hypothetical prote
42	262.5	9.9	445	2 T42203	serotonin receptor
43	260	9.8	430	2 T16079	hypothetical prote
44	259.5	9.8	589	2 B29514	muscarinic acetylch
45	258	9.8	460	2 A31897	muscarinic acetylch

ALIGNMENTS

RESULT 1

A35546 muscarinic acetylcholine receptor M4 - chicken
C/Species: Gallus gallus (chicken)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C/Accession: A35546
R/Tietje, K.M.; Goldman, P.S.; Nathanson, N.M.
J. Biol. Chem. 265, 2828-2834, 1990
A/Title: Cloning and functional analysis of a gene encoding a novel muscarinic acetylch
A/Reference number: A35546; PMID:90153912; PMID:2154460
A/Accession: A35546
A/Molecule type: DNA
A/Residues: 1-490 <TIE>
A/Cross-references: UNIPROT:P17200; UNIPARC:UP100004E75B; GB:J05218; NID:G211067; PIDN
C/Superfamily: Vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmem
F/42-67/Domain: transmembrane #status predicted <TM1>
F/80-104/Domain: transmembrane #status predicted <TM2>
F/117-138/Domain: transmembrane #status predicted <TM3>
F/158-181/Domain: transmembrane #status predicted <TM4>
F/203-226/Domain: transmembrane #status predicted <TM5>
F/413-433/Domain: transmembrane #status predicted <TM6>
F/445-466/Domain: transmembrane #status predicted <TM7>

Query Match 13.0%; Score 343.5; DB 2; Length 490;
Best Local Similarity 23.7%; Pred. No. 1.1e-15;

Matches 116; Conservative 94; Mismatches 176; Indels 103; Gaps 17;

QY	36	TVLVIFLA-----	ASFGNIVLALVQRKPOLQVNRPIFNLTVDL-----	QISL 83
		::	::	::
QY	84	VAPWVATSVPLFWPLNSHFTALVSLTLFAFASVNTIVLVSVDRLYSIHPLSYSKRM 143		
		::	::	::
DB	39	TVELVFIATVTSGLSLVTVSGNLVWLSIKNRQLOTUNNYLFSLACDILIGVSSML 98		
QY	99	YTVYTIKG---YWPFGAVVCDMLALDLYVNSNANWMLISFDYFCVTKELTPARR 154		
		::	::	::
QY	144	TQRRGVLLIXGTWIVAILLOSTPPLYGM---GQAADENALCSMTWGSPTTILSVYS 199		
		::	::	::
DB	155	TYKMGAGLMTAAWILSFIIMAPALIFWQPIVSKRTVHERE--CYIOFLSNPAVTFGTATA 212		
QY	200	FIVIPLIWVIACSVYFCARROHALLVNKRHSLEVR-----VKDCVEN 244		
		::	::	::
DB	213	APFLPVIMTVLYIHLSLSRSR-----VRHKHPSRKRRKSKLSFKAPPVYKONNN 266		
QY	245	EDEGAKEKEEFQDESEFRQHEGYKAKGMEAKDGLKAKESGTGTSSESVEARGE 304		
		::	::	::
DB	267	SPRAVEVKEEVRN-----GKV-----DDPSAQTEATGQOE-----KE 301		
QY	305	EYRESSTVASDSMEKESGTVKEENSMKADKRTVNCSDIDLGDDMEFEGDDINPSE 364		
		::	::	::
DB	302	TSNESSTVSMOTYTKDP--TTEILPAGGQSPAHPRVPTSS-----KMSKIKLVTKO 352		

Qy 365 DDVEAVNIPESLP-----DSRRN--SNSNP--LPRCY-----OQKAAKV 400
Db 353 TGTSEVTEIEIVPAGASDHNSLSNSRPNVARKFASIASQYAKKQMAAREKKVTRT 412
Qy 401 IFFIIFSVLSGRCPCFLAVLAWVDVETQPOWVITTIIMFLPQCCIHPPVGVYMKT 460
Db 413 IFAILALITLWTFPNNVNLINTF--CEICVPEIWSIGYMLCVNSTINPACTALCNAT 470
Qy 461 IKKEIQDML 469
Db 471 FKTFKHL 479

RESULT 2
138209
serotonin receptor 1A - human
N.Alternate names: 5-hydroxytryptamine receptor 1A (5-HT1A)
C.Species: Homo sapiens (man)
C.Date: 06-Sep-1996 #sequence revision 15-May-1998 #text_change 09-Jul-2004
C.Accession: I38209; I37104; S07343; I56176; S31438
R.Jacobson, J.S.; Refolo, L.M.; Conley, M.P.; Sambamurti, K.; Humayun, M.Z.
Mutat. Res. 179, 89-101, 1987
A.Title: DNA replication-blocking properties of adducts formed by aflatoxin B1-2,3-dichl
A.Reference number: I38209; MUID:87258013; PMID:3110609
A.Accession: I38209
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-422 <JAC>
A.Cross-references: UNIPROT:P08908; UNIPARC:UPI0000124F1A; EMBL:X57829; NID:g36428; PIDN
R.Park, C.L.; Chang, L.S.; Shenk, T.
Nucleic Acids Res. 19, 7155-7160, 1991
A.Title: A polymerase chain reaction mediated by a single primer: cloning of genomic seq
A.Reference number: I37104; MUID:92115564; PMID:1766875
A.Accession: I37104
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-9 <PAR>
A.Cross-references: UNIPARC:UPI00000077A; EMBL:211168; NID:g1033027; PIDN:CAA77560.1; F
R.Koblika, B.K.; Friele, T.; Collins, S.; Yang-Peng, T.; Koblika, T.S.; Francke, U.; Le
Nature 329, 75-79, 1987
A.Title: An intronless gene encoding a potential member of the family of receptors coupl
A.Reference number: S07343; MUID:87153569; PMID:3041227
A.Accession: S07343
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-151, 'PR', 155-171, 'I', 173-417, 'N', 419-422 <KOB>
A.Cross-references: UNIPARC:UPI00000503DD; EMBL:X13565; NID:g35523; PIDN:CAA31908.1; PID
A.Note: the authors translated the codon ATC for residue 172 as Met
R.Aune, T.M.; McGrath, K.M.; Sarr, T.; Bombard, M.P.; Kelley, K.A.
J. Immunol. 151, 1175-1183, 1993
A.Title: Expression of 5HT1a receptors on activated human T cells. Regulation of cyclic
A.Reference number: I56176; MUID:93329096; PMID:8393041
A.Accession: I56176
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 'RPV', 203-227, 'R', 229-244, 'A', 245-354, 'T', 356-362, 'MRP' <AUN>
A.Cross-references: UNIPARC:UPI0000116D78; GB:S64045; NID:9404416; PIDN:AA013945.1; PID:
C.Genetics:
A.Gene: GDB:HTT1A; ADBR2RL1; ADBRRL1
A.Cross-references: GDB:120686; OMIM:109760
A.Map position: 5cen-5q11
C.Superfamily: vertebrate rhodopsin
C.Keywords: G protein-coupled receptor; glycoprotein; 11oprotein; neurotransmitter rece
F.37-62/Domain: transmembrane #status predicted <TM1>
F.74-98/Domain: transmembrane #status predicted <TM2>
F.110-132/Domain: transmembrane #status predicted <TM3>
F.153-178/Domain: transmembrane #status predicted <TM4>
F.192-217/Domain: transmembrane #status predicted <TM5>
F.346-367/Domain: transmembrane #status predicted <TM6>
F.379-403/Domain: transmembrane #status predicted <TM7>
F.10-11, 24/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.109-187/Diulfide bond: #status predicted
F.420/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 12.9%; Score 340.5; DB 2; Length 422;
Best Local Similarity 22.0%; Pred. No. 1.5e-15;
Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

Qy 26 ISLAHGIIRSTVVIIFLAASFVGN--IVLALVLRKQQLQVTRFIINLLVTLQISL 83
Db 31 VTSSVQVTTSLTLGLTFCAVLGNACVAAALALR--SLQNVAVYLGLSLDLMVSVL 88
Qy 84 VAPWVATSVPLFWPLNSHFTALVSLTHLPFASVNTIVLVSDRYLSIHPLSYSKM 143
Db 89 VLPMALYQVLNKKMTLGGVTCDDLFLALDVLCCTSSILHCAIALDRWALIDPIDYVKR 148
Qy 144 TORRGYLLVGTWVAIIQSTPPLYGWGOAFAEDRNALCSITWASPSYITLVSFVI 203
Db 149 TPRBAALISLTWLGFLISIPMLGWRT--EDRSPDCACTISKDHGYITVSTFGAFYI 206
Qy 204 PLIYVIAACYSVFCAARQHALLVNVRKHSLEVVKOCVENDEGAKEKEEPQDESFR 263
Db 207 PLLMLLVLYGRIFRAAR-----FPIKTVKVEKGTADTRHGASAPAPQK 251
Qy 264 RQHEGVYAKKGRM--EAKDGL-----KAKGSGTGSSESVFARGSEVESESTVASDG 316
Db 252 KSVNGSESSRWRLGVESKAGALCANAVAGDGAALVEIVH----- 296
Qy 317 SMEGKSGSTKYEENSMKADKGRTEVNCSDLDGEDMEFEGDDINPSEDVAVNIPESL 376
Db 297 ----RVGNSK-EHPLPSEAGPTPCAPASF----- 322
Qy 377 PPSRRNSNSNPPLPRCYCKAAKVIIFIIISVLSLGPYCFVLAVWVDVETQPOWVI 436
Db 323 RKNENNAAKRKMALARRKTKVLTGIIMGFIILCWLPFFVALVLPCESSCHMPTLLG 382
Qy 437 TIIVLFPQCCIHPPVYGVYMKTIKKEIQDMLKKFPCKE 476
Db 383 AIIMVLGYSNLSLNPVIYAVFNKDFQNAFKIIRCKKPERQ 422

RESULT 3
571323
alpha-1A adrenergic receptor - Japanese medaka
C.Species: Oryzias latipes (Japanese medaka)
C.Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
C.Accession: S71323
R.Yasuoka, A.; Abe, K.; Arai, S.; Emori, Y.
Eur. J. Biochem. 235, 501-507, 1996
A.Title: Molecular cloning and functional expression of the alpha-1-A-adrenoceptor of Me
A.Reference number: S71323; MUID:96184522; PMID:8654394
A.Accession: S71323
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-477 <YAS>
A.Cross-references: UNIPARC:UPI00001778AD; EMBL:D63859
A.Note: it is uncertain whether Met-1 or Met-8 is the initiator
C.Superfamily: vertebrate rhodopsin

Query Match 12.9%; Score 340; DB 2; Length 477;
Best Local Similarity 23.8%; Pred. No. 1.8e-15;
Matches 119; Conservative 66; Mismatches 180; Indels 134; Gaps 14;

Qy 12 SNSGHTCMPLSKMPSISLAHGIIRSTVVIIFLAASFVGNIVLALVLRKQQLQVTRFI 71
Db 18 SNCSHVLP----ELNTKAVAVLGVGLGIFLFGVIGILVLSVCHRHQQTIVYVYI 73
Qy 72 NLVTVDLQISLVAPWVATSVPLFWPLNSHFTALVSLTHLPFASVNTIVLVSDRYL 131
Db 74 NLAVALDLLSTVLPFSAIFFELDRWVGKVFCAINAAVDVLCCTASIMSLCVISVDRIY 133
Qy 132 SIHPLSPSKMTORRGYLLVGTWVAIIQSTPPLYGWGOAFAEDRNALCSITWASPS 191
Db 134 GVSYLRKRPALMTKRRALLAWMLVLSVIISIGLFPWKRP--PEDTVCKIT--EERG 190
Qy 192 YTIISVSVIYIPLIWMACYSVFCAARQHALLVNVRKHSLEVVKOCVENDEBGAE 251

```

Db      191 YAIFAVSGSYFLPLAILIILAMCYRVYVNAKESRGL-----KEG-Q 229
Qy      252 KKEEFODESEFRQHEGEVAKEGHWEAKDGLKAKESGTSTSESSVEARGSEVRESST 311
Db      230 KIEKSDSEQVILIRMRG-----NTT 249
Qy      312 VASDGSMEGKSGSTKVEENSMKADKGRTEVNOCSIDLGEDMEFGEEDINFSEDDVEAVN 371
Db      250 VSED-----EALRSRT-----HFLRLRLKFSREK----- 273
Qy      372 IPESLPSPSRNSNSNPRLPRCYQCKAKIYIFIIISYVLSLQPYCPFLAVLAWVDVETOV 431
Db      274 -----KAAKTLGIWGCFLVLCWLP--FFVLPLPGISIFPAYR 307
Qy      432 P-QWVITIIIMLFLOCCIHPIYVGYGMHTIKKEIOMDKKPFCKEKPKEDSHDPLPST 490
Db      308 PSDYVFKITFMGLYRNSCINPIIYLCSSNOEFKAPQSL-GVHCILMTFRAHH-HLSVG 365
Qy      491 EGGTEG-KIVPSYDSATFP 508
Db      366 QSGTGHSLTSLDCKGAP 384

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RESULT 4

```

alpha-1C adrenergic receptor - rat
157959
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: 157959; 152862; PC2179
R:Laiz, T.M.; Forray, C.; Smith, K.E.; Bard, J.A.; Vaysse, P.J.; Branchek, T.A.; Weinshan
Mol. Pharmacol. 46, 414-422, 1994
A>Title: The rat homologue of the bovine alpha 1C-adrenergic receptor shows the pharmac
A:Reference number: 157959; MUID:95021119; PMID:7935320
A:Accession: 157959
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-466 <RES>
A:Cross-references: UNIPROT:P43140; UNIPARC:UPI00004E761; EMBL:U07126; NID:9595275; PID
R:Stewart, A.F.; Rokosh, D.G.; Bailey, B.A.; Karns, L.R.; Chang, K.C.; Long, C.S.; Katly
Circ. Res. 75, 796-802, 1994
A>Title: Cloning of the rat alpha 1C-adrenergic receptor from cardiac myocytes. alpha 1C
A:Reference number: 152862; MUID:95008062; PMID:7923624
A:Accession: 152862
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-38,'L',40-66,'G',68-466 <RE2>
A:Cross-references: UNIPARC:UPI000016761; EMBL:U13368; NID:9555851; PIDN:AAA52103.1; PI
R:Rokosh, D.G.; Bailey, B.A.; Stewart, A.F.R.; Karns, L.R.; Long, C.S.; Simpson, P.C.
Biochem. Biophys. Res. Commun. 200, 1177-1184, 1994
A>Title: Distribution of alpha 1C-adrenergic receptor mRNA in adult rat tissues by RNase
A:Reference number: PC2179; MUID:94241969; PMID:8185565
A:Accession: PC2179
A:Molecule type: mRNA
A:Residues: 102-279 <R0K>
A:Cross-references: UNIPARC:UPI00001778AF
A:Experimental source: cardiac myocyte
C:Comment: This factor comprises a multigene family. As do alpha-2 and beta-adrenergic r
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor; transmembrane protein
F:26-42/Domain: transmembrane #status predicted <TM1>
F:73-89/Domain: transmembrane #status predicted <TM2>
F:104-120/Domain: transmembrane #status predicted <TM3>
F:147-163/Domain: transmembrane #status predicted <TM4>
F:195-211/Domain: transmembrane #status predicted <TM5>
F:276-292/Domain: transmembrane #status predicted <TM6>
F:306-329/Domain: transmembrane #status predicted <TM7>

```

```

Query Match      12.7%; Score 336; DB 2; Length 466;
Best Local Similarity 21.3%; Pred. No. 3,3e-15;
Matches 108; Conservative 79; Mismatches 186; Indels 134; Gaps 11;
7 NSTRESNHSHTCMPKSPISLAHGIIRSTVLVIFLAASFVGNIVLALVLOKRPQLQVT 66

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Db      7 NASEGNSCTH-----PPAPVNIISKAILLGVLLGLIIFGVAGNIIIVLSVACHRIHAST 61
Qy      67 NRIFFNLVTDLQISTLAPVWVATSVPLPMLNSHFCCTALVSLTHLPAPASVNTIVLVS 126
Db      62 HYIYNLAVADLLTSTVLPSPALFEIIGYNAFGVFCINAAVYVLCCTASIMGLCTIS 121
Qy      127 VDRYLSTIHPLSYSPKMTQRRGYLLYGTWIVAILQSTPTPLYGWQAAFDERNALCSMIW 186
Db      122 IDRYIGVSPYLRPYTFIVQRRGVALLCWVLSTVISIGPLFGMRQPA-PEDETICQI-- 178
Qy      187 GASESTYLLSVSFVIFPLIVMIACYSVYFCAARQHLLNVNKHSLSEVRKDCVENED 246
Db      179 NEEPYVLFSAIAGSYVPLAIILVWYCRVYVAKR-----ESRG 217
Qy      247 EBGAKKEEPQDESEFRQHEGEVAKEGHWEAKDGLKAKESGTSTSESSVEARGSEEV 306
Db      218 LKSGLKTDSSEQVTLIHKRVPAEG-----GVSSA----- 251
Qy      307 RESSTVASDGSMEGKSGSTKVEENSMKADKGRTEVNOCSIDLGEDMEFGEEDINFSEDD 366
Db      252 -----KXKT-----HPSVRLKFSREK 268
Qy      367 VEAVNIPESLPSPSRNSNSNPRLPRCYQCKAKIYIFIIISYVLSLQPYCPFLAVLAWVD 426
Db      269 -----KAAKTLGIWGCFLVLCWLP--FLWMPIGSF 298
Qy      427 VETQVPOWVITIIIMLFLOCCIHPIYVGYGMHTIKKEIOMDKKPFCKEKPKEDS--- 483
Db      299 PDFKSEVYFKIVPLGYLNSCINPIIYPCSSQEFKAPQNVLRIOCLRRQSSKHALGY 358
Qy      484 --HPDLPTGEGTEGKI-VPSYDSATFP 507
Db      359 TLHPSSQALEGHRMVRIPVSSGETF 385

```

RESULT 5

```

149375
serotonin receptor 1A - mouse
N:Alternate names: 5-hydroxytryptamine receptor 1A (5-HT1A)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 149375; A57508
R:Charcst, A.; Wainer, B.H.; Albert, P.R.
J. Neurosci. 13, 5164-5171, 1993
A>Title: Cloning and differentiation-induced expression of a murine serotonin1A receptor
A:Reference number: 149375; MUID:94076019; PMID:8254366
A:Accession: 149375
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-421 <CHA>
A:Cross-references: UNIPROT:064264; UNIPARC:UPI000029964; EMBL:U9391; NID:91066325; PI
R:Milkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G.
Genomics 18, 175-184, 1993
A>Title: Identification, chromosomal location, and genome organization of mammalian G-pr
A:Reference number: A48909; MUID:94116980; PMID:8288218
A:Accession: A57508
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 136-176,'T',178-241,'L',243-246,'V',248-262,'W',264-303,'H',305-329,'I',331-
A:Cross-references: UNIPARC:UPI00001778E8; GB:I20339
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
F:37-62/Domain: transmembrane #status predicted <TM1>
F:74-98/Domain: transmembrane #status predicted <TM2>
F:110-132/Domain: transmembrane #status predicted <TM3>
F:153-178/Domain: transmembrane #status predicted <TM4>
F:192-217/Domain: transmembrane #status predicted <TM5>
F:346-367/Domain: transmembrane #status predicted <TM6>
F:379-403/Domain: transmembrane #status predicted <TM7>
F:410,11,24,30/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:109-187/Disulfide bonds: #status predicted

```

```

Query Match      12.7%; Score 335.5; DB 2; Length 421;
Best Local Similarity 23.2%; Fred. No. 3.2e-15;
Matches 106; Conservative 88; Mismatches 190; Indels 73; Gaps 12;

Qy 26 ISLAGIIRSTVLYIFLAASFVGN--IYLAIVLQKRPOLLQVTRFIFNLVTDLLQSL 83
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 31 VTFSYQVITSLILGLTIFCAVGNACVAAIALER--SLQNVANLISLAVTDLMVSL 88
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 84 VAPWVATSVPLFPLNSHFCTALVSLTHLPFAFSVNTIVLVSDRYLSIHPISPSKM 143
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 89 VLPMALVQVANKMTLGGVTCDFIALDLCTSSILHLCAIALDRYWAITDPIDYVKR 148
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 144 TORRGYLLVGTWVAIIQSTPPLVYGQAAPDENALCGSMINCASTYITLVSVSTV 202
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 149 TPRAAALISLTWILGFLISIPMLGM--RAPEDRSNPECTI--SKDHGYITISFGAFY 205
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 203 IPLVMTACYSVFCARQHALLYNVKHSLEVRKDCVENDEDEGAKEEEDSEF 262
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 206 IPLMLLVYGRIRRAAR-----PRIKTVKKVEKKA----- 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 263 RROHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVARGSEVRESSTVASDGSMEGK 321
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 239 -----GTSFGTSAPPKKSLNG--QPSGDCRGRSAENRAVGTPCANGAVRGE 285
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 322 EGSF--KYEENSMKADKRTETVNOCSIDLGEDMFEGBDDINFSEDDVEAVNIPESLP-P 378
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 286 DDATLEVLEVHVRVNGSK-----DLPLPSGATSVVPACLERK 324
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 379 SRRSNSNPPLPRCYQCAKAVIFIIISYVLSLGPYCFLAVLAWVETQVPMWITI 438
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 325 NERTAEARKKALAREKTVITLIGIMGTIFLCMLPFITVALVLPFCSSSCHMBELGAI 384
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 439 IIVLFLOCCIHPPVYVGYMAKTIKEIQDMLKFFCK 475
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 385 INMLGYSNLNPVLYAYFNKDPQVAFKKIKCKFCR 421
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
565556
alpha-1C-adrenergic receptor splice form 3 - human
N/Alternate names: alpha-1C-adrenoceptor isoform 3
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C/Accession: S65556; MUID:95255557; PMID:7737411
R/Tanaka, T.
submitted to the EMBL Data Library, July 1994
A/Reference number: S65556
A/Accession: S65556
A/Molecule type: mRNA
A/Residues: 1-429 <TAN>
A/Cross-references: UNIPROT:Q13729; UNIPARC:UPI000004E75F; EMBL:D32201; NID:9927210; PID:
R:Hiraasawa, A.; Shibata, K.; Horie, K.; Takei, Y.; Obika, K.; Tanaka, T.; Muramoto, N.;
FEBS Lett. 363, 256-260, 1995
A/Title: Cloning, functional expression and tissue distribution of human alpha1(C)-adren
A/Reference number: S65554; MUID:95255557; PMID:7737411
A/Accession: S65554
A/Molecule type: mRNA
A/Residues: 424-429 <HIR>
A/Cross-references: UNIPARC:UPI00001778AF; EMBL:D32201
C/Genetics:
A/Gene: GDB:ADRA1C, ADRA1L1
A/Cross-references: GDB:128088; OMIM:104221
A/Map position: 8p21-8p11.2
C/Superfamily: vertebrate rhodopsin
C/Keywords: alternative splicing; neurotransmitter receptor

Query Match      12.6%; Score 333.5; DB 2; Length 429;
Best Local Similarity 21.1%; Fred. No. 4.4e-15;
Matches 107; Conservative 79; Mismatches 189; Indels 131; Gaps 10;

Qy 8 STRESNSHTCMPLSKMPISLAHGIRSTVLYIFLAASFVNGVYALVLAQKRPOLLQVTR 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 SGNSSDSNCTOP--PAFVNISKALLVGLILFGLVGLNITLVLSVACHRHLSVTH 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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```

Qy 68 RFINLVTDLLQISLVAPWVATSVPLFPLNSHFCTALVSLTHLPFAFSVNTIVLVSV 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 YVIVNLAVADLLILSTVLPFGSAIEVLGYWAFGRVFCNIMAAVDVLCCTASIMELCIISI 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 128 DRVYSIIHPLSYSPKMQRQRYGLLYGTWVAIIQSTPPLVYGQAAPDENALCGSMINCA 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 DRYIGVSTPLRPVITVQRKLMALLCVMWALSVISIGPLFGMRQPA-PEDETICQI--N 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 188 ASPSTYILSVSFYIVPLVIWACYSVFCARQHALLYNVKHSLEVRKDCVENEDE 247
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 180 EEPGVYLFSAIGSYPLPLAITLVNVCRIYVAKR-----ESRGL 218
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 248 EGAEKKEEFODESEFRROHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVARGSEEV 307
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 219 KSGLTKDKSDSEQVTLIHRKNAPA-----GSGSMASAKTKTHFSVRL- 261
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 308 ESSVTSADSGMEGEGSTKVEENMKADKRTETVNOCSIDLGEDMFEGBDDINFSEBDV 367
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 262 -----LKFSREK- 268
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 368 EAVNIPESLPSRRNSNPPLPRCYQCAKAVIFIIISYVLSLGPYCFLAVLAWVDV 427
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 269 -----KAKTGIYVGCFLVLCMLPF-FLVMPIGSFPP 299
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 428 ETQVPQWYITIIIVLFLOCCIHPPVYVGYMAKTIKEIQDMLKFFCKEKPCKEDS---- 483
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 300 DFKSESTVFKEVFMVGYLNCINPIIYPCSOEKKAFQVNLRIQCLRRKQSGHALGYT 359
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 484 -HPDLPTEGSGTEGI--VPSYDSATF 507
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 360 LHPPSQAVEGQKDMVRNIPVGSRET 385
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
JN0765
alpha-1C-adrenergic receptor - human
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C/Accession: JN0765; I84635; J02333; G01419
R:Hiraasawa, A.; Horie, K.; Tanaka, T.; Takagaki, K.; Mural, M.; Yano, J.; Tsujimoto, G.
Biochem. Biophys. Res. Commun. 195, 902-909, 1993
A/Title: Cloning, functional expression and tissue distribution of human cDNA for the al
A/Reference number: JN0765; MUID:93384619; PMID:8396931
A/Accession: JN0765
A/Molecule type: mRNA
A/Residues: 1-466 <HIR>
A/Cross-references: UNIPROT:P53348; UNIPARC:UPI0000503E6; GB:L31774; NID:9666892; PID:;
R:Diehl, N.L.; Shreeve, S.M.
Eur. J. Pharmacol. 268, 393-398, 1994
A/Title: Identification of the alpha 1c-adrenoceptor in rabbit arteries and the human ear
A/Reference number: I47013; MUID:95104335; PMID:7805763
A/Accession: I84635
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 202-344 <DIE>
A/Cross-references: UNIPARC:UPI000016B46A; GB:S76001; NID:9913817; PID:AA014205.1; PID:;
Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
A/Title: Cloning, expression and characterization of human alpha adrenergic receptors al
A/Reference number: J02331; MUID:94296402; PMID:8024574
A/Accession: J02333
A/Molecule type: mRNA
A/Residues: 1-130, 'F', 132-140, 'P', 142-166, 'C', 168-247, 'H', 249-337, 'C', 339-430, 'Q', 432-466,
A/Cross-references: UNIPARC:UPI00001778AC; GB:S70782; NID:9547219; PID:AA031163.1; PID:;
R:Ellstrom, K.O.
submitted to the EMBL Data Library, April 1994
A/Reference number: G06938
A/Accession: G01419
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 296-346, 'C', 348-430, 'Q', 432-466 <ELL>
A/Cross-references: UNIPARC:UPI0000000534; EMBL:U08994; NID:9497243; PID:AAA18783.1; PI

```


C/Comment: This protein plays critical roles in the regulation of a variety of physiolog
C/Genetics:
A/Gene: GDB:ADRA1C; ADRA1L1
A/Cross-references: GDB:128088; OMIM:104221
A/Map position: 8p21-8p11.2
A/Introns: 295/3
A/Note: the list of introns may be incomplete
C/Superfamily: vertebrate rhodopsin
C/Keywords: alternative splicing; glycoprotein; receptor; transmembrane protein
F:26-31/Domain: transmembrane #status predicted <TM1>
F:66-90/Domain: transmembrane #status predicted <TM2>
F:101-122/Domain: transmembrane #status predicted <TM3>
F:144-165/Domain: transmembrane #status predicted <TM4>
F:183-205/Domain: transmembrane #status predicted <TM5>
F:274-298/Domain: transmembrane #status predicted <TM6>
F:306-329/Domain: transmembrane #status predicted <TM7>
F:7,13,22/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.6%; Score 333.5; DB 2; Length 466;
Best Local Similarity 21.1%; Pred. No. 4.8e-15;
Matches 107; Conservative 79; Mismatches 189; Indels 131; Gaps 10;

```
QY      8 STRESNSSHTCMPLSKMPSISLAHGIRSTVIVIFLAASFVGNIVLALVQRKPOLQVYN 67
      5 SGNADSSNCTOP--PAPVNISKAILLGVLGGLLFGVLGNILVLSVACHRHLSVTH 62
      68 RIFNILVTDLIQISLVAPWVAVTSVPLFMPINSHFCTALVSLTHLFAFASVNTIVLSV 127
      63 YIIVNLAVADLLTSTVLPFSAIFEVLGYWAFGRVCNMAADVLCCTASIMGLCIISI 122
      128 DRYLSIHPLSYPSKMTORRGVLLLYGTWIVALLDSTPPLYGWGAAPDERNALCSMIG 187
      123 DRYIGVYPLRYPITYVTOGRGLMALLCWALSLVISIGLFGWRQPA-PEDETCOI--N 179
      188 ASPSTYILSVSFIVYPLVIMTACSVVFCARQHALLYNKRHSLERVKDCVENDE 247
      180 EEPGYVLPFALGSFYLPALILVMYCRYVYVAKR-----ESRGL 218
      248 EGAEKKEEFODESEPRROHGEVKAKEGMEAKDGLKAKEGSTGTSSESVEARGSEYR 307
      219 KSGLKTDKSDSEQVTLRIHRKNAFA-----GSGMASAKTKTHFSVRL- 261
      308 EESTVADSGSMGKSGSTVEENSMKADKGRTEVNQCSIDLGEDDMFEGEDINPEDEVD 367
      262 -----LKFSREK- 268
      368 EAVNIPESLPSPRRNSNPNPLPRCYOCAKATFIIFISYVLSLGPYCFPLAVLAWVDV 427
      269 -----KAAKTIGIVGCFVLCWLPF-FLVMPIGSFPP 299
      428 ETQVPQWVITITIIWLFLOCCIHPPVYGYMAKTIKEIDMLKKFFCKEKPRKEDS---- 483
      300 DKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKAFQVNLRIQCLRRKQSSKHALGYT 359
      484 -HPDLPTGTEGTEGKI-VPSYDSATP 507
      360 LHPPSQAVEGQHKDMWRIPVGSRETF 385
```

RESULT 8
S65657
N:Alternate names: alpha-1C-adrenoreceptor splice form 2 - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C/Accession: S65657; S65655
R/Tanaka, T.
submitted to the EMBL Data Library, July 1994
A/Reference number: S65656
A/Accession: S65657
A/Molecule type: mRNA
A/Residues: 1-499 <TAN>
A/Cross-references: UNIPROT:Q13675; UNIPARC:UPI000004875E; EMBL:D32202; NID:927208; PID

R.Hirasawa, A.; Shibata, K.; Horie, K.; Takei, Y.; Obika, K.; Tanaka, T.; Muramoto, N.;
FEBS Lett. 363, 256-260, 1995
A/Title: Cloning, functional expression and tissue distribution of human alpha(1C)-adre
A/Reference number: S65654; MUID:95255557; PMID:7737411
A/Accession: S65655
A/Molecule type: mRNA
A/Residues: 424-499 <HIR>
A/Cross-references: UNIPARC:UPI00001778AB; EMBL:D32202
C/Genetics:
A/Gene: GDB:ADRA1C; ADRA1L1
A/Cross-references: GDB:128088; OMIM:104221
A/Map position: 8p21-8p11.2
C/Superfamily: vertebrate rhodopsin
C/Keywords: alternative splicing; neurotransmitter receptor

Query Match 12.6%; Score 333.5; DB 2; Length 499;
Best Local Similarity 21.1%; Pred. No. 5.2e-15;
Matches 107; Conservative 79; Mismatches 189; Indels 131; Gaps 10;

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QY      8 STRESNSSHTCMPLSKMPSISLAHGIRSTVIVIFLAASFVGNIVLALVQRKPOLQVYN 67
      5 SGNADSSNCTOP--PAPVNISKAILLGVLGGLLFGVLGNILVLSVACHRHLSVTH 62
      68 RIFNILVTDLIQISLVAPWVAVTSVPLFMPINSHFCTALVSLTHLFAFASVNTIVLSV 127
      63 YIIVNLAVADLLTSTVLPFSAIFEVLGYWAFGRVCNMAADVLCCTASIMGLCIISI 122
      128 DRYLSIHPLSYPSKMTORRGVLLLYGTWIVALLDSTPPLYGWGAAPDERNALCSMIG 187
      123 DRYIGVYPLRYPITYVTOGRGLMALLCWALSLVISIGLFGWRQPA-PEDETCOI--N 179
      188 ASPSTYILSVSFIVYPLVIMTACSVVFCARQHALLYNKRHSLERVKDCVENDE 247
      180 EEPGYVLPFALGSFYLPALILVMYCRYVYVAKR-----ESRGL 218
      248 EGAEKKEEFODESEPRROHGEVKAKEGMEAKDGLKAKEGSTGTSSESVEARGSEYR 307
      219 KSGLKTDKSDSEQVTLRIHRKNAFA-----GSGMASAKTKTHFSVRL- 261
      308 EESTVADSGSMGKSGSTVEENSMKADKGRTEVNQCSIDLGEDDMFEGEDINPEDEVD 367
      262 -----LKFSREK- 268
      368 EAVNIPESLPSPRRNSNPNPLPRCYOCAKATFIIFISYVLSLGPYCFPLAVLAWVDV 427
      269 -----KAAKTIGIVGCFVLCWLPF-FLVMPIGSFPP 299
      428 ETQVPQWVITITIIWLFLOCCIHPPVYGYMAKTIKEIDMLKKFFCKEKPRKEDS---- 483
      300 DKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKAFQVNLRIQCLRRKQSSKHALGYT 359
      484 -HPDLPTGTEGTEGKI-VPSYDSATP 507
      360 LHPPSQAVEGQHKDMWRIPVGSRETF 385
```

RESULT 9
JH0315
N:Alternate names: 5-hydroxytryptamine receptor 1A (5-HT1A)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C/Accession: JH0315; A35181
R/Fujiwara, Y.; Nelson, D.L.; Kashiwara, K.; Varga, E.; Roecke, W.R.; Yamamura, H.I.
Life Sci. 47, 127-132, 1990
A/Title: The cloning and sequence analysis of the rat serotonin-1A receptor gene.
A/Reference number: JH0315; MUID:90355775; PMID:2167416
A/Accession: JH0315
A/Molecule type: DNA
A/Residues: 1-422 <FUJ>
A/Cross-references: UNIPROT:P19327; UNIPARC:UPI00001778BE
R/Albert, P.R.; Zhou, Q.Y.; Van Tol, H.H.M.; Bunzow, J.R.; Civelli, O.
J. Biol. Chem. 265, 5825-5832, 1990

```

A>Title: Cloning, functional expression, and mRNA tissue distribution of the rat 5-hydroxytryptamine 1A receptor
A>Reference number: A35181; MUID:90202832; PMID:2156831
A>Accession: A35181
A>Molecule type: DNA
A>Residues: 1-372, 'S', 374-422 <AB>
A>Cross-references: UNIPARC:UPI0000124F1B; GB:J05276; NID:G202540; PIDN:AAA0612.1; PID:
C:Superfamily: vertebrate rhodopsin
C>Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane
F:37-62/Domain: transmembrane #status predicted <TM>
F:74-98/Domain: transmembrane #status predicted <TM>
F:109-134/Domain: transmembrane #status predicted <TM>
F:153-178/Domain: transmembrane #status predicted <TM>
F:252-277/Domain: transmembrane #status predicted <TM>
F:346-371/Domain: transmembrane #status predicted <TM>
F:379-404/Domain: transmembrane #status predicted <TM>

Query Match 12.5% Score 331.5; DB 2; Length 422;
Best Local Similarity 23.5% Pred. No. 5,9e-15;
Matches 111; Conservative 76; Mismatches 181; Indels 105; Gaps 12;

QY ISLHGIIINSTVLVIFLAASFVGN--IVLALVLRKPOLLOVYNRFNMLVTLDLQISL 83
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB VFESYQYITSLIGTLIFCAVLGNACVAALALER--SLQNVANVYLIGSLAVTDLMAVS 88
84 VAPWVAVTSPLPMPNLNHFCTALVSLTHLAFASVNTIVLSVDVRYLSIHPLSPSK 143
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB VLPMAALQVLRKNTLQVTCDFLADLVLCCTSSILHLCAIALDRYMAITDPIDVYNR 148
144 TORRGVLLVGYMTVALTOSTPPLPGMGQAFAFDESNALCSMTMGASPSYTLISVSFIY 203
149 TPRRAALLISLTWILIGLISLPMLGMRT--EDRSDPDACTISKDHGYTISTGCAFYI 206
QY PLVIIMACYSVVFCAARQHALLVNKRHSLEVRKDCVENEDEBGAKEKEFEDESERR 263
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB PLLMLVLYGRIFPRAR-----FRIRKTVKYEKKGA----- 238
QY RQHEGEVKAKEGRNEAKDGSILKAKEGSTGTSESSVEANGSEVRESSTVASDGSMEK 323
264 :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 239 -----GTS-----LGTSSAPPKKSLNGQP 259
QY S---TKVEENSMKADKGRTEVNOCSIDLGEDDMERGEDINFSDDVEAV-NIPESLP-P 378
324 :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB SGDMRRRAEN-----RAVGTPCT---NGAVRGDDDEATLEVLRHVGSKENLPLP 308
379 SRNNSNP-----LPRCYOCKAKAVYIIIFSVLSLGPYCFPLAVLA 422
DB SEEGSNVYAPACLERKNERNEAKRKMALEBKIVTKLIGIMGFILCMLPRFIYALV 368
QY 423 VWDVETQVQWVTTITIMLFFLQCCIHPIYVGYGMKTIKKEIQDMLKPFCK 475
369 PFCNSCHMWALLGAIINMILGYSNLSLNPVIYAYFNKQFAFKIICKFCR 421

RESULT 10
alpha-1-adrenergic receptor - bovine
A35375
C:Species: Bos primigenius taurus (cattle)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C>Accession: A35375
R>Schimim, D.A.; Lomaney, J.W.; Lorenz, W.; Szklut, P.J.; Fremeanu Jr., R.T.; Yang-Feng,
J. Biol. Chem. 265, 8183-8189, 1990
A>Title: Molecular cloning and expression of the cDNA for a novel alpha-1-adrenergic rec
A>Reference number: A35375; MUID:90243698; PMID:1970822
A>Accession: A35375
A>Molecule type: mRNA
A>Residues: 1-466 <SCH>
A>Cross-references: UNIPROT:P19130; UNIPARC:UPI00004E762; GB:J05426; NID:G162663; PIDN:
C:Superfamily: vertebrate rhodopsin
C>Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
Query Match 12.3% Score 325.5; DB 2; Length 466;
Best Local Similarity 20.4% Pred. No. 1.7e-14;
Matches 107; Conservative 78; Mismatches 182; Indels 157; Gaps 10;

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QY      7 NSTRESNSHCTMPLSKMPISLAHGIIIRSVLVIFLAASFVGNIVLALVLRKPOLLOYT   66
Db      7 NASDSNCR-----PPPVNISAKILLGVILGGLLFVGVLGNILVLISVACHRHLSVT   61
QY      67 NREIFALLTDLLOISLVAPMWVATSVLPFLPMLNSHCFTALVSLTHLFAPASVNTIVVS   126
Db      62 HYIYNLAVADLLLTSTVPFSALIFELIGWAGRVACVNMAADVLCCTSIIMDLCTIS    121
QY      127 VDRYSIIHPLSYPSKMTORRGVLLYGTVIIVALOSTPPLYGMGOAFAEDERNALCSMIW   186
Db      122 IDRYIGVSYPLRPYITVOTKRGLMALCVWALSIVISIGFLCWRQPA-PEDETICQT--   178
QY      187 GASPEYTLISVSVFYIPLVMACSVMFCARROHALLYNRGRHSLEVAVKDCVENBD     246
Db      179 NEEPGVLSALGSFYVPLTLLVMYCVRVVVAR-----                213
QY      247 EEGAEEKEEFODESEFRROHEGEVKAKEGRMEAKDGLKAKEGSTGTSSESSVEARGSEBV   306
Db      214 -----ESRG-----                217
QY      307 RESSTVASDGSGEKGEGSTKVTEENSMAKDGRTEVNOCSI DLGEDNEFEGBDDINFSBDD   366
Db      218 -----LKSGLKTDKSDS---EQVTLRIHRKNAQVGSQGTSAKNKTHFSRLLKFSEBK   268
QY      367 VEANVINPESLPSPRRSNSNPRLPRCYOCCAIAVFIIIFISYVLSLGPYCLAVIALAWVD   426
Db      269 -----RAAKTLGIvGCFFVCWLPF-FLVMPDTSGF   298
QY      427 VETOVPOWVITIIIMFLFOCCIHPYVGYMHKTIKEIDMLKKFFCKEKRPK-----   480
Db      299 PPFRESEYTFKLAFWLGYNLNCINPIIIPCSSQEKFKAFOFNVALIQCLRARRQSSGHITGY   358
QY      481 -----EDSHPDL-----PGTEGGTEGKI VPS 501
Db      359 TLHAPSHVLEGGHKDLVRIPVGSAEFTFYKISKTDGCEWKFISS 402

RESULT 11
A47174
serotonin receptor - great pond snail
N:Alternate names: 5-hydroxytryptamine receptor (5-HT1)
C:Species: Lymnaea stagnalis (great pond snail)
C>Date: 21-Sep-1993 #sequence_rev=18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A47174
R:Sugamori, K.S.; Sunahara, R.K.; Guan, H.C.; Bullloch, A.G.; Tensen, C.P.; Seeman, P.; N
Proc. Natl. Acad. Sci. U.S.A. 90, 11-15, 1993
A>Title: Serotonin receptor cDNA cloned from Lymnaea stagnalis.
A:Reference number: A47174; MUID:93126323; PMID:8093556
A:Accession: A47174
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-509 <SUG>
A:Cross-references: UNIPROT:Q25414; UNIPARC:UP1000004E75D; GB:L06803; NID:g159458; PIDN:
A:Experimental source: central nervous system
A>Note: sequence extracted from NCBI backbone (NCBIN:121945, NCBIRef:121952)
C:Superfamily: octopamine receptor type I
C:Keywords: neurotransmitter receptor

Query Match          12.1%; Score 319; DB 2; Length 509;
Best Local Similarity 22.3%; Pred. No. 5,le-14;
Matches 108; Conservative 96; Mismatches 205; Indels 76; Gaps 14;

QY      3 STCTNSTRESNSHTCMPLSKMPISLAHGIIIRSVLVIFLAASVGN--IYLALVLRKP   60
Db      74 TSATNMTRDRYMSLV-----YSHELVLTSLIQLFVLCCTIIGCFVIAAWLER--   124
QY      61 OLLOVTRREFIENLVLDLOISLVAPMVVATSVLPFLPMLNSHCFTALVSLTHLFAPASVN   120
Db      125 SLHNANYIILSLAVADMVAULVLMPLSVSEISKWFHSEVCDMMISDVVLCTASTL    184
QY      121 TLVLVSVDYRLSLIHPLSPSKMTORRGVLLLYGTWIVAILQSTPPLYGMGOAFD-ERN    179
:
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Db      185 HLVAIMANDRYMAVT-SIDYIRRRSARRILIMTMVIMVALFISIPPLFGWRDPNDPDKT 243
Qy      180 ALCSMIWGASPSYTIISVSVFIVPIIWMIACTSVVFCARROHALLVYKHSLEVRK 239
      244 GTC--IIISGDKGTYITSTGAPFLPMLVMMIYIRIWLVARSR-----IRDKPQMTGA 295
Qy      240 DCVENDEEGAEKKEEFODESEFRQHEGEVAKEGRMEA-----KDSLIK 285
Db      296 RLKTEETTLVVASPKTEYSVAVSDCNGCNSPDSTTEKKRRAPFKSYGCSPPREKKRRAK 355
Qy      286 AREGSGTSESSVEANGSEVR-ESSTVSDSGMEKEGKSTAKVEENSMADKRTVNOG 344
Db      356 LPENANGVSNSSSSRLKQIOLITVAPANGCAE--EASIMLE-----RQC 401
Qy      345 SIDLGEDMEFGEEDINFSEDDVEAVNIPESLPPSRNSNSNPPLPRCYCKAKAVIFII 404
Db      402 N-----NGKKISNDTPYRTREKLEKRR-----KAAKTLAII 436
Qy      405 IFSYVLSLGPYCFPLAVLAVVDVETQVPQWVITIIIMLFLOCCHPYVYGMHTIKKE 464
Db      437 TCAFLICMLPFFIILALIGFVDPB-CIPPFASFLVMLGLFNSLNPITITIFSPEFRSA 495
Qy      465 IODML 469
Db      496 FQKIL 500

RESULT 12
JH0447
alpha-1A-adrenergic receptor - human
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #ext_change 09-Jul-2004
C/Accession: JH0447
R/Bruno, J.F.; Whitaker, J.; Song, J.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 179, 1485-1490, 1991
A/Title: Molecular cloning and sequencing of a cDNA encoding a human alpha 1A adrenergic
A/Reference number: JH0447; MUID:9202892; PMID:1656955
A/Accession: JH0447
A/Molecule type: mRNA
A/Residues: 1-501 <BRU>
A/Notes: references: UNIPROT:P25100; UNIPARC:UPI0000149ED3; GB:M76446; NID:g177806; PIDN:
A/Experimental source: h1ppocampus
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; transmembrane protein
F:56-79/Domain: transmembrane #status predicted <TM1>
F:93-116/Domain: transmembrane #status predicted <TM2>
F:128-151/Domain: transmembrane #status predicted <TM3>
F:172-196/Domain: transmembrane #status predicted <TM4>
F:210-233/Domain: transmembrane #status predicted <TM5>
F:308-331/Domain: transmembrane #status predicted <TM6>
F:339-363/Domain: transmembrane #status predicted <TM7>

Query Match      11.9%; Score 314.5; DB 2; Length 501;
Best Local Similarity 23.0%; Pred. No. 1e-13;
Matches 102; Conservative 64; Mismatches 158; Indels 119; Gaps 10;

Qy      29 AHGIIRSTVLVIFLAASFVGNIVLALVLRKQQLQVTRFIFNLVTLDTLOISLAVPV 88
Db      52 AGGVGVGLFILAFLMAVAGNLVILVASCNRRLQTVNYFVNLAVADLLSATVLPSS 111
Qy      89 VATSVPLFWPLNSHCTALVSLTLHPAFASVNTIVLVSDRYLSIIHPLSYSPSKMTORG 148
Db      112 ATMEVLGFMAFGARCFDWAADVLCCTASISLCTISIDRYVGNHSLKPAIMTERKA 171
Qy      149 YLLIGTWTVALIQSTPPYLGWGQ-AAFDERNAKSMIMGASPSYTIISVSEFIVPLIV 207
Db      172 AAILALMVAALVAVSGPLGKKEPPDPB--FCGITEEA--GVAVFSSVCSFYLPMAV 227
Qy      208 MIACYSVVFCAARQHALLVYKHSLEVRVDCVENDEEGAEKKEEFODESEFRQHE 267
Db      228 IYVMTKRVVVA-----STTRSL 247
Qy      268 GEVKAEGMEAKDGLKAKEGSTGTSSESVEARGSEVEESSTVASDGSMEKEGSTVY 327

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Db      248 AGCKRERG-----KASEVLR--IHCRAATGADCA--- 276
Qy      328 EENSKADKGRTEVNOCSIDLGEDMEFGEEDINFSEDDVEAVNIPESLPPSRNSNSNP 387
Db      277 --HGMSAKGHTFRSLSLRL-----LKSRER----- 302
Qy      388 PLPRCYCKAKAVIFIIIFSYYLSLGPYCFPLAVLAVVDVETQVPQWVITIIIMLFLOC 447
Db      303 -----KAAKTLAIVGVFVLCWPFPPFFVLPDS-LFPQKPSGVEKVFVWLGXFNS 353
Qy      448 CIHPYVYGMHTIKKEIODMLK 470
Db      354 CVNPILYPCSSREFKRAFLRLR 376

RESULT 13
I39369
alpha-1A-adrenergic receptor - human
C/Species: Homo sapiens (man)
C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #ext_change 09-Jul-2004
C/Accession: I39369; J02331
R/Sbenshade, T.A.; Hirasawa, A.; Tsujimoto, G.; Tanaka, T.; Yano, J.; Mineman, K.P.;
Mol. Pharmacol. 47, 977-985, 1995
A/Title: Cloning of the human alpha 1A-adrenergic receptor and inducible expression of
A/Reference number: I39369; MUID:95265059; PMID:7746284
A/Accession: I39369
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-572 <RES>
A/Cross-references: UNIPROT:P25100; UNIPARC:UPI000003B078; GB:D29952; NID:g914933; PIDN:
R/Leiberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borikowski, D.;
Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
A/Title: Cloning, expression and characterization of human alpha adrenergic receptors
A/Reference number: J02331; MUID:94296402; PMID:8024574
A/Accession: J02331
A/Molecule type: mRNA
A/Residues: 1-30, 'G', 32-521, 'P', 523-572 <WEI>
A/Cross-references: UNIPARC:UPI000016B433
A/Notes: the authors translated the codon CCC for residue 522 as Arg
C/Genetics:
A/Gene: GDB:ADRA1A; ADRA1; ADRA1R
A/Cross-references: GDB:118749; OMIM:104219
A/Map position: 20pter-20qter
A/Introns: 37/3
C/Superfamily: vertebrate rhodopsin
C/Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F:89-123/Domain: transmembrane #status predicted <TM1>
F:132-162/Domain: transmembrane #status predicted <TM2>
F:172-197/Domain: transmembrane #status predicted <TM3>
F:208-235/Domain: transmembrane #status predicted <TM4>
F:254-278/Domain: transmembrane #status predicted <TM5>
F:344-374/Domain: transmembrane #status predicted <TM6>
F:380-414/Domain: transmembrane #status predicted <TM7>
F:55/2/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      11.9%; Score 314.5; DB 2; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.2e-13;
Matches 102; Conservative 64; Mismatches 158; Indels 119; Gaps 10;

Qy      29 AHGIIRSTVLVIFLAASFVGNIVLALVLRKQQLQVTRFIFNLVTLDTLOISLAVPV 88
Db      94 AGGVGVGLFILAFLMAVAGNLVILVASCNRHLQTVNYFVNLAVADLLSATVLPSS 153
Qy      89 VATSVPLFWPLNSHCTALVSLTLHPAFASVNTIVLVSDRYLSIIHPLSYSPSKMTORG 148
Db      154 ATMEVLGFMAFGARCFDWAADVLCCTASISLCTISIDRYVGNHSLKPAIMTERKA 213
Qy      149 YLLIGTWTVALIQSTPPYLGWGQ-AAFDERNAKSMIMGASPSYTIISVSEFIVPLIV 207
Db      214 AAILALMVAALVAVSGPLGKKEPPDPB--FCGITEEA--GVAVFSSVCSFYLPMAV 269
Qy      208 MIACYSVVFCAARQHALLVYKHSLEVRVDCVENDEEGAEKKEEFODESEFRQHE 267

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Db 270 IVMYCRYVVAR-----STTSLE 289
Qy 268 GEVKAEGREMAKODSLKAKEGSTGTSSESVARGSEFEVRESSTVADSGMEKGGSTKV 327
Db 290 AGVRRERG-----KASEVLR---IHCGAALGADGA--- 318
Qy 328 EENSMKADKGRTEVNOCSIDIGEDDMFEGEDDINFSEDVEAVNIPESLPPSRNSNSNP 387
Db 319 --HGMRSAKHGHTFRSSLSVRL-----LKFSREK----- 344
Qy 388 PLPRCYOCKAKAVITIIIFSVYLSGIPYCFVLAVLWMDVETQVQWVITIIIMLPLOC 447
Db 345 -----KAKTLIAIVGVFVLCWFPPEFVPLIGS-LFPOLKPEGVFKVIFWLGYNSS 395
Qy 448 CIHPYVGYMHKTIKEIODMLK 470
Db 396 CVNPLIPCSSREFKAFRLRL 418

RESULT 14

S48657

muscarinic acetylcholine receptor MR - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C/Accession: S48657; S24948

C/Herrera, L.; Carvallo, P.; Antoneilli, M.; Olate, J.

FEBS Lett. 352, 175-179, 1994

A/Title: Cloning of a Xenopus laevis muscarinic receptor encoded by an intronless gene.

A/Reference number: S48657; MUID:95010703; PMID:7925970

A/Accession: S48657

A/Molecule type: mRNA

A/Residues: 1-484 <HER>

A/Cross-references: UNIPROT:P30544; UNIPARC:UPI0000178CB; GB:X65865; NID:G64900; PIDN:CR:Olate, J.

Submitted to the EMBL Data Library, April 1992

A/Reference number: S24948

A/Accession: S24948

A/Molecule type: mRNA

A/Residues: 1-131, 'X', 133-484 <OLA>

A/Cross-references: UNIPARC:UPI00001252BD; EMBL:X65865; NID:G64900; PID:G64901

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane

F/33-58/Domain: transmembrane #status predicted <TM1>

F/71-95/Domain: transmembrane #status predicted <TM2>

F/108-139/Domain: transmembrane #status predicted <TM3>

F/148-172/Domain: transmembrane #status predicted <TM4>

F/194-217/Domain: transmembrane #status predicted <TM5>

F/407-427/Domain: transmembrane #status predicted <TM6>

F/439-460/Domain: transmembrane #status predicted <TM7>

Query Match 11.8%; Score 312.5; DB 2; Length 484;

Best Local Similarity 21.0%; Pred. No. 1.3e-13;

Matches 110; Conservative 105; Mismatches 209; Indels 99; Gaps 16;

Qy 7 NSTRESNHTCMPLKMPISLAHGIIRSTVLVFLA-----ASFVGNITVLVLQR 58

Db 3 NDYTESNSASHMSIDENTIVEIRGKY--QTMEMIFLATVGSLSLVTVVGNILWLSIKF 60

Qy 59 KPQLQVNNRPFNLVLDL---QISLVARVAVATSVPLFWPLNSHCTLVSLTHLF 114

Db 61 NRQLQTVNNYFLFSACADLLIGVSMNLSLYIKG---YMPLGPIVCDMLMLADYV 116

Qy 115 APASVTVLVSVVDYLSIHPISYPSKVTORGVLVLTGTVIVVILGSTPLVYGGOA 174

Db 117 SNASVWMLIISLEKIFCTKPLTPARTTGMAGLMIAMWLSFELMAPILFW-QPI 175

Qy 175 FDER---NALCSMIGASPSYTLISVSPFIVPLVIMTACSVVFCARQHALYNNR 231

Db 176 VGORIVPSEGEVIGPLSNPAVTFGTAIAFYLPVIMTILYIHISLASR-----VRR 229

Qy 232 HSLERVVDQVENEDEGAKEEFPQDSSEFRQHEGVEKAKEGREMAKODSLKAKEG-S 290

Db 220 HCPETR-----QEKKPISSMKSLIKOTKNIP---KQADGKXVEKANGVS 273
Qy 291 TGTSESVYARGSEFEVRESSTVADSGM-----EKGEGSTKVEENSMK--ADKG 337
Db 274 NGKTEKSMNTNQTAEKETSNESSASLSHNHPKQPLSEASSGVVLAPQSGMPLPAKA 333
Qy 338 RTE-----VNOCSIDIGEDDMFEGEDDINFSEDVEAVNIPE 374
Db 334 NTASKMSKIKIVTKOTGNECVTAIEIPECAIPIPE-----QANNRPVVAR 380
Qy 375 SLPPSRNSNSNPPLPRCYOCKAKAVITIIIFSVYLSGIPYCFVLAVLWMDVETQVQW 434
Db 381 KFASTARQVRKKROMAREKVTTRTIPALLAFITMTPTVNMWMLNTF---COTCIPE 438
Qy 435 VITIIIMLPLOCIPHYPYGYMHKTIKEIODMLKFFCKEX 477
Db 439 IWIYGVWLCYNNSTINPACVALCNATFKTKHL---MCGYK 478

RESULT 15

A38731

alpha-1A adrenergic receptor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004

C/Accession: A38731; A53280

C/Romanney, J.W.; Cotecchia, S.; Lorenz, W.; Leung, W.Y.; Schwinn, D.A.; Yang-Feng, T.L.

J. Biol. Chem. 266, 6365-6369, 1991

A/Title: Molecular cloning and expression of the cDNA for the alpha-1A-adrenergic receptor.

A/Reference number: A38731; MUID:91177889; PMID:1706716

A/Accession: A38731

A/Molecule type: mRNA

A/Residues: 1-560 <LOW>

A/Cross-references: UNIPROT:P23944; UNIPARC:UPI000015AB77; GB:M60654; NID:G202761; PIDN:R.Perez, D.M.; Piacick, M.T.; Graham, R.M.

Mol. Pharmacol. 40, 876-883, 1991

A/Title: Solution-phase library screening for the identification of rare clones: isolation

A/Reference number: A53280; MUID:92100054; PMID:1661838

A/Accession: A53280

A/Molecule type: mRNA

A/Status: preliminary; not compared with conceptual translation

A/Residues: 1-36, 'P', 38-58, 'Y', 60-202, 'I', 204-305, 'R', 307-366, 'I', 368-370, 'I', 372-559 <F

A/Cross-references: UNIPARC:UPI0000057159

A/Experimental source: hippocampus

A/Note: sequence extracted from NCBI backbone (NCBI:73541)

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 11.6%; Score 306.5; DB 2; Length 560;

Best Local Similarity 23.0%; Pred. No. 3.9e-13;

Matches 102; Conservative 59; Mismatches 163; Indels 119; Gaps 10;

Qy 29 AHGIRSTVLVFLASFPVGNIVLVLVQRKPOLQVNNRPFNLVTDLQISLVAPMV 88

Db 88 AOGVGVGFLLAFITAVAGNLVLSVACNRHLOTNNYITVNLVADLLSAVLPFS 147

Qy 89 VATSVPLFWPLNSHCTLVSLTHLFAFASVNTIVLVSVDRYLSIHPISYPSKVTORG 148

Db 148 ATMEVLGFMARGRCFCDVMAVADVLCCTAISTLCISTISVDHYGVGRHSIKTPALWTERKA 207

Qy 149 YLLYGTIVVILGSTPLVYGWQ-AAPDERNALCSMTWGSPTTISVSVFIVPLIV 207

Db 208 AAILLALVAVALVSVGLLQMKKEVPDER--FCGIT--EEVGAIFSSVCSFYLPAV 263

Qy 208 MIACSVVFCARQHALYNNKRSLEVRVVDQVENEDEGAKEEFPQDSSEFRQHE 267

Db 264 IVMYCRYVVAR-----TRSLAAGIK-----REP 290

Qy 268 GEVKAEGREMAKODSLKAKEGSTGTSSESVARGSEFEVRESSTVADSGMEKGGSTKV 327

Db 291 GKASEVLRHICRGAAATSAK-GYPETGSS----- 318

Qy 328 EENSMKADKGRTEVNOCSIDIGEDDMFEGEDDINFSEDVEAVNIPESLPPSRNSNSNP 387

Db 319 -----KGHTLRSSLSVRL-----LKFSREK----- 338
QY 388 PLPRCYQCKAKVIFIIISYVLSLGPYCFEVLAVWVVDVETQVPQWVITIIIMLFLQC 447
Db 339 -----KAAKTLAIWGVFLCWFPPFVFLPLGS-LFPQDKPSSEGVFKVIFWLGYNFS 389
QY 448 CIHPYVGYMHTIKKEIQDMLK 470
Db 390 CVNPLIYPCSSRERFKAFRLRLR 412

Search completed: December 3, 2005, 06:31:38
Job time : 31.8636 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:23:01 ; Search time 170.873 Seconds

(without alignments)
2097.517 Million cell updates/sec

Title: US-10-712-615-2

Perfect score: 2644

Sequence: 1 MTSTCTNSREBSNSHTCMP.....GTGGTGGKIVPSYDSATFP 508

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2641	99.9	508	1	Q96P66 homo sapien
2	2641	99.9	508	2	Q5JSM8 HUMAN
3	588	22.2	229	2	Q4RPS9 tetraodon n
4	576	21.8	200	2	Q4SUM2 tetraodon n
5	392.5	14.8	526	2	Q90X46 BRAKE
6	391	14.8	407	2	Q5TGK0 HUMAN
7	391	14.8	529	2	GP161 HUMAN
8	391	14.8	529	2	Q5TGK1 HUMAN
9	373	14.1	535	2	Q4S0K3 TETNG
10	343.5	13.0	490	1	ACM4_CHICK
11	343	13.0	77	1	GP101_MOUSE
12	343	13.0	466	2	Q96RE8 HUMAN
13	341	12.9	427	2	Q8BUE5 MOUSE
14	341	12.9	466	2	Q8BV77 MOUSE
15	340.5	12.9	422	1	5HT1A_HUMAN
16	340.5	12.9	422	1	5HT1A_PANTR
17	340.5	12.9	422	2	Q5ZGX3 HUMAN
18	340	12.9	425	2	Q9MZU2 RABIT
19	340	12.9	429	2	Q9MZU3 RABIT
20	340	12.9	466	1	ADALA1 RABIT
21	340	12.9	470	1	ADALA1_ORYX
22	339.5	12.8	408	2	Q98998 XENLA
23	339.5	12.8	422	1	5HT1A_GORGO
24	339.5	12.8	490	2	Q5MBX1 COLLI
25	338.5	12.8	466	1	ADALA1_HUMAN
26	337.5	12.8	466	1	ADALA1_CAVPO
27	336	12.7	466	1	ADALA1_RAT
28	335.5	12.7	421	1	5HT1A_MOUSE
29	335.5	12.7	422	1	5HT1A_PONY
30	334.5	12.7	423	1	5HT1A_VULVU
31	333.5	12.6	423	2	Q8HYB0_CANFA

32	333.5	12.6	466	2	Q4VBW7 HUMAN	Q4VBW7 homo sapien
33	333	12.6	423	1	5HT1A_FUGRU	Q4Z385 fugu rubrip
34	333	12.6	466	1	ADALA1_MOUSE	P97718 mus musculu
35	332.5	12.6	422	1	5HT1A_RAT	P19327 rattus norv
36	331.5	12.5	421	2	Q8BGS4 MOUSE	Q8BGS4 m mus muscu
37	331.5	12.5	423	1	5HT1A_CANFA	Q6KXK9 canis fami1
38	330.5	12.5	421	2	Q8BZP1_MOUSE	Q8BZP1 mus musculu
39	330	12.5	422	2	Q4T0Z1 TETNG	Q4T0Z1 tetraodon n
40	328.5	12.4	436	2	Q4T2Y7 TETNG	Q4T2Y7 tetraodon n
41	325.5	12.3	466	1	ADALA1_BOVIN	P18130 bos taurus
42	324	12.3	416	2	Q6KXP2 OREMO	Q6KXP2 oreochromis
43	324	12.3	466	2	Q9TSM7_PIG	Q9TSM7 sus scrofa
44	321	12.1	481	2	Q5U3D9_BRAKE	Q5U3D9 brachydanto
45	320	12.1	341	2	Q4RX90_TETNG	Q4RX90 tetraodon n

ALIGNMENTS

RESULT 1	ID	GP101_HUMAN	STANDARD;	PRT;	508 AA.
AC	Q96P66; Q8NG93;				
DT	10-OCT-2003 (Rel. 42, Created)				
DT	10-OCT-2003 (Rel. 42, Last sequence update)				
DT	10-MAY-2005 (Rel. 47, Last annotation update)				
DE	Probable G-protein coupled receptor 101.				
GN	Name=GPR101;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;				
OC	Homio.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=21458557; PubMed=11574155; DOI=10.1016/S0378-1119(01)00651-5;				
RA	Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantl W.B., Arkhileko O.,				
RA	Lewis T., Evans J.F., George S.R., O'Dowd B.F.;				
RT	"Discovery and mapping of ten novel G protein-coupled receptor				
RT	genes."				
RL	Gene 75:83-91(2001).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;				
RA	Takeda S., Kadowaki S., Haga T., Takeasu H., Mitaku S.;				
RT	"Identification of G protein-coupled receptor genes from the human				
RT	genome sequence."				
RL	FEBS Lett. 520:97-101(2002).				
RN	[3]				
RP	NUCLEOTIDE SEQUENCE.				
RA	Suwa M., Sato T., Okouchi I., Arita M., Putami K., Matsumoto S.,				
RA	Tsutsun S., Aburatani H., Asai K., Akiyama Y.;				
RT	"Genome-wide discovery and analysis of human seven transmembrane helix				
RT	receptor genes."				
RL	submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.				
RN	[4]				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;				
RA	Strussberg R.L., Feingold E.A., Grose L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,				
RA	Altshul S.F., Zeeberg B., Burow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carinici P., Prange C.,				
RA	Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bosch S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko V., Boultard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schenker A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Orphan receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC
 DR EMBL; AF411115; AAL26486.1; -; Genomic DNA.
 DR EMBL; AB083588; BAB89301.1; -; Genomic DNA.
 DR EMBL; AB065937; BAC06152.1; ALT_INIT; Genomic DNA.
 DR EMBL; BC069439; AA069439.1; -; mRNA.
 DR Ensembl; ENSG00000165370; Homo sapiens.
 DR HGNC; HGNC:14963; GPR101.
 DR MIM; 300393; -.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
 KW Transmembrane.
 FT TOPO_DOM 1 35 Extracellular (Potential).
 FT TRANSMM 35 56 1 (Potential).
 FT TOPO_DOM 57 68 Cytoplasmic (Potential).
 FT TRANSMM 69 89 2 (Potential).
 FT TOPO_DOM 90 106 Extracellular (Potential).
 FT TRANSMM 107 127 3 (Potential).
 FT TOPO_DOM 128 149 Cytoplasmic (Potential).
 FT TRANSMM 150 170 4 (Potential).
 FT TOPO_DOM 171 196 Extracellular (Potential).
 FT TRANSMM 197 217 5 (Potential).
 FT TOPO_DOM 218 399 Cytoplasmic (Potential).
 FT TRANSMM 400 420 6 (Potential).
 FT TOPO_DOM 421 433 Extracellular (Potential).
 FT TRANSMM 434 454 7 (Potential).
 FT TOPO_DOM 455 508 Cytoplasmic (Potential).
 FT CARBOHYD 7 13 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).
 FT DISULFID 104 182 By similarity.
 SQ SEQUENCE 508 AA; 56716 MW; E20A409F65C95B5 CRC64;

Query Match 99.9%; Score 2641; DB 1; Length 508;
 Best Local Similarity 99.8%; Pred. No. 3,8e-147;
 Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTSTCTNSTRESNSHTCMPLSKMPSISLAHGIRSTVLVIFLAASFVGNIVLALVLRKP 60
 DB 1 MTSTCTNSTRESNSHTCMPLSKMPSISLAHGIRSTVLVIFLAASFVGNIVLALVLRKP 60
 QY 61 QLLQVTNRFINLVTDLQISLVAPWVAVTSVLPFWPLNSHFCALVSLTHLFAFASVN 120
 DB 61 QLLQVTNRFINLVTDLQISLVAPWVAVTSVLPFWPLNSHFCALVSLTHLFAFASVN 120
 QY 121 TIVVSVDRYLSIIHPLSPSKMTQRGYLLVGTWIVAILQSTPPLVGMQQAADFERN 180
 DB 121 TIVVSVDRYLSIIHPLSPSKMTQRGYLLVGTWIVAILQSTPPLVGMQQAADFERN 180
 QY 121 TIVVSVDRYLSIIHPLSPSKMTQRGYLLVGTWIVAILQSTPPLVGMQQAADFERN 180
 DB 121 TIVVSVDRYLSIIHPLSPSKMTQRGYLLVGTWIVAILQSTPPLVGMQQAADFERN 180
 QY 181 LCSMTWGSPSYTTISLVSVFIVPLIWIACYSVVFCAARQHALLVNKRSHLEVRKYD 240
 DB 181 LCSMTWGSPSYTTISLVSVFIVPLIWIACYSVVFCAARQHALLVNKRSHLEVRKYD 240
 QY 241 CVENDEGAKKEKFEODESEFRROHEGEVAKKGRMEAKDGLAKEGSTGTSSEV 300
 DB 241 CVENDEGAKKEKFEODESEFRROHEGEVAKKGRMEAKDGLAKEGSTGTSSEV 300

QY 301 RGESEVRESSVVAADSGMEKSGSTKYBENSMKADKRTENOCSDLDGDMRFGEDDI 360
 DB 301 RGESEVRESSVVAADSGMEKSGSTKYBENSMKADKRTENOCSDLDGDMRFGEDDI 360
 QY 361 NFESEDDVAVVIPSPLPSRRNSNPPLPFCYCKAKAVYFIIFFSYVSLGFCFLAV 420
 DB 361 NFESEDDVAVVIPSPLPSRRNSNPPLPFCYCKAKAVYFIIFFSYVSLGFCFLAV 420
 QY 421 LAVVVDVETQVQVWVITIIWLFLLQCCIHPEYVGYWVKTIKKRIGDMLKKKFKKRPK 480
 DB 421 LAVVVDVETQVQVWVITIIWLFLLQCCIHPEYVGYWVKTIKKRIGDMLKKKFKKRPK 480
 QY 481 EDSHPDLPGTEGTEGKIVPSYDSATRP 508
 DB 481 EDSHPDLPGTEGTEGKIVPSYDSATRP 508

RESULT 2
 Q5JSM8_HUMAN PRELIMINARY; PRT; 508 AA.
 ID Q5JSM8; HUMAN
 AC Q5JSM8; 10-MAY-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE G-protein-coupled receptor, 101.
 GN Name=GPCR1; ORFNames=RP11-308D16.5-001;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lawlor S.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 DR EMBL; AL390879; CA14047.1; -; Genomic DNA.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signaln...; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 SQ SEQUENCE 508 AA; 56716 MW; E20A409F65C95B5 CRC64;

Query Match 99.9%; Score 2641; DB 2; Length 508;
 Best Local Similarity 99.8%; Pred. No. 3,8e-147;
 Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTSTCTNSTRESNSHTCMPLSKMPSISLAHGIRSTVLVIFLAASFVGNIVLALVLRKP 60
 DB 1 MTSTCTNSTRESNSHTCMPLSKMPSISLAHGIRSTVLVIFLAASFVGNIVLALVLRKP 60
 QY 61 QLLQVTNRFINLVTDLQISLVAPWVAVTSVLPFWPLNSHFCALVSLTHLFAFASVN 120
 DB 61 QLLQVTNRFINLVTDLQISLVAPWVAVTSVLPFWPLNSHFCALVSLTHLFAFASVN 120
 QY 121 TIVVSVDRYLSIIHPLSPSKMTQRGYLLVGTWIVAILQSTPPLVGMQQAADFERN 180
 DB 121 TIVVSVDRYLSIIHPLSPSKMTQRGYLLVGTWIVAILQSTPPLVGMQQAADFERN 180
 QY 121 TIVVSVDRYLSIIHPLSPSKMTQRGYLLVGTWIVAILQSTPPLVGMQQAADFERN 180
 DB 121 TIVVSVDRYLSIIHPLSPSKMTQRGYLLVGTWIVAILQSTPPLVGMQQAADFERN 180
 QY 181 LCSMTWGSPSYTTISLVSVFIVPLIWIACYSVVFCAARQHALLVNKRSHLEVRKYD 240
 DB 181 LCSMTWGSPSYTTISLVSVFIVPLIWIACYSVVFCAARQHALLVNKRSHLEVRKYD 240
 QY 241 CVENDEGAKKEKFEODESEFRROHEGEVAKKGRMEAKDGLAKEGSTGTSSEV 300
 DB 241 CVENDEGAKKEKFEODESEFRROHEGEVAKKGRMEAKDGLAKEGSTGTSSEV 300


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QY 301 RSSEVEBSSTVASDQSMGKSGSTVEBNSMKADGRTEVNOCSIDLGEDMEFGEDDI 360
DB 301 RSSEVEBSSTVASDQSMGKSGSTVEBNSMKADGRTEVNOCSIDLGEDMEFGEDDI 360
QY 361 NFSEDDVEAVNIPESLPSPRRNSNPPLPRCYQCAAAVFIPIISYVLSIGPYCELA 420
DB 361 NFSEDDVEAVNIPESLPSPRRNSNPPLPRCYQCAAAVFIPIISYVLSIGPYCELA 420
QY 421 LAAVWVDEVOVQWVTTIIIMLFLOCCIHPPVYGMHTIKREIOMDKKPFCKEKKPK 480
DB 421 LAAVWVDEVOVQWVTTIIIMLFLOCCIHPPVYGMHTIKREIOMDKKPFCKEKKPK 480
QY 481 EDSDPDLPGTEGTEGKIVPSYDSATFP 508
DB 481 EDSDPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 3
O4RP59 TETNG PRELIMINARY; PRT; 229 AA.
ID O4RP59_
AC O4RP59_
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Chromosome 1 SCAF15008, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00031265001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_Taxid=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Catolico L., Poulain J., De Bernardinis V.,
RA Cruaud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McGowan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Sautin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -! SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -! SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DB EMBL, CAEB01015008; CAG09823.1; -; Genomic_DNA.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON TER 229
SQ SEQUENCE 229 AA; 25449 MW; 6CEB5B9850A9AA6 CRC64;
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Query Match 22.2%; Score 588; DB 2; Length 229;
Best Local Similarity 49.3%; Pred. No. 6.9e-27;
Matches 113; Conservative 47; Mismatches 57; Indels 12; Gaps 3;

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QY 6 TNSSTESNSHTCMPISKAPISLAHGIIRSTVLVIFLAASFVGNITVALVLRKPDLLQV 65
DB 11 TNNSTD-----ARGYSTVDSVVMVIALILCSLGGNVVLLVFPKRKQLLHV 60
QY 66 TNRFFNLVLDLQISLVAPNVAVTSVPLFPLNSHFTALVSLTHLFAFASVNTIVLV 125
DB 61 ANRFVNLILLADLQTVLWMPALAAVGVWPLDARLQALVLMHLFAPAGVNTIIVV 120
QY 126 SVDRVLSITHPSYSKMTQRRGYLLVCTWVALQSPRPVYGCQAADFERNLCSMI 185
DB 121 SVDRVLSITHPSYPTRMTPHGLTNLLICTWVLSLQSTPPVYGVGTVDFDRKVCSSV 180
QY 186 MGASPSYITL-SVGSFIVPLIWMIACTSVVPCARRQHALLVNVRHS 233
DB 181 WSSLSYSTIMVSTLSF-WLPVIMLGCTMMVRRARRQNALVHPVQYOS 228

RESULT 4
O4SUM2 TETNG PRELIMINARY; PRT; 200 AA.
ID O4SUM2_
AC O4SUM2_
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Chromosome undetermined SCAF13862, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00012395001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_Taxid=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Catolico L., Poulain J., De Bernardinis V.,
RA Cruaud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McGowan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Sautin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -! SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -! SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DB EMBL, CAEB01013862; CAF95660.1; -; Genomic_DNA.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON TER 200
SQ SEQUENCE 200 AA; 22473 MW; 8D0A26D8F99489C CRC64;
```

Query Match 21.8%; Score 576; DB 2; Length 200;
Best Local Similarity 55.1%; Pred. No. 3e-26;
Matches 109; Conservative 39; Mismatches 48; Indels 2; Gaps 2;

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QY 37 VLVLFLAASFGVGNIVLALVLRKPOLLOVTRNFNNLVTDLIQISLVAPWVATSPLE 96
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 LIALILCVSLFGNVVLLVLFQKRPOLLHVANRFVNLILLADLIQVLVMPFALAASVPGV 62
QY 97 WPLNSHFTALVSLTLHLPAPASVNTIVVSVDRYLSIIHPLSPSKRMQRBYLLXGTW 156
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 WPLDRRLCOALVNLHLFAPAGVNTIVVSDRYLIIHPLSLPYTRMTPLHGTNLIICTW 122
QY 157 IVAILQSTPPLVGMQAAFDERNALCSMIWGAAPSYTIL-SVVSFVIPLVIMACYSV 215
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 VLSLIQSTPPLVGMGTVPDRRYKVCVWSSSLYSIMVSTLSF-WLPVIMLCGMV 181
QY 216 FCARROHALLVYVKRHS 233
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 FRAARQNALVHPIDOTOS 199
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RESULT 5

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Q90X46_BRARE PRELIMINARY; PRT; 526 AA.
ID Q90X46;
AC Q90X46;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Novel protein similar to human G-protein coupled receptor RE2.
GN ORFNames=D22015.4-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
RX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lloyd D.;
RL Submitted (DEC-2004) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AL590146; CAC94897.2; -; Genomic DNA.
DR Ensembl; ENSDARG0000000007; Danio rerio.
DR ZFIN; ZDB-GENE-030616-58; sl:rp71-2015.4.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . ; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR00276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 526 AA; 58485 MW; CACE795D638B5B3E CRC64;
```

Query Match 14.8%; Score 392.5; DB 2; Length 526;
Best Local Similarity 23.6%; Pred. No. 4.9e-15;
Matches 110; Conservative 75; Mismatches 137; Indels 145; Gaps 10;

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QY 7 NSTRSNSHTCMPISLAHGIIRSTVIFPLAASFGVGNIVLALVLRKPOLLOV 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 NGTAVANSITNGDDNGLM-----VLESVSIITIIAIIACLNLIIVTLVYKPYLLPS 58
QY 67 NRIFFNLVTDLIQISLVAPWVATSPLEPMLNSHFC--TALVSLTLHLPASVNTIVL 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 NKFVSLSSNLLSLVLMPLFVYASSVRDMMFGVWCMFTALLH--LVSSSSMLTLIGA 116
QY 125 VSVDRYLSIIHPLSPSKRMQRBYLLXGTWIVAILQSTPPLVGMQAAFDERNALCSM 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 117 IALIDRYVALVYIMYIMKITGNRAVALAIYVIMLSHVGCLPLFGWSPFEDRFKMTCTV 176
QY 185 IMGASPSYTIISVSVFIVPLVIMACYSVVFCAARROHALLVYVKRHSLEVRVADCVEN 244
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Db 177 SMHKEISTAFWWTWCCLLPVLVAMLVCYGFVRAR----- 212
QY 245 EDEBGAKEKEBFODESEFRQHEGEVAKEGMEAKDGLKAKGSGTSTGSSVEARGSE 304
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 213 -----IAKRYCG----- 221
QY 305 EVRESSTYASDGMGKEGKSTKVEENSMKADKGTENVQCSIDIDGEDDMERGEDDINSE 364
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 222 -----SVVVS-----QESSSQNNGRKNSVTSISSG----- 248
QY 365 DDVEAVNIPESLPSRRN---SNSNPPLPRCYOCKAAKVFIIIFSYLSLGPYCFGLAVL 421
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 249 -----SRKSLISGS-----QCKAFITLVIGTFLITGSPYVVIST 286
QY 422 AVWVDVETQDPQWYITIIIMLFPLQCCIHPIVYGYMHTIKKEIQDM 468
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 287 EALIGKNSVSPQ-VETLVSWLSFTSAVCHPLITGYLMNKTVAKELLGM 332
```

RESULT 6

```
Q5TGK0_HUMAN PRELIMINARY; PRT; 407 AA.
ID Q5TGK0;
AC Q5TGK0;
DT 01-FEB-2005 (Tremblrel. 29, Created)
DT 01-FEB-2005 (Tremblrel. 29, Last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
DE G protein-coupled receptor 161.
GN Name=GPRI61; ORFNames=RP4-745114.2-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
RX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Martin S.;
RL Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AL033532; CA12624.1; -; Genomic DNA.
DR Ensembl; ENSG00000143147; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . ; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR00276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 407 AA; 45363 MW; 00078B8EB5BC1F21 CAC64;
```

Query Match 14.8%; Score 391; DB 2; Length 407;
Best Local Similarity 23.6%; Pred. No. 4.6e-15;
Matches 106; Conservative 67; Mismatches 130; Indels 146; Gaps 11;

```
QY 31 GIIRSTVIFPLAASFV--GNIVLALVLRKPOLLOVTRNFNNLVTDLIQISLVAPWV 88
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 GVIITQPIAIVITTFVCLGNLVIVTYLTKKSYLLTSNKKVFSLTLSNPLSLVLPFV 84
QY 89 VATSVLPFWPLNSHFTALVSLTLHLPAPASVNTIVVSVDRYLSIIHPLSPSKRMQRG 148
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 85 VTSSIRREMIGVWCMNSALLYLLISSASMLTIGVAILDRYVALVYPMYPMKITGNRA 144
QY 149 YLLVGTWIVAILQSTPPLVGMQAAFDERNALCSMIWGAAPSYTIIISVSVFVIPLVIM 208
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 145 VVALVYIMLSHVGCLPLFGWSPFEDRFKMTCTVAFWQIICALFPPLVM 204
QY 209 IACYSVVFCAARROHALLVYVKRHSLEVRVADCVENDEBGAKEKEBFQDSEFRQHEG 268
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 205 LVCTGIFFRVAR-----YKARKVHCGTIVIVE-BDAQ----- 235
```

QY	269	EYKAEGNRHADGSLAKAEGSTGTSSSEVARGSEFVBSSTVADGSEKGE	328
DB	236	---RTGR-----KNSSTISSG-----	250
QY	339	ENSMKADKRGRTVNOCSI DLGEGDMEFGEDDINFESDDEAVANIPE	383
DB	251	-----SRNNAQGVV	260
QY	364	NSNPPLPRCYOCCAKAKVFIITFSVLSGPR-CFLAVIAWV-VDVETQ	439
DB	261	YSAN-----QCKALITLIVLGLFMVMTWGPYVIAESALMGKSSVS	309
QY	440	IWLFLQCCIHPRYVGYMKHTIKKEIQDM	468
DB	310	TWLSFASAVCHPLITGLMKNKTVKELGLM	338

RESULT 7

ID	GP161_HUMAN	STANDARD;	PRT;	529 AA.
AC	Q8NEU8; 075963;			
DT	05-JUL-2004 (Rel. 44, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Probable G-protein coupled receptor 161 (G-protein coupled receptor RE2).			
GN	Name=GPRI61;			
OS	homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;			
OC	Homo.			
OX	NCBI_TaxId=9606;			
RP	[1]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 1).			
RC	TISSU=Brain;			
RA	Warren C.N., Aronstam R.S., Sharma S.V.;			
RT	"Isolation of cDNA coding for G-protein coupled receptor RE2."			
RL	Submitted (Apr-2003) to the EMBL/GenBank/DBD databases.			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 2).			
RC	TISSU=Brain;			
RX	PubMed=9932290;			
RA	Raming K., Konzelmann S., Breer H.;			
RT	"Identification of a novel G-protein coupled receptor expressed in			
RL	distinct brain regions and a defined olfactory zone."			
RN	Recept. Channels 6:141-151(1998).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM 1).			
RC	TISSU=Brain;			
RX	MEDLINE=22389857; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,			
RA	Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,			
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Boesk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hele S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield V.S.N., Krzyminski M.I., Skalska U., Smalins D.E.,			
RA	Schuerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC	-1- FUNCTION: Orphan receptor.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			

[illegible]

QY 329 ENSKADKGRTEVNCSTIDLGEDDMEFGEDDINFESEDDVEAVNIPESLPSPRRNS----- 383
Db 251 -----SRNAFGQGV 260
QY 384 -NSNPPLRCYQCKAKAVYFIIFISYVLSGPY-CFLAVLAW--VDVETQVPOQVITII 439
Db 261 YSAN-----QCKALITILVLGAFVMTWGPVNVVIASEALMGKSSVPSLETMA----- 309
QY 440 IWLFLQCCIHPPYVGYNMHTIKKEIODM 468
Db 310 TWLSFASAVCHPLIYGLMKNKTVRKELLGM 338

RESULT 8
ID 05TGK1 HUMAN PRELIMINARY; PRT; 529 AA.
AC 05TGK1
DT 01-FEB-2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE G-protein-coupled receptor 161.
GN Name=GPRI61; ORFNames=RP4-745114.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Martin S.;
RL Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AL033533; CA122623.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1. 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 529 AA; 58559 MW; FC7D1AC0894DC3F3 CRC64;

Query Match 14.8%; Score 391; DB 2; Length 529;
Best Local Similarity 23.6%; Pred. No. 66-15;
Matches 106; Conservative 67; Mismatches 130; Indels 146; Gaps 11;

QY 31 GIRSTVVIIFLAASFV--GNIVLALVLRQKPOLQVTRFIFNLITVDLQISLVAPV 88
Db 25 GVIIHQFALIVITITFVLCGNIVIVTLYKSYLLTSKPFSLTSLFSLSVLVPV 84
QY 89 VATSVPLFWPLNSHFCALVSLTHLPAPASVNTIVLVSDRYLSIHPISYSPKXTORRG 148
Db 85 VTSSIRREMIFGVWNCFSALTYLLISSASMLTIGVIALDRYAVLYPVMYPMKITGRRA 144
QY 149 YLLVGTWIVALTGSTPLPYGCGAAPDERNALCGMIMWASSYITLVSSTIVPLVM 208
Db 145 VVALVYIMLHSLIGCLPPLFGMSVVEPDEFKWMCVAAHREGEYTAFWQIMCALPPLVM 204
QY 209 IACYSVFCAARQHALLYNVRHSLLEVVKDCVENEDDEGAKKEEFQDESEFRHQEG 268
Db 205 LVTCYGFIRVAR-----VAKYKHCCTVIVE-EDQ----- 235
QY 269 EYKAGEGRMEAKDGLKAKESGTGTSSESVARGSEBEVESSTVASDGSMEGEGSTKYE 328
Db 226 ---RTGR-----KNSSTSSSSG----- 250
QY 329 ENSMADKGRTEVNCSTIDLGEDDMEFGEDDINFESEDDVEAVNIPESLPSPRRNS----- 383

Db 251 -----SRNAFGQGV 260
QY 384 -NSNPPLRCYQCKAKAVYFIIFISYVLSGPY-CFLAVLAW--VDVETQVPOQVITII 439
Db 261 YSAN-----QCKALITILVLGAFVMTWGPVNVVIASEALMGKSSVPSLETMA----- 309
QY 440 IWLFLQCCIHPPYVGYNMHTIKKEIODM 468
Db 310 TWLSFASAVCHPLIYGLMKNKTVRKELLGM 338

RESULT 9
ID 04SOK3_TETNG PRELIMINARY; PRT; 535 AA.
AC 04SOK3;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome 2 SCAR14781, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0025981001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorph; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dobas C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Authouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Catcicollo L., Poulian J., De Bernardis V.,
RA Crnaud C., Duprat S., Brotier P., Couanseau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schacherer V., Coster F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAE01014781; CAG05829.1; -; Genomic DNA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1. 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON TER 535
SQ SEQUENCE 535 AA; 58074 MW; 5203973C7F10E8E4 CRC64;

Query Match 14.1%; Score 373; DB 2; Length 535;
Best Local Similarity 23.0%; Pred. No. 6.9e-14;
Matches 112; Conservative 72; Mismatches 136; Indels 168; Gaps 13;

QY 13 NSSHTCMPVLSKMPISLHGIIRSVLVIFLAASVGVIVLALVLRQKPOLQVTRFIF 71
Db 2 NTSRNCIVVAGGEGIALAESVMTVTLL-----ACLSULLVATILYRPFYLLTSNKRVF 57
QY 72 NLVLTDLQISLVAPVWVATSVPLFWPLNSHFCALVSLTHLPAPASVNTIVLVSD--- 128
Db 58 SLTSLNLLSVLVLPFVAVSVVREMLFGVWNCFTALTYLLISSASMLTIGALAIIDRSV 117
QY 129 -----RYLSIHPISYSPKXTORRGYLLVGTWIVALTGSTP 165

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Db      118 FSPSPSCGATLWVLTSLVLTTRYAVVLPMTPKIGNRAVVAISYVWLHSLVGLP 177
Qy      166 PLVGMGQAFDERNALCSMIMGASPSYTLISVSVFVPLIMICYSVPCARQNAL 225
Db      178 PLFGMSSEFFDLKRTCVASMRBSPYFWIMCLPLCYWLACVYIFVVAR----- 232
Qy      226 LYNVRHSLSEVAVKDC---VENEDEGAKEKEEFQDESEFRQHEGVEAKEGMEARD 281
Db      223 -----MKARKVHCITVVGPPDDAGAG-----RSGR----- 258
Qy      262 GSLKAKESGTSESSVEARGSEEVRESSTVASDSGMEKESGTVKENSMAKDKGRTEV 341
Db      259 -----KNSSTSTS-----SNGS---RSLVYA-----GS----- 279
Qy      342 NCGSIDLGEDDMFEGEDINPSEDDVEAVNIPESLPSPRRNSNPPLPRCYQCKRAKY 401
Db      280 -----OQKAFVTI 287
Qy      402 FIIFSVYLSGPGYC-FLAVLAVWVDETQVPOWVITIIIMFLQCCIHPPYVGYMHT 460
Db      288 LVVIGTFVITWKPYPYGVCTEALM--GQGSVAPEGELTVAMSLCSAVCHPLIYGFMMKT 345
Qy      461 IKKEIQDM 468
Db      346 VKKELGM 353

RESULT 10
ACM4_CHICK STANDARD; PRT; 490 AA.
ID ACM4_CHICK STANDARD; PRT; 490 AA.
AC P17200;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Muscarinic acetylcholine receptor M4.
GN Name=CHRM4;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90153912; PubMed=2154460;
RT Tietje K.M., Goldman P.S., Nathanson N.M.;
RT "Cloning and functional analysis of a gene encoding a novel muscarinic
RT acetylcholine receptor expressed in chick heart and brain.";
RL J. Biol. Chem. 265:2828-2834(1990).
CC -!- FUNCTION: The muscarinic acetylcholine receptor mediates various
CC cellular responses, including inhibition of adenylylate cyclase,
CC breakdown of phosphoinositides and modulation of potassium
CC channels through the action of G proteins. Primary transducing
CC effect is inhibition of adenylylate cyclase. May couple to multiple
CC functional responses in cell lines.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in heart and brain.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; J05218; AAA48563.1; -; Genomic_DNA.
CC
CC DR PIR; A35546; A35546.
CC DR HSSP; P02699; 1BOU.
CC DR Ensembl; ENSGALG00000008365; Gallus gallus.
CC DR GO; GO:0016021; C:intracellular membrane; IC.
CC DR GO; GO:0004981; F:muscarinic acetylcholine receptor activity; NAS.
CC DR GO; GO:0007194; P:negative regulation of adenylylate cyclase ac. .; NAS.
CC DR GO; GO:000384; P:phosphoinositide metabolism; NAS.

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DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR001432; M4_receptor.
DR InterPro; IPR000995; MusA2C_receptor.
DR PANTHER; PTHR19266:SF85; M4_receptor; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR00541; MUSCARINICR.
DR PRINTS; PR00541; MUSCARINICR.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1.
DR PROSITE; PS00262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Multigene family;
KW Phosphorylation; Postsynaptic membrane; Receptor; Transducer;
KW Transmembrane.
FT TOPO_DOM 1 42 Extracellular (Potential).
FT TRANSMEM 43 64 1 (Potential).
FT TOPO_DOM 65 78 Cytoplasmic (Potential).
FT TRANSMEM 79 99 2 (Potential).
FT TOPO_DOM 100 116 Extracellular (Potential).
FT TRANSMEM 117 138 3 (Potential).
FT TOPO_DOM 139 158 Cytoplasmic (Potential).
FT TRANSMEM 159 181 4 (Potential).
FT TOPO_DOM 182 203 Extracellular (Potential).
FT TRANSMEM 204 226 5 (Potential).
FT TOPO_DOM 227 412 Cytoplasmic (Potential).
FT TRANSMEM 413 433 6 (Potential).
FT TOPO_DOM 434 447 Extracellular (Potential).
FT TRANSMEM 448 467 7 (Potential).
FT TOPO_DOM 468 490 Cytoplasmic (Potential).
FT CARBOHYD 3 3 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 15 15 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 20 20 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 25 25 N-linked (GlcNAc...) (Potential).
FT DISULFID 115 195 By similarity.
SQ SEQUENCE 490 AA; 54937 MW; 2CDFB5FAD72298E CRC64;

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Query Match 13.0%; Score 343.5; DB 1; Length 490;
Best Local Similarity 23.7%; Pred. No. 3,4e-12;
Matches 116; Conservative 94; Mismatches 176; Indels 103; Gaps 17;

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Qy 36 TVLVFLA-----ASVGNIVAVLQKRPQLQOTNRIFFLVLTDL-----QISL 83
Db 39 TVELVFIAVTGSLSLVTVGNILVMSIKVRQLOQTANNVFLFSLACADLIIGVPSMWL 98
Qy 84 VAPWVAVSVPLFVFNHPTALVSLTLFAPASVNTIVAVSVRYLSIHPLSYPSM 143
Db 99 YTVYIIKG---YVFLGAVVCDLWMLADYVNSASVWMLISFPRICTVTEPLTPARR 154
Qy 144 TORRGYLLYGTVIAVLIQSTPPLYG---GQAAFDERNALCSMIMGASPSYTLISVVS 199
Db 155 TTKMAGLMTAAWMLISFILMAPALIFWQFIYVGRITVHERE--CYIPLSNPAVTFGTALA 212
Qy 200 FIVIPLIYIACYSVVFCAARQNALLVNKRHSLEVR-----YVDCVN 244
Db 213 AFVLPVIMTVIYIHSLSRSR-----VRHKKESRERKRGKLSFFKAPVYQNNNN 266
Qy 245 EDEGAKEKEEFQDESEFRQHEGVEAKEGMEAKDGLSKAKESGTSESSVEARGSE 304
Db 267 SKRAVEVKEEVRN-----GKV-----DDQPSQATATGQOE-----KE 301
Qy 305 EVRESSTVASDSGMEKESGTVKENSMAKDKGRTEVNCSIDLGEDDMFEGEDINPSE 364
Db 302 TENESSTVSMGTQTKDP-TTEILPAGQGQSPAHPRVNPST-----KMSKIKIVTKQ 352
Qy 365 DVEAVNIPESLP-----PSRRN--SNSNP-LPRCY-----OQKAAKY 400
Db 353 TGTESVTALEIVPARAGASDNHLSNSRPANVARRPASIARSQVKKQMAAREKVVYT 412
Qy 401 FIIFSVYLSGPGYCFLAVLAVWVDETQVPOWVITIIIMFLQCCIHPPYVGYMHT 460
Db 413 FVAILLAFILTTPTFNWVLIITF--CETCVETWMSIGYWLCCYNSTINPACVLCNAT 470
Qy 461 IKKEIQDM 469

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Db 471 FKTFKILL 479

RESULT 11
GP101 MOUSE STANDARD; PRT; 77 AA.

AC Q80762;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable G-protein coupled receptor 101 (Fragment).
GN Name=Grp101;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]

NP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22584407; PubMed=12679517; DOI=10.1073/pnas.0230374100;
RA Vasiliadis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.E.,
Rastrud M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,
R Bergmann J.E., Galanaris G.A.;
RT "The G protein-coupled receptor repertoire of human and mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908(2003).
CC -1- FUNCTION: Orphan receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL: AY255576; AA085088.1; -. mRNA.
DR Ensembl; ENSMUSG0000036357; Mus musculus.
DR MGI; MGI:2685211; Gpr101.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1, 1.
DR PRINTS; PR00237; GPCRHOPOSN.
DR PROSITE; PS50262; G_PROTEIN_REC_P1_2, 1.
KM G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT TOPO_DOM <1 9 Cytoplasmic (Potential).
FT TRANSMEM 10 30 4 (Potential).
FT TOPO_DOM 31 56 Extracellular (Potential).
FT TRANSMEM 57 77 5 (Potential).
FT DISULFID <1 42 By similarity.
FT NON_TER 1 1
FT NON_TER 77 77
SQ SEQUENCE 77 AA; 8517 MW; C760758CB179D114 CRC64;

Query Match 13.0%; Score 343; DB 1; Length 77;
Best Local Similarity 81.6%; Pred. No. 5.6e-13; Indels 0; Gaps 0;
Matches 62; Conservative 6; Mismatches 8;

Qy 141 SKMTQRSGYLLIGTWIVAIIGSTPPLYGWGAQAFDERNALCSMTMGASPSYTIISVSF 200
Db 1 SKMTRRSGYLLIGTWIVAIIGSTPPLYGWGAQAFDERNALCSMTMGASPSYTIISVSF 60

Qy 201 IIVPLIWIACYSVVF 216
Db 61 IIVPLIWIACYSVVF 76

RESULT 12
Q96RE8_HUMAN PRELIMINARY; PRT; 466 AA.
AC Q96RE8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Adrenergic receptor alpha-1a.

GN Name=ADRA1A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]

NP NUCLEOTIDE SEQUENCE.
RA Banerjee A.G.N., Aarti A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: This alpha-adrenergic receptor mediates its action by
CC association with G proteins that activate a phosphatidylinositol-
CC calcium second messenger system. Its effect is mediated by G(q)
CC and G(11) proteins (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL: AF395806; AA07197.1; -. mRNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004937; F: alpha1-adrenergic receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P: signal transduction; IEA.
DR InterPro; IPR001004; A_receptor1Gs.
DR InterPro; IPR00276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1, 1.
DR PRINTS; PR00557; ADRENERGICAL.
DR PRINTS; PR00237; GPCRHOPOSN.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1, 1.
DR PROSITE; PS50262; G_PROTEIN_REC_P1_2, 1.
KM G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 466 AA; 51431 MW; 876CBFB3323B7A1 CRC64;

Query Match 13.0%; Score 343; DB 2; Length 466;
Best Local Similarity 21.6%; Pred. No. 3.5e-12; Indels 130; Gaps 10;
Matches 106; Conservative 76; Mismatches 178;

Qy 8 STRESNSHTCMPLSKPISLAHGIIRSTVLVIFLAASFVGNIVLALVLRKPOLLOVYN 67
Db 5 SGNASDSNGCTP--PAVNVISKAILLGVILGGLILRGVGNILVILSVACHRLHSTH 62

Qy 68 RPIRLVTDLLQISLVAAPVAVTSVPLFPLNHFCTALVSLTHLPFASVNTIVLSV 127
Db 63 YVIVLAADLLISTVLPSAIFEVILGVAFGRVFCINMAADVLCCTASIMGLCIISI 122

Qy 128 DRYLSIHPILSPKMTQRSGYLLIGTWIVAIIGSTPPLYGWGAQAFDERNALCSMTMG 187
Db 123 DRYIGVSHPLPPIVIVQKRLMALLCWMLSLVISTIGPLFGWQRA-PEDETICQI--N 179

Qy 188 ASPSTIISVSVFTVPLIWIACYSVVFCAARRQHALLVNKKHSLDEVVKDCVENDE 247
Db 180 EEPGVLPFSAIGSFYLPFLAIIIVMYCRVYVAKR-----ESRGL 218

Qy 248 EGAKEKEPQDESEFRQHESEVAKEGRMKAKGSLKAKGSGTGTSSSVYARGSEVR 307
Db 219 KSGLKTDSDSEQVTLRIHRNAPA-----GGSGMSAKTKTFPSVYL 261

Qy 308 ESSYVASDGSNEKGSGTKVENSMKADKRTENVQCSIDLGEEDMERGEDIDFSEDDV 367
Db 262 -----LFRSKK- 268

Qy 368 EAVNIPESLPPSRNSNSNPPLPRCYQCAKAVIFIIIFSYLSLGPYCLAVLAWVDV 427
Db 269 -----KAKTIGIVGCFVLCMLPR-FLVMPIGSFPF 299

Qy 428 ETQVPQWYITIIIMFLQCCIHPPYVGYWKTIKGIDMLK-KPFCKEKPPE---D 482
Db 300 DKFSETVFKIVFLGYNSCINPIYPCSSQEFKAFQNVLRICLCRKQSSKHALGYT 359

Qy 483 SHPDLPTGEG 492
Db 360 LHPDSQAVEG 369

RESULT 13	Q8BUE5_MOUSE PRELIMINARY;	PRF:	427 AA.
AC	Q8BUE5;		
DT	01-MAR-2003 (TREMBLrel. 23, Created)		
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone: D63050N06 product: adrenergic receptor, alpha 1a, ALPRA		
DE	1A-ADRENOCPTOR, full insert sequence.		
GN	Name=Adrala;		
OS	Mus musculus (Mouse).		
OC	Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Mus.		
OK	NCBI Taxid=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=C57BL/6J; TISSUE=Kidney;		
RX	MEBLINE=99279253; Pubmed=10349656; DOI=10.1016/S0076-6879(99)03004-9;		
RA	Carninci P., Hayashizaki Y.;		
RT	"High-efficiency full-length cDNA cloning.";		
RL	Mech. Enzymol. 303:19-44(1999).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=C57BL/6J; TISSUE=Kidney;		
RX	MEBLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;		
RA	Kawai T., Shinagawa A., Shihata K., Yoshino M., Itoh M., Ishi Y.,		
RA	Arkawa T., Hara A., Fukunishi Y., Komu H., Adachi J., Fukuda S.,		
RA	Atawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,		
RA	Salto T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Salto R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Glisic C., King B., Kochia H.,		
RA	Kuehl P., Lewis S., Metzuo T., Nikaide I., Pesole G., Quackenbush J.,		
RA	Schirrl L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bersh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Guertlich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Maestri M., Mazzarelli U., Kombo N.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shihata Y., Storch K.-F.,		
RA	Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RL	Nature 409:685-690(2001).		
RN	[3]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=C57BL/6J; TISSUE=Kidney;		
RA	The FANTOM Consortium		
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;		
RT	"Analysis of the mouse transcriptome based on functional annotation of		
RT	60,770 full-length cDNAs.";		
RL	Nature 420:563-573(2002).		
RN	[4]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=C57BL/6J; TISSUE=Kidney;		
RX	MEBLINE=20499374; Pubmed=11076861; DOI=10.1101/gr.152600;		
RA	Carninci P., Shihata Y., Hayatsu N., Sugihara Y., Shihata K., Itoh M.,		
RA	Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;		
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to		
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";		
RL	Genome Res. 10:1617-1630(2000).		
RN	[5]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=C57BL/6J; TISSUE=Kidney;		
RX	MEBLINE=20530913; Pubmed=11076861; DOI=10.1101/gr.152600;		
RA	Shihata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,		
RA	Kono H., Akiyama U., Nishi K., Kikunai T., Tachino H., Itoh M.,		
RA	Sumi N., Ishii Y., Nakamura S., Hachima S., Nishino T., Harada A.,		
RA	Yamamoto K., Matsunoto H., Sakaguchi S., Ikegami T., Kasaiwagi K.,		

RA Fujitake S., Inoue K., Togawa Y., Tanaka T., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Itanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RL sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata N., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohmoto N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Saeki D., Shibata K., Shinagawa A., Shitaki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Kahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases
 CC -!- FUNCTION: This alpha-adrenergic receptor meditates its action by
 CC association with G proteins that activate a phosphatidylinositol-
 CC calcium second messenger system. Its effect is mediated by G(q)
 CC and G(11) proteins (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC EMBL; AK085653; BAC39495.1; -; mRNA.
 DR MGI; MGI:104773; Adra1a.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0008217; P:regulation of blood pressure; IMP.
 DR InterPro; IPR0001004; A_receptor1CS.
 DR InterPro; IPR000276; GPCR_RecepDsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO0557; ADRENRCALAR.
 DR PROSITE; PRO0237; GPCRKHODOSP.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 427 AA; 47516 MW; 3810B5D5F5A09317 CRC64;

Query Match 12.9%; Score 341; DB 2; Length 427;
 Best Local Similarity 22.7%; Pred. No. 4.2e-12;
 Matches 115; Conservative 75; Mismatches 183; Indels 134; Gaps 13

QY NSTEENSNRHCHMPLSKMPISLARGIIRSYLVIFLASPVGNYIALVLQRKPOLQYT 66
 DB 7 NASGSGNCTH--PPAQNISKA--ILLGVILGGLIGVIGNLIVILSVACHRHLSVT 61
 QY 67 NRFENLVTDLTQLSLVAPWVAATVPLFPLNSHCFCTALVSLTHLPAPASVNTIVLVS 126
 DB 62 HYIYLAIVADLLLTSTYLPFSALPELIGYVAFGRVFCVMAADVLCCTASIMELCIIS 121
 QY 127 VDRYLSIIHPLSYPSKMTQRRGQYLLYGTWTVAILQSTPPIYWGQAAFDERNALCSMTW 186
 DB 122 IDRYIGVYPRPYFTYIQRGVABALLCVMALSLVISIGLPIFGMRQQA--PEDETICQI-- 178
 QY 187 GASSTYLLSVSFIVPLIYMIACYSVPCAAQRQHALLYNKRHSLEVAVKQCVENBD 246
 DB 179 NEEPRGYVFSALSGFPYPLTIIILWYCRVYVAKR-----ESRG 217
 QY 247 EGAQKEKEFODESEFRQHEGVEVAKRGREMAKDGSLKAKEGSTGTSESSVEARGSEEV 306
 DB 218 LKSGLKTDKSSQVQTLRIHKRNPV-----EGS--GVSSA----- 251
 QY 307 RESSTVASDGSMEGKEGSGTKVENSMMKADKCRTEVYNQCSIDLGEDMEFGEBDLINFSEDD 366
 DB 252 -----KTKT-----HFSVRLLFKSRKK 268
 QY 367 VEAVNIPESLPPSRNSNSNPPLRCVCGKAKAYIFIIIFSYVLISLGVCYFLAVLAVWVD 426
 DB 269 -----KAAKTLGIIVGCGVLCWLPDF--PLWVPIGSEFF 298


```

Qy 427 VETQVQWVITIIITFLFLOCIHRYVYGVYMAKTIKKEIQDMLKKFCKEKPCKEDS--- 483
Db 299 ENFKRPETVFKIVFVLGYLNSCINPIIYPCSSQEFKKAFOVNLRIQRRRSSGHALGY 358
Qy 484 --HPDLPTGEGTEGKI-VPSYDSATF 507
Db 359 TLHPESQAVBQGRGMVRIPIVSGSGTF 385

RESULT 14
Q8BV77_MOUSE PRELIMINARY; PRT: 466 AA.
ID Q8BV77_MOUSE
AC Q8BV77
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Mus musculus adult male spinal cord cDNA, RIKEN full-length enriched
DE library, clone:A330054N1 product:adrennergic receptor, alpha 1a, ALPHA
DE 1A-ADRENOCEPTOR, full insert sequence.
GN Name=Adrala;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OK NCBI_taxid=10090;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20499374; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsumoto Y., Nakai I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Steinhilber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakei K., Okido T., Furuno M., Aono H., Baladrelli R., Barash G.,
RA Blake J., Boffelli D., Boujunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guernich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).

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RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitayama T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kahtani K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA Adachi J., Aizawa K., Akiyama T., Aikawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: This alpha-adrennergic receptor mediates its action by
CC association with G proteins that activate a phosphatidylinositol-
CC calcium second messenger system. Its effect is mediated by G(q)
CC and G(11) proteins (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL, AK079357; BAC37694.1; -; mRNA.
DR Ensembl; ENSMUSG0000045875; Mus musculus.
DR MGI; MGI:104773; Adrala.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0008217; P:regulation of blood pressure; IMP.
DR InterPro; IPR001004; A_receptor1Acs.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00557; ADRENRGALAR.
DR PRINTS; PR00237; GPCRRODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 466 AA; 51744 MW; 8C5FE5C67E885795 CRC64;

Query Match 12.9%; Score 341; DB 2; Length 466;
Best Local Similarity 22.7%; Pred. No. 4.6e-12;
Matches 115; Conservative 75; Mismatches 183; Indels 134; Gaps 13;

Qy 7 NSTRESNSHTCMPLSKMPISLANGIIRSTVLVFLAASPVGNIVLALVLRKPOLLOVT 66
Db 7 NASEGSNCTH---PAQVNISKA--ILGVLGGILIRGVGNILVILSVACHRLHLSVT 61
Qy 67 NRIFNVLVTLDTLQISLVAPVNVATSVLPFPLNSHFTALVSLTHLPAFASVNTIVLV 126
Db 62 HYYIVNLVAVDLLLSTVLPFSALFELIGYVAFGRVFENINMAVDVLLCTTASIMLCIIS 121
Qy 127 VDRVLSIHPISYSPKMTQRRGVLLYGTGTVAIILQSPPTPYGMOAFAFDERNALCSMIM 186
Db 122 IDRYIGVSPRLRPIYVIRGRVALLCVMAISLVISIGPLFGMRQA--PEDETTCQL-- 178
Qy 187 GASPSYLLISVSVFIVPLIWMACYSVFCAARQHALLVNKKHSLVLRKVCVENED 246
Db 179 NEEPEYVLFALSGSYVFLTLIILVMYCRVYVAKR-----ESRG 217
Qy 247 EBGAKKEEFODESFRQHEGEVYAKGRWADGSLAKEGSGTGESSEYVARGSEEV 306
Db 218 LKSGIKTKDSSEQVTLRIHRKNVPA-----EGS-GVSSA----- 251

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Qy 307 RESSTVADSGSMGKSGSTKVEENSMKADKGRTEVNOQSIDGEGDMEGEDDINSEDD 366
Db 252 -----KNKT-----HFSVRLKTSRKK 268
Qy 367 VEAVNIPESLPSRRNSNSNPPLPRCYCKAAKAVITIIIFSYVLSGPICFLAVALVWD 426
Db 269 -----KAAKTGIVGCGFVLCWLPF-FLVMPISGFF 298
Qy 427 VETQVQWVITIIIMLFPOCCIPHYVGYGMHTIKKEIODMKKPFCKEKKPKEDS---- 483
Db 299 PNFKEPEYFKIVFMVGLNSCINPFIIPCSSOEFFKAFQVNRICLRRROSSKHALGY 358
Qy 484 --HPDLPGETGTEGKI-VPSYDSATP 507
Db 359 TLHPPEQAVEGQHRGVRIPIVSGGCTP 385

RESULT 15
SH1A_HUMAN
AC P08908; O6LA87; STANDARD; PRT; 422 AA.
ID 1
DT 01-NOV-1988 (rel. 09, Created)
DT 01-APR-1993 (rel. 25, Last sequence update)
DT 13-SEP-2005 (rel. 48, Last annotation update)
DE 5-hydroxytryptamine 1A receptor (5-HT-1A) (Serotonin receptor 1A) (5-HT1A) (G-21).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=87315369; PubMed=3041227; DOI=10.1038/329075a0;
RA Koblika B.K., Friele T., Collins S., Yang-Feng T.L., Koblika T.S., Francke U., Lefkowitz R.J., Caron M.G.;
RT "An intronless gene encoding a potential member of the family of receptors coupled to guanine nucleotide regulatory proteins.";
RL Nature 329:75-79(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Saltzman A.G., Morse B., Felder S.;
RT Submitted (FEB-1991) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver project.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Puhl H.U., Iikeda S.R., Aronstam R.S.;
RT "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Bhat N.K., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stappleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.R., Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C., Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Miliaty S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muray D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy E., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Rauterfeld Y.S.N., Krzywicki M.J., Skalska U., Smailus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE OF 1-9.
RX MEDLINE=92115564; PubMed=1766875;
RA Parks C.L., Chang L.S., Shenk T.;
RT "A polymerase chain reaction mediated by a single primer: cloning of genomic sequences adjacent to a serotonin receptor protein coding region.";
RL Nucleic Acids Res. 19:7155-7160(1991).
RN [7]
RP NUCLEOTIDE SEQUENCE OF 200-365.
RX MEDLINE=93329096; PubMed=8393041;
RA Aune T.M., McGrath K.M., Sarf T., Bombara M.P., Kelley K.A.;
RT "Expression of SH1A receptors on activated human T cells. Regulation of cyclic AMP levels and T cell proliferation by 5-hydroxytryptamine.";
RL J. Immunol. 151:1175-1183(1993).
RN [8]
RP FUNCTION.
RX MEDLINE=88334700; PubMed=3138543; DOI=10.1038/335358a0;
RA Farzin A., Raymond J.R., Lohse M.L., Koblika B.K., Caron M.G., Lefkowitz R.J.;
RT "The genomic clone G-21 which resembles a beta-adrenergic receptor sequence encodes the 5-HT1A receptor.";
RL Nature 335:358-360(1988).
RN [9]
RP VARIANTS SER-22 AND VAL-28.
RX MEDLINE=95275307; PubMed=7755630;
RA Nakai B., Nielsen D.A., Linnoila M., Goldman D.;
RT "Two naturally occurring amino acid substitutions in the human 5-HT1A receptor: glycine 22 to serine 22 and isoleucine 28 to valine 28.";
RL Biochem. Biophys. Res. Commun. 210:530-536(1995).
RN [10]
RP VARIANTS LEU-16 AND ASP-273.
RX MEDLINE=98425601; PubMed=9754630;
RA DOI=10.1002/(SICI)1096-8628(19980907)81:5<434::AID-AMG13>3.0.CO;2-D;
RA Kawanishi Y., Harada S., Tachikawa H., Okubo T., Shirashi H.;
RT "Novel mutations in the promoter and coding region of the human 5-HT1A receptor gene and association analysis in schizophrenia.";
RL Am. J. Med. Genet. 81:434-439(1998).
CC -I- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that inhibit adenylyate cyclase activity.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC EMBL; M28269; AAA36440.1; -; Genomic DNA.
CC EMBL; X13556; CAA31908.1; -; Genomic DNA.
CC EMBL; X57829; CAA40962.1; -; Genomic DNA.
CC EMBL; M83181; AAA66493.1; -; Genomic DNA.
CC EMBL; AB041403; BAA94488.1; -; Genomic DNA.
CC EMBL; BC069159; BAA69159.1; -; mRNA.
CC EMBL; AF498978; AAM21125.1; -; mRNA.
CC EMBL; Z11168; CAA75560.1; -; Genomic DNA.
CC PIR; I38209; I38209.
CC HSPB; P08913; IHLU.
CC EMBL; ENSG00000178394; Homo sapiens.
CC HGNC; HGNC:5286; HTR1A.
CC MIM; 109760; -.

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DR GO: GO:0004993; F:serotonin receptor activity; TAS.
DR GO: GO:0007610; P:behavior; TAS.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR GO: GO:0008284; P:positive regulation of cell proliferation; TAS.
DR InterPro: IPR000610; SH1A_receptor.
DR InterPro: IPR002231; SHT_receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR Pfam: PF00512; 5HT1ARECEPTR.
DR PRINTS: PRO1101; 5HTARECEPTR.
DR PRINTS: PRO0237; GPCRHOODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
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KW Polymorphism; Receptor; Transducer; Transmembrane.
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FT VARIANT 28 28 I -> V (1n dbSNP:1799921).
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FT VARIANT 220 220 P -> L (1n dbSNP:1800043).
FT VARIANT 220 220 /FTid=VAR_011828.
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FT VARIANT 273 273 G -> D (1n dbSNP:1800042).
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FT CONFLICT 200 202 M -> I (1n Ref. 1).
FT CONFLICT 228 228 TFG -> RPR (1n Ref. 7).
FT CONFLICT 244 244 K -> R (1n Ref. 7).
FT CONFLICT 244 244 A -> AA (1n Ref. 7).
FT CONFLICT 355 355 I -> T (1n Ref. 7).
FT CONFLICT 363 365 IVA -> MKP (1n Ref. 7).
FT CONFLICT 418 418 K -> N (1n Ref. 1).
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Query Match 12.9%; Score 340.5; DB 1; Length 422;

Best local Similarity 22.0%; Pred. No. 4,4e-12; Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

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DB 31 VTVSVQVITSLILGLIFCAVGNACVVAIALER--SLQNVANVILGSLAVTDLMVSVL 88
QY 84 VAPWVAATSVPLFWPLNHFCTALVSLHLFAFASVNTIVLVSDRYLSIIHPLSYPSKM 143
DB 89 VLPMAALVQVANKMTLIGQVTCOLFALDVLCTSSILHLCAIALDRYVAITDPIDYVNR 148
QY 144 TORRGVLLLYGTWYVAILLOSTPPLVGMGQAAPDERNALCSMTWGASPTTILSVVSFIYI 203
DB 149 TPRRAAALISLTWLIGFLISIPMLGWRP--EDRSDDPACTISKDHGYTIYSTFGAFYI 206

QY 204 PLIWIACYSVVFCAARRQHALLVNVKRHSLEIVVKOCVENEDEGAEKKEEFODESEFR 263
DB 207 PLLMLVLVYGRIFRAAR-----FRIKTVKKVEKTAGDTRHGASPAPOPK 251
QY 264 RQHEGEYVAKEGRM--EAKDGL-----KAKGSTGTSSESVEARGSEVNESTVASDG 316
DB 252 KSVNGESGRNRWRLGVESKAGALCANGAVRQDGDGAALLEIVEH----- 296
QY 317 SMEKGSTKYEENSMKADKRTVENQCSIDLGEDMEFGEDINFSRDDVEAVNIPESL 376
DB 297 ----RVGNSK-EHLPLPSEAGPTPCARASF----- 322
QY 317 PPSRRNSNPPLPFCYQCKAKVIFITISYVLSLGRYCFVLAVAVWDVETQVPMVI 436
DB 323 RKNERNNAKRKMALAREKTKTILGIMGTFLICWLPFFIVALVLPFCSSCHMPTLLG 382
QY 437 TTIWLPLOCCIHPIYVGVYHKTIKKEIQOMLKKFPCKE 476
DB 383 AIIWMLGYNSLNPVIVAYFNKDPQNAFKKIKCKPCRO 422

Search completed: December 3, 2005, 06:36:43
Job time : 176.873 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 10, 2005, 04:47:24 ; Search time 5052 Seconds

(without alignments)
5715.850 Million cell updates/sec

Title: US-10-712-615-2

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Delop	6.0	Delext	7.0

Searched: 5883141 segs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blomum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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-NMAP -LANG=JUTERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: GenBml:*
2: gb_ba:*
3: gb_in:*
4: gb_env:*
5: gb_om:*
6: gb_ov:*
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10: gb_scs:*
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12: gb_un:*
13: gb_vl:*
14: gb_ncg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	2644	100.0	1524	6	BD173594	BD173594 Novel G p
2	2644	100.0	1527	6	BD095705	BD095705 Novel gua
3	2644	100.0	1527	6	AX497863	AX497863 Sequence

	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45																																																																																																																																																																																																																		
	2644	100.0	1580	6	AX497909	AX497909 Sequence	2644	100.0	175465	14	AL356783	AL356783 Homo sapi	2641	99.9	1524	6	BD173595	BD173595 Novel G p	2641	99.9	1527	6	BD144320	BD144320 Novel G-P	2641	99.9	1527	6	CO736967	CO736967 Sequence	2641	99.9	1527	6	AR679058	AR679058 Sequence	2641	99.9	1527	6	AX148174	AX148174 Sequence	2641	99.9	1527	6	AX230165	AX230165 Sequence	2641	99.9	1527	6	AX355868	AX355868 Sequence	2641	99.9	1527	6	AX497907	AX497907 Sequence	2641	99.9	1527	6	AX543321	AX543321 Sequence	2641	99.9	1527	6	AX549287	AX549287 Sequence	2641	99.9	1527	6	AB083588	AB083588 Homo sapi	2641	99.9	1527	6	AF411115	AF411115 Homo sapi	2641	99.9	1527	8	BC069439	BC069439 Homo sapi	2641	99.9	1527	6	AX646733	AX646733 Sequence	2641	99.9	1527	6	AB065937	AB065937 Homo sapi	2641	99.9	1520	6	AX355867	AX355867 Sequence	2641	99.9	2781	6	AR679128	AR679128 Sequence	2641	99.9	2781	6	AX148262	AX148262 Sequence	2641	99.9	7524	6	AX543323	AX543323 Sequence	2641	99.9	140628	14	AC016468	AC016468 Homo sapi	2641	99.9	172280	8	AL390879	AL390879 Human DNA	2637	99.7	1659	6	AX080495	AX080495 Sequence	2637	99.7	1659	6	AX497906	AX497906 Sequence	2636	99.7	1527	6	AR679119	AR679119 Sequence	2636	99.7	1527	6	AX148250	AX148250 Sequence	2636	99.7	1527	6	AX497908	AX497908 Sequence	2628	99.4	1527	6	AX497910	AX497910 Sequence	2619	99.1	1527	6	AX459697	AX459697 Sequence	2619	99.1	1704	6	AX459693	AX459693 Sequence	2518	95.2	1458	6	AX342674	AX342674 Sequence	2245.5	84.9	212696	14	AC156524	AC156524 Bos tauru	2021	76.4	1197	6	AX543324	AX543324 Sequence	2021	76.4	1330	6	AX286523	AX286523 Sequence	1903	72.0	135462	14	AC123439	AC123439 Rattus no	1903	72.0	250681	14	AC099159	AC099159 Rattus no	1897.5	71.8	179648	9	AL672122	AL672122 Mouse DNA	1360	51.4	951	6	AX657432	AX657432 Sequence	1330	50.3	835	10	BV208535	BV208535 GPR101_20	1087	41.1	1697	6	AX647119	AX647119 Sequence	1087	41.1	70254	14	AC024415	AC024415 Homo sapi

ALIGNMENTS

RESULT 1
LOCUS BD173594 1524 bp DNA linear PAT 18-FEB-2003
DEFINITION Novel G protein-coupled receptor protein and DNA thereof.
ACCESSION BD173594
VERSION BD173594.1 GI:28414925
KEYWORDS WO 02059304-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 1524)
REFERENCE
AUTHORS Miwa,M., Ito,T., Shintani,Y. and Miyajima,N.
TITLE Novel G protein-coupled receptor protein and DNA thereof
JOURNAL Patent: WO 02059304-A 1 01-AUG-2002;
TAKEDA CHEMICAL INDUSTRIES LTD, MASANORI MIWA, TAKASHI ITO, YASUSHI
SHINTANI, NOBUYUKI MIYAJIMA
OS Homo sapiens (human)
PN WO 02059304-A/1
PD 01-AUG-2002
PE 22-JAN-2002 WO 2002JP0000405
PR 23-JAN-2001 JP 01P 015050.30-MAR-2001 JP 01P 102560 PI
MASANORI MIWA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA PC
C12N15/12, C12P21/02, C07K14/705, C07K16/28, A61K45/00, A61P25/00, PC
A61P29/00,
PC A61P9/00, A61P35/00, A61P37/00, A61P1/00, G01N33/566, PC

GOIN33/50,
 CC GOIN33/15
 Novel G protein-coupled receptor protein and DNA thereof FH
 Key Location/Qualifiers
 FT source 1..1524
 FT Location/Qualifiers
 1..1524
 /organism="Homo sapiens"
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ORIGIN

Alignment Scores:
 Pred. No.: 3,8e-207 Length: 1524
 Score: 2644.00 Matches: 508
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-10-712-615-2 (1-508) x BD173594 (1-1524)

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 DB 121 TTCCTGCGCGCTCTTCTGCGGCAACATAGTGTGCGCTAGTGTGCGGCGCAAGCGG 180
 QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuValThrAsnLeuGln 80
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RESULT 2
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 LOCUS Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use.
 DEFINITION
 ACCESSION BD095705.1 GI:22641293
 VERSION WO 0148188-A/17.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 1527) Saito, Y., Noriyuki, Morikawa, Yoshida, K., Matsumoto, S., Oda, T., Sugiyama, T., Kishimoto, T., Kanzaki, K., Yasuda, S. and Inoue, Y.
 Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use

REFERENCE
 AUTHORS
 TITLE

JOURNAL Patent: WO 0148188-A 17 05-JUL-2001;
HELIX RESEARCH INSTITUTE, SHUNICHIRO MATSUMOTO, TAMAKI ODA, YOKO
SAITO, NORIYUKI MORIKAWA, KENJI YOSHIDA, MAKIKO SUWA, TOMOYASU
SUGIYAMA, TOSHIMITSU KISHIMOTO, KOJI KANZAKI, SHINICHIRO
YASUDA, YOSHIOHISA INOUE
COMMENT OS Homo sapiens (human)
PN WO 0148188-A/17
PD 05-JUL-2001
PR 28-DEC-2000 WO 2000JP009408
PF 28-DEC-1999 JP 99P 375152,31-MAR-2000 JP 00P 101339 PI
SHUNICHIRO MATSUMOTO, TAMAKI ODA, YOKO SAITO, NORIYUKI PI
MORIKAWA, KENJI YOSHIDA,
PI MAKIKO SUWA, TOMOYASU SUGIYAMA, TOSHIMITSU KISHIMOTO, KOJI
KANZAKI,
PI SHINICHIRO YASUDA, YOSHIOHISA INOUE
PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C07K14/705, PC
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G01N33/15,
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CC Novel guanosine triphosphate-bound protein-coupled receptors
CC encoding them, and their production and use
FH Key Location/Qualifiers
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ORIGIN

Alignment Scores:

Pred. No.:	3,81e-207	Length:	1527
Score:	2644.00	Matches:	508
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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US-10-712-615-2 (1-508) x BD095705 (1-1527)

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QY 501 SerTyrAspSerAlaThrPhePro 508
DB 1501 TCCTACGATTCGCTACTTTTCT 1524

RESULT 3
LOCUS AX497863 1527 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1 from Patent WO0240670.
ACCESSION AX497863
VERSION AX497863.1 GI:23342970
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS 1
TITLE Battaglini, P., Feder, J., Mintler, G., Nelson, T., Ramanathan, C.,
Westphal, R., Cacace, A., Barber, L., Hawken, D. and Kornacker, M.
A novel human g-protein coupled receptor, hgrprmy8, expressed
highly in brain
JOURNAL Patent: WO 0240670-A 1 23-MAY-2002;
Bristol-Myers Squibb Company (US)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 3,81e-207 Length: 1527
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeuGln 80
DB 181 CAGTGTCTCAGAGTGACCAACCGTTTATCTTTAACTCTCGTCAACGACCTGCTGACG 240
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DB 1441 GAAAGATACCAACCCAGACCTGCCGGAACAGAGGTGTGAGACTGAAGGCAAGATTGTCCCT 1500
QY 501 SerIleAspSerAlaThrPhePro 508
DB 1501 TCTTACGATTCGCTACTTTTCT 1524
RESULT 4
LOCUS AX497909 1580 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 47 from Patent WO0240670.
ACCESSION AX497909

VERSION AX497909.1 GI:23342984
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
AUTHORS 1 Battaglini, P., Feder, J., Muntler, G., Nelson, T., Ramanathan, C.,
Westphal, R., Cacace, A., Barber, L., Hawken, D. and Kornacker, M.
TITLE A novel human g-protein coupled receptor, hgrprny8, expressed
highly in brain
JOURNAL Patent: WO 0240670-A 47 23-MAY-2002;
Bristol-Myers Squibb Company (US)
FEATURES
source 1.1580
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ORIGIN
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Pred. No.: 3,98e-207 Length: 1580
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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QY 361 AsnPheSerGluAspAspValGluAlaValAlaenIleProGluSerLeuProProSerArg 380
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ACCESSION AL356783
VERSION AL356783.20 GI:14456213
KEYWORDS HTG; HTGS PHASE1; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 Hominidae; Homo.
AUTHORS Heath, P.
TITLE Direct Submission
JOURNAL Submitted (09-Jul-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On Jun 14, 2001 this sequence version replaced gi:1432943.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: B13JL21
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Et-amersham; 35% of reads
Dye-terminator Big Dye; 64% of reads
Consensus quality: 173062 bases at least Q40
Consensus quality: 174012 bases at least Q30
Consensus quality: 174525 bases at least Q20
Insert size: 174865; sum-of-ctnigs
Quality coverage: 5.89x in Q20 bases; sum-of-ctnigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 ctnigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the ctnigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 102859: contig of 102859 bp in length
* 102860 102959: gap of 100 bp
* 102960 126878: contig of 23919 bp in length
* 126879 126978: gap of 100 bp
* 126979 132924: contig of 5946 bp in length
* 132925 133024: gap of 100 bp
* 133025 136361: contig of 3337 bp in length
* 136362 136461: gap of 100 bp
* 136462 142243: contig of 5782 bp in length
* 142244 142343: gap of 100 bp
* 142344 150640: contig of 8297 bp in length
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QY	101 SerHisPheCysThrAlaLeuValSerIleuThrHisLeuPheAlaPheAlaSerValAsn	120	
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LOCUS BD144320
DEFINITION Novel G-protein coupled receptors.
ACCESSION BD144320
VERSION BD144320.1 GI:27850078
KEYWORDS JP 2002112793-A/45.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Hase, T., Takeda, S. and Miyake, N.
TITLE Novel G-protein coupled receptors
JOURNAL Patent: JP 2002112793-A 45 16-APR-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT
PS Homo sapiens (human)
PD JP 2002112793-A/45
PD 16-APR-2002

PF 09-FEB-2001 JP 2001034434
PI TATSUYA HAGA, SHIGEKI TAKEDA, NARIKI MIYAKE
PC
C12N15/09, A01K67/027, A61K38/00, A61K39/395, A61K39/395, A61K45/00, PC
A61K48/00.
PC A61P33/00, C07K14/705, C07K16/28, C07K19/00, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, PC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
JOURNAL Patent: WO 02068579-A 22901 06-SEP-2002;
PE Corporation (NY) (US)
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Pred. No.: 6 71e-207 Length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
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QY 21 LeuSerLysMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
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QY 41 PheLeuAlaLysSerPheValIGluAsnIleValLeuAlaLeuValIleGluArgLysPro 60
Db 121 TTCTGCGGCTCTTCTGTCGACATATGCTGCGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuValThrAspLeuLeuGln 80
Db 181 CAGCTGCTGAGGTGACCAACGCTTTATCTTTAACTCTGCTGCTGCTGCTGCTGCTG 240
QY 81 IleSerLeuValAlaProThrValIleValAlaIleThrSerValProLeuPheThrProLeuAsn 100
Db 241 ATTTGCTGCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
Db 301 AGCCACTTCTGCAAGGCGCTGTTAGCTTACCTCACCTGCTGCTGCTGCTGCTGCTG 360
QY 121 ThrIleValLeuValSerValAspArgThrLeuSerIleIleHisProLeuSerThrPro 140
Db 361 ACCATTGCTGAGTGTCAAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 141 SerLysMetThrGlnArgArgGlyThrLeuLeuLeuThrGlyThrTrpIleValAlaIle 160
Db 421 TCCAAATGACCCAGAGCGCGGTTACTGCTCTCTATGAGCAGCTGATTTGGGCATC 480
QY 161 LeuGlnSerThrProProLeuThrArgIleThrGluAlaAlaPheAspGluGluAsnAla 180
Db 481 CTGCAGAGCACTCTCACCTGACCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 540
QY 181 LeuCysSerMetIleThrGlyAlaSerProSerThrThrIleLeuSerValIleSerPhe 200
Db 541 CTCTGCTCATGATCTGGGGGGGCAAGCCAGCTATCATATTTCCAGCGTGGTCTTCC 600
QY 201 IleValIleProLeuIleValMetIleAlaCysThrSerValIlePheCysAlaAlaArg 220
Db 601 ATCGTATTCACATGATTGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 221 ArgGlnHisAlaLeuLeuTyrAsnValIysArgHisSerLeuGluValArgValIysAsp 240
Db 661 AGGCAGCATGCTCTGCTGTAACAATGTCAGACAGACAGCTTGGAAGTGCAGCAAGAC 720
QY 241 CysValIGluAsnGluAspGluGluGluValAGluLysLysGluLysGluAspGluSer 260

Db 721 TGTGTGAGAAATGAGATGAAAGGAGGAGCAAGAAAGAGAGTCCAGATGAGACT 780
Qy 261 GIUPEAARGAGLNIHISGLUGLUGLVALLYSALALYSGLUGLYARGMETGIUALYS 280
Db 781 GAGTTTCGGCCGACAGATGAAGTGAAGTCAGAGGCCAAGAGGCGAGATGAGAGCCAG 840
Qy 281 AAGGLYSERLEUVALALYSGLUGLYSERTHRGLYTHSERGIUSERSERVALGIUALA 300
Db 841 GACGCGACGCTGAAGGCCAAGAGAGAGACAGCGGGACACAGTAGAGTGTAGAGGGCC 900
Qy 301 ARGGLYSERGLUGLVALARGLUSERSERTHVALALASERAPGLYSERMETGIULY 320
Db 901 AAGGGCAGGAGAGAGTCAAGAGACAGACGAGTGGCCAGCGACGAGCTGAGAGGGT 960
Qy 321 LYSGLUGLYSERTHRYVALGLUGLUAENSERMETLYSALASPLYSGLYARGTHRGU 340
Db 961 AAGGAAGGACAGCACCAAGTTGAGAGAGACAGATGAAGCAGACAGAGGTGGCACAG 1020
Qy 341 VALAENGILCYSESERILEASPLEUGLYLUASPAAPSMERCGLUPHEGLYLUASPAPI 360
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Qy 361 AAPHSESERGLUASPAAPVALGILUALAVALANLIEPROGLUSERLEUPROBROSERARG 380
Db 1081 AATTTTCAGAGAGATGACCTCGAGGACATGACATCCGAGAGCCTCCACCCAGTCT 1140
Qy 381 ARGANSEASERSEANPROBLEUPROARGCYSTYRGILCYSELYSALALALYSVAL 400
Db 1141 CGTAAACAGACAGCAACCTCTCTGCCAGGTGTATACAGTGCAAACTGCTAAAGTG 1200
Qy 401 ILEPHEILEIIEPHESESTYRVALLEUSERLEUGLYPROTYCYAPHELEUALVAL 420
Db 1201 ATCTTCATCATATTTCTCTATGTGCTATCCCTGGGCGCCCTACTGCTTTTAAAGCAGTC 1260
Qy 421 LEUALAVALITRYVALASPAVALGILURHGINVALPROGLINTRYVALILEHRIELLE 440
Db 1261 CTGGCCGCTGGGTGATGATCGAAACCCAGTACCCAGTGGGTGATCCCAATACATC 1320
Qy 441 TRPLEUPHEPHELEUGILNCYSCYSLIEHISPROTYRYVALTYRGITYRMECHISLYTHR 460
Db 1321 TGGCTTTCTTCTCTGAGTGCAGTCCACCCCTATGTCTATGCTACATGCAACAGACC 1380
Qy 461 ILELYLYSGILILEGINASPMETLEULYSLYSPHEPHECYALYSGLULYSPROPLY 480
Db 1381 ATTTAAGAGAGAAATCCAGAGACATGCTGAAGAAATTCTTCTGCAAGAAAAGCCCGAAA 1440
Qy 481 GIUASPSERHIAPROASPLEUPROGLYTHRGILUGLYLTHRGILUGLYLYSALVAL 500
Db 1441 GAAGATAGCCACCCAGACCTGCCCGGAGACAGAGGTGGAGCTGAAAGGCAAGATTGCCCT 1500
Qy 501 SEPTYASPSERIALATHRPHEPRO 508
Db 1501 TCCTAGATTCTGCTACTTTTCT 1524

RESULT 9
AR679058 1527 bp DNA linear PART 13-JUN-2005
LOCUS AR679058
DEFINITION Sequence 15 from patent US 6902902.
ACCESSION AR679058
VERSION AR679058.1 GI:67620281
KEYWORDS
SOURCE
ORGANISM Unknown.
UNCLASIFIED.
REFERENCE 1 (bases 1 to 1527)
AUTHORS Unett,D.J., Chen,R., Richman,J.G., Connolly,D.T., Hakak,Y.,
Behan,D.P. and Chalmers,D.T.
TITLE Human G protein-coupled receptors and modulators thereof for the
JOURNAL treatment of metabolic-related disorders
Parent: US 6902902-A 15 07-JUN-2005;
FEATURES
Location/Qualifiers

source 1. 1527
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 6 71e-207 Length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: 6 Gaps: 0

US-10-712-615-2 (1-508) x AR679058 (1-1527)

Qy 1 METTRSERTHCYSTHASNERTHARGLUSERAENSERILETHRCYMETPRO 20
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Db 61 CTCTCAAAATGCCATCAGCCTGGCCCAAGGCATCATCCGCTCAACCGTCTGTTATC 120
Qy 41 PHEUALAALASERPHVALGLYASNLIEVALLEUALLEUALARGLYSPRO 60
Db 121 TTCCTGGCGGCTCTTGTGGCAACATAGTGGCTGAGTGTTCAGGCGCAAGCCG 180
Qy 61 GINLEUENGILVALITHRASNAHPHEILEPHEANLEUVALITHRASPLEUENGIL 80
Db 181 CAGCTGCTGAGAGTACCAACCGTTTATCTTTAACTCTCTGTCACCGACCTGTCAG 240
Qy 81 ILESERLEUVALALAPROTRYVALVALATHRSERVALPROLEUPHETRYPROLEUAN 100
Db 241 ATTTGCTGCTGGCCCCCTGGGTGGTGCCACTGTGGCTCTTCTGCGCCCTCAAC 300
Qy 101 SERHISPECYETHALILEUVALSERLEUTHRHSLEUPHEALAPHEALASERVAL 120
Db 301 ACCCACTTCGACGCGCTGTGATGCTCAACCCAGTGTGCTTGCCAGCGCTCAAC 360
Qy 121 THRILEVALLEUVALSERVALASPARGTYRLEUSERILEIIEHISPROLEUSERTRYPRO 140
Db 361 ACCATTGTGCTGTGCTAGTGAATGCTACTGTCTATCATCATCAACCTCTCTCAACCG 420
Qy 141 SEPTYSMETTHRGILARGARGGLYTRYLEULEULEUTYRGILYTHRTPILEVALIIE 160
Db 421 TCCAAGATGACCCACGCGCGGCTTACCTGCTCTGTGGCACTGGAATGTGGCCATC 480
Qy 161 LEUGINSETRHPROBLEUTYRGILYTHRGILUGILALAPHEASGLUARGHENA 180
Db 481 CTGCAGACATCTCTCACTCTACGCGTGGGCGCAGGCTGCCCTTGATGAGCGCATGCT 540
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Db 541 CTCTGCTCATATATCTGGGGGGCGCCAGCCCAAGCTACATATTCAGCGGTGTCCTTC 600
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Qy 261 GIUPEAARGAGLNIHISGLUGLUGLVALLYSALALYSGLUGLYARGMETGIUALYS 280
Db 781 GAGTTTCGGCCGACAGATGAAGTGAAGTCAGAGGCCAAGAGGCGAGATGAGAGCCAG 840
Qy 281 AAGGLYSERLEUVALALYSGLUGLYSERTHRGLYTHSERGIUSERSERVALGIUALA 300

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Qy ArgGlySerGluGluValArgGlySerSerThrValAlaSerAspGlySerMetGluGly 320
Db 901 AGGGGAGGAGGAGGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Qy 321 LysGluGlySerThrIleValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
Db 961 AAGGAGGAGGAGAGCAAGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy 341 ValAsnGlnCysSerIleLeuAspLeuGlyValAspAspMetLysPheGlyValAspAsp 360
Db 1021 GTCACACAGGAGCAATGACTTGCTGGGTGAAGAGACATGAGAGTTGGTGAAGAGCATC 1080
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Qy 421 LeuAlaValThrValAspValGluThrGlnValProGluThrValIleThrIleIleIle 440
Db 1261 CTGGCGGTGGGTGAGTGTGAAACCCAGAGTACCCAGAGGTGAGTACACATATCATC 1320
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Qy 461 IleLysLysGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysProProLys 480
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Qy 501 SerTyAspSerAlaThrPhePro 508
Db 1501 TCCTACGATTCTGCTACTTTTCT 1524
RESULT 10
AX148174 1527 bp DNA linear PAT 08-JUN-2001
LOCUS AX148174
DEFINITION Sequence 15 from Patent WO0136471.
ACCESSION AX148174
VERSION AX148174.1 GI:14347080
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
AUTHORS Chen, R., Dang, H.T. and Lowitz, K.P.
TITLES Endogenous and non-endogenous versions of human g protein-coupled
JOURNAL Patent: WO 0136471-A 15 25-MAY-2001;
ARENA Pharmaceuticals, Inc. (US)
FEATURES
SOURCE Location/Qualifiers
1..1527
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Alignment Scores: 6.71e-207 Length: 1527
Pred. No.:

Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: 6 Gaps: 0
US-10-712-615-2 (1-508) x AX148174 (1-1527)
Qy 1 MetThrSerThrCysThrAsnSerThrArgGlySerAsnSerSerThrCysMetPro 20
Db 1 ATGACCTTCACCTGACCAACAGCAGCCGCGAGATTAACAGACACCACTGCATGCC 60
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Qy 41 PheLeuAlaAlaSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLysPro 60
Db 121 TTCCTGCGCGCTCTTTCGTGGCAATATGCTGGCCCTAGTGTTCAGCGCGCAAGCCG 180
Qy 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeuGln 80
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Qy 81 IleSerLeuValAlaProThrValValAlaIleThrSerValProLeuPheThrProLeuAsn 100
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Qy 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
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Qy 121 ThrIleValLeuValSerValAspArgTyLysSerIleIleIleAspProLeuSerTyPro 140
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Qy 141 SerLysMetThrGlnArgArgGlyTyLysLeuLeuLeuTyGlyThrTrpIleValAlaIle 160
Db 421 TCCAGATATCCAGAGCGCGCGGTTACTGCTCTTATAGCACTCGAATTGGGCCATC 480
Qy 161 LeuGlnSerThrProProLeuTyGlyTyPheGlnAlaAlaPheAspGluArgAsnAla 180
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Qy 181 LeuCysSerMetIleThrPheValAspProSerTyThrIleLeuSerValIleSerPhe 200
Db 541 CTCTGCTCATATCTGGGAGGCGCAGCCCACTACATATCTTCAAGCGTGTCTTCT 600
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Db 721 TGTGTGAAGAAATGAGATGAGAGGAGGAGAGAGAGAGAGAGAGAGTTCAGAGTGAAGT 780
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Db 781 GAATTTGCGCGCCAGCATGAGTGAAGTGAAGGTCAGAGCCAAAGAGGAGCAATTCAGAGCC 840
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Db 841 GACGCGAGCTGAAGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Qy 301 ArgGlySerGluGluValArgGlySerSerThrThrValAlaSerAspGlySerMetGluGly 320
Db 901 AGGGGAGGAGGAGGTGAG 960
Qy 321 LysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340

Db	961	AAGGAAGCAGACCAAAAGTTGAGGAGAAACAGCATGAAGGACAGACAAAGGCTGCACAGAG	1020
Qy	341	ValaAngInCySer11eAspLeuGlyIuAspAspMetGluPheGlyIuAspAsp11e	360
Db	1021	GTCAACCACTGCAGCATTTGACTTGGGTGAAGATGACATGAGATTGGTGGAAAGACACACTC	1080
Qy	361	AenPheSerGIuAspAspValGIuAlaValAen11eProGluSerLeuProProSerArg	380
Db	1081	AATTTCACTGAGAGAGACGTGCAGGCACTGAACATCCCGAGAGCCTCCACCCAGTCTGT	1140
Qy	381	ArgAenSerAenSerAenProProleuProArgCyTyrgInCyValAlaAlaValVal	400
Db	1141	CGTAAACACCAACAGCAACCCCTCTCTGCCAGGTCTACAGTGCMAAGCTGCTAAAGTG	1200
Qy	401	11ePhe11e11e11ePheSerTyValIuSerLeuGlyProTyrCyPheLeuAlaVal	420
Db	1201	ATCTTCATCATCATTTTCTCTCATGTGCTATCCCTGGGGCCCTACTGCTTTTGTAGCACTC	1260
Qy	421	LeuAlaVal11rPpValAspValGIuThrgInValProGlnTrpVal11eThr11e11e	440
Db	1261	CTGGCGCTGTGGGTGATGTGAAACCCAGGATACCCAGTGGGTATCACCATTATCATTC	1320
Qy	441	TrpLeuPhePheLeuGlnCyCysVal11eH1sProTyrVal11rGlyTy11rMetH1s11rThr	460
Db	1321	TGGCTTTTCTCTCCAGTGCATCCACCCCTATGTCTATGGCTACATCACAAAGCC	1380
Qy	461	11e11s11rGlu11eG11AspMetLeu11s11rPheCy11s11rGlu11rPro11rH1s	480
Db	1381	ATTAAAGAAAGAAATTCAGGACACTGCTGAAGAAATTTCTTCTGCAAGAAAGACCCCGAAA	1440
Qy	481	GluAspSerH1sProAspLeuProGlyThrgInGlyGlyThrgInGly11s11rValPro	500
Db	1441	GAAAGTACGACCAACCCAGACCTGCCGGAACAGAGGGTGGAGCTGAAGCAAGATTGTCCCT	1500
Qy	501	SerTyrrAspSerAlaThrPhePro	508
Db	1501	TCTTACGATTCTGTACTATTTTCTCT	1524
RESULT 11			
AX230165		1527 bp	DNA linear PAT 11-SEP-2001
LOCUS	AX230165		
DEFINITION	Sequence 52 from Patent WO0162797.		
ACCESSION	AX230165		
VERSION	AX230165.1		
KEYWORDS	GI:15592183		
SOURCE			
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homidae; Homo.		
REFERENCE	1		
AUTHORS	Vogel1,G., Wood,L.S., Parodi,L.A. and Lind,P.		
TITLE	Novel 9 protein-coupled receptors		
JOURNAL	Patent: WO 0162797-A 52 30-AUG-2001;		
	PHARMACIA & UPJOHN COMPANY (US)		
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ORIGIN			
Alignment Scores:			
Pred. No.:	6,71e-207	Length:	1527
Score:	2641.00	Matches:	507
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.80%	Mismatches:	0
Query Match:	99.89%	Indels:	0
DB:	6	Gaps:	0

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DB	1	ATGACGCTCCACTGTGACCAACAGCAGCGGCGAGAGTAAACAGACGACACGTCGATGCCC	60
QY	21	LeuSerIlyMetProIleSerIleuAlaHisGlyIleIleArgSerThrValIleuValIle	40
DB	61	CTCTCCAAAATGCCATCAGCTTGGCCCAACGGCATCATCCGCTCAACCGTGTGATTATC	120
QY	41	PheIleuAlaAlaSerPheValGlyAsnIleValIleuAlaIleuValIleuGlnArgIlyPro	60
DB	121	TTCTCGCGCGCTCTTTGTGTGGGCAATAGTGCTGGGCGTATGTTGTGACGGCAAGCCG	180
QY	61	GlnIleuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspleuGln	80
DB	181	CAGCTGCTGACGGTGACCAACCGTTTATCTTTAACTCTCTGTACCGACTGTGTGACG	240
QY	81	IleSerIleuValAlaProIleValValAlaIlePheSerValProIleuPheIleProIleuAsn	100
DB	241	ATTTCGCTGTGGCCCTCTGGGTGTGGCACCTGTGGCTCTCTTCTTGGCCCTTCAAC	300
QY	101	SerHisPheCysThrAlaIleuValSerIleuThrHisIleuPheAlaPheAlaSerValAsn	120
DB	301	AGCACCTTCTGACGGGCCCTGGTTATGCTCAACCCACCTGTTGCTTGGCCGCGTCAAC	360
QY	121	ThrIleValIleuValSerValAspArgIlyIleuSerIleIleHisProIleuSerIlyPro	140
DB	361	ACCATTTGCTGGTGTGATGATGCTGCTACTTGTTCATCATCTCACCTCTCTCCATCCG	420
QY	141	SerIlyMetThrGlnArgArgGlyIlyIleuLeuLeuIlyIlyThrIleValIleAlaIle	160
DB	421	TTCAAGATGACCCACGCGCGGGTTACCTGCTCTTATGGCACCTGGATTGGCCATC	480
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DB	601	ATCGCATTTCCACTGATTTGTCATGATTCCTCTGACTCCGCTGTGTCTGTGCACCCGG	660
QY	221	ArgGlnHisAlaIleuLeuIlyAsnValIlyAsnArgHisSerIleuGluValAlaValIlyAsp	240
DB	661	AGGCAGCATGCTCTCTGCTACATTCATGACAGACACACACTTGGAGTGGAGTCAAAGAC	720
QY	241	CysValGluAsnGluAspGluGluGlyValIleGluIlyIlyGluGluPheGlnAspGluSer	260
DB	721	TGTGTGGAGATAGAGATGAGAGAGGACAGAGAAAGAGAGAGATTCACGAGTATGAGAT	780
QY	261	GluPheAlaArgGlnHisIleGluGlyGluValIlyAlaIlyGluGlyValArgMetGluAlaIys	280
DB	781	GAGTTTCCCGCCACACATGAGGTGAGTCAAGGCCCAAGAGGAGGACGAATGGAAACCAAG	840
QY	281	AspGlySerLeuValAlaIysGluGlySerThrGlyIlyThrSerGluSerSerValGluAla	300
DB	841	GACGGCACCTGAAAGGCCAAGAGAGAAAGCACCGGGGACCATGAGAGTATGTTAAGGCC	900
QY	301	ArgGlySerGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGly	320
DB	901	AGGGCAGACGAGAGAGTACAGAGAGACAGACGCTGTGGCCAGCGACGATGAGGGGT	960
QY	321	LysGluGlySerThrIlyValGluGluIleuAsnSerMetIlyAlaAspIlyGlyArgThrGlu	340
DB	961	AAGGAAGGACAGACCAAAAGTTGAGAGAAACAGCATGAAGGCGCAGAAAGGTGTGCACAG	1020
QY	341	ValAsnGlnCysSerIleAspLeuGlyGluIleuAspMetGluPheGlyGluAspAspIle	360
DB	1021	GTCAAACCACTGACGATTGACTGTGGGTGAAGTGAATGACATGGAATTTGGTGAACAGCATATC	1080
QY	361	AsnPheSerGluAspAspValGluValAlaAsnIleProGluSerIleuProIleSerArg	380

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Qy 421 LeuAlaValTrrPValAspValGluThrGlnValProGlnTrrPValIleThrIleIleIle 440
Db 1261 CTGGCCGTGGGTGGATGTCGAACCCAGATACCCCAAGGTGGATCACCATATATCATC 1320
Qy 441 TrpLeuPhePheLeuGlnCysIleIleProTyrValTyrGlyTyrMetHisIysThr 460
Db 1321 TGCGTTTCTTCTCTGCGAGTCTGCTGATCCCTCTATGTCTATGGCTACATGCAAGACC 1380
Qy 461 IleIysIysGlnIleGlnAspMetLeuIysPhePheCysIysGlnIysProProIys 480
Db 1381 ATTAAGAGGAATCCAGGACATGCTGAAGAAGTTCTTTCGAAGGAAAGCCCGGAA 1440
Qy 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyIleValPro 500
Db 1441 GAAGATAGCCACCCAGACCTGCCCGGAACAGAGGTGGAGCTGAAGGCAGATTTGTCCT 1500
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Db 1501 TCCTACGATTCCTCTACTTTTCT 1524

RESULT 12
AX35868 1527 bp DNA linear PAT 06-FEB-2002
LOCUS AX35868
DEFINITION Sequence 2 from Patent WO0188126.
ACCESSION AX35868
VERSION AX35868.1 GI:18620521
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 Ramakrishnan,S.
AUTHORS Regulation of human_g(a)1a2adrenergic receptor-like G
TITLE protein-coupled receptor
JOURNAL Patent: WO 0188126-A 2 22-NOV-2001;
Bayer Aktiengesellschaft (DE)
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/db_xref="taxon:9606"

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Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
Gaps: 0
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US-10-712-615-2 (1-508) x AX35868 (1-1527)

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AX497907 1527 bp DNA linear PAT 26-SEP-2002
LOCUS AX497907 Sequence 45 from Patent WO0240670.
DEFINITION AX497907
ACCESSION AX497907
VERSION AX497907.1 GI:23342982
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homnidae; Homo.
REFERENCE
1 Batteaglinio, P., Feder, J., Muntier, G., Nelson, T., Ramanathan, C.,
Westphal, R., Cacace, A., Barber, L., Hawken, D. and Kornacker, M.
A novel human g-protein coupled receptor, hgrbny8, expressed
highly in brain
JOURNAL Patent: WO 0240670-A 45 23-MAY-2002;
Bristol-Myers Squibb Company (US)
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Query Match: 99.89% Indels: 0
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US-10-712-615-2 (1-508) x AX497907 (1-1527)

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AX543321 1527 bp DNA linear PAT 23-NOV-2002

LOCUS Sequence 1 from Patent WO02059151.

DEFINITION AX543321

ACCESSION AX543321

VERSION AX543321.1 GI:25276744

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Li, Z., Cravchik, A., Milshina, N., Wei, M. H., Ketchum, K. A., di Francesco, V., and Beasley, E. M.

TITLE Isolated human g-protein coupled receptors, nucleic acid molecules encoding human gpcr proteins, and uses thereof

JOURNAL Patent: WO 02059151-A 1 01-AUG-2002; PE Corporation (NY) (US)

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Location/Qualifiers

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ORIGIN

Alignment Scores:

Pred. No.: 6,71e-207 Length: 1527

Score: 2641.00 Matches: 507

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 99.80% Mismatches: 0

Query Match: 99.89% Indels: 0

DB: 6 Gaps: 0

US-10-712-615-2 (1-508) x AX543321 (1-1527)

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VERSION AX549297.1 GI:25813959
KEYWORDS
SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homnidae; Homo.
REFERENCE
1 Burner,G.C., Roush,C.L. and Brown,J.P.
AUTHORS Antigenic peptides, such as for G protein-coupled receptors
TITLE (GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 582 08-AUG-2002;
LifeSpan Biosciences, Inc. (US)
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Percent Similarity: 100.00% Conservatave: 1
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US-10-712-615-2 (1-508) x AX549297 (1-1527)

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Copyright (c) 1993 - 2005 CompuGen Ltd.

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Maximum Match 100%
Listing first 45 summaries

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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=tni -MATRIX=biosum62 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10712615 @CGN 1.1 143 @runat.02122005.103723.24090 -NCPH=6 -ICPH=3
-NO_WMAP -LARGEBUERY -NEG_SCORES=0 -WAIT -DSPBLLOC=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2641	99.9	1527	3	US-10-314-048A-15 Sequence 15, Appl1
2	2641	99.9	1527	3	US-10-314-048A-103 Sequence 103, App
3	2636	99.7	1527	3	US-10-314-048A-91 Sequence 91, Appl1
4	391.5	14.8	1382	3	US-09-364-425B-22 Sequence 22, Appl1
5	389	14.7	1584	2	US-08-748-485-2 Sequence 2, Appl1
6	389	14.7	1584	2	US-09-016-434-284 Sequence 284, App
7	371	14.0	2481	2	US-08-467-568-1 Sequence 1, Appl1
8	371	14.0	2481	2	US-09-030-582-1 Sequence 1, Appl1
9	368	13.9	2481	6	PCT-US94-09051-1 Sequence 1, Appl1

10	338.5	12.8	1639	2	US-08-334-698-5 Sequence 5, Appl1
11	338.5	12.8	1639	2	US-08-228-932-5 Sequence 5, Appl1
12	338.5	12.8	1639	2	US-08-468-933-5 Sequence 5, Appl1
13	338.5	12.8	1639	2	US-08-406-855A-5 Sequence 5, Appl1
14	338.5	12.8	1639	2	US-08-722-190-5 Sequence 5, Appl1
15	338.5	12.8	1639	2	US-08-244-354-5 Sequence 5, Appl1
16	338.5	12.8	1639	3	US-09-206-899-5 Sequence 5, Appl1
17	338.5	12.8	1639	3	US-09-444-783-5 Sequence 5, Appl1
18	338.5	12.8	1639	3	US-09-688-415-5 Sequence 5, Appl1
19	338.5	12.8	1639	3	US-09-444-783-5 Sequence 5, Appl1
20	338.5	12.8	1639	6	PCT-US95-04203-5 Sequence 5, Appl1
21	338.5	12.8	1997	2	US-08-722-001-27 Sequence 27, Appl1
22	333.5	12.6	2290	2	US-08-722-001-11 Sequence 11, Appl1
23	333.5	12.6	2290	3	US-09-016-434-1368 Sequence 1368, App
24	333.5	12.6	2536	3	US-09-919-039-5 Sequence 5, Appl1
25	325	12.3	1579	3	US-09-016-434-1243 Sequence 1243, Ap
26	324	12.3	1266	3	US-09-826-509-424 Sequence 424, App
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28	314.5	11.9	1776	2	US-08-722-001-29 Sequence 29, Appl1
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32	314.5	11.9	2140	2	US-08-468-933-1 Sequence 1, Appl1
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35	314.5	11.9	2140	3	US-08-244-354-1 Sequence 1, Appl1
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43	300.5	11.4	1987	2	US-08-722-001-26 Sequence 26, Appl1
44	293	11.1	1440	3	US-09-826-509-518 Sequence 518, App
45	287	10.9	2108	3	US-09-032-742-6 Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-10-314-048A-15
; Sequence 15, Application US/10314048A
; Patent No. 6902902
; GENERAL INFORMATION:
; APPLICANT: Unet, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Hong T.
; APPLICANT: Choi, Bryan
; APPLICANT: Leonard, James
; APPLICANT: Hakak, Yaron
; APPLICANT: Law, Chen
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; FILE REFERENCE: 22 US6.CIP
; CURRENT APPLICATION NUMBER: US/10/314,048A
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/096,511
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/995,543
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/399,917
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/404,761
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/410,747
; PRIOR FILING DATE: 2002-09-13

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; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-314-048A-15

Alignment Scores:
Pred. No.: 3,72e-278 Length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: Gaps: 0

US-10-712-615-2 (1-508) x US-10-314-048A-15 (1-1527)

QY 1 MetThrSerThrCythTrpAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
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DB 61 CTCTCAAAATGCCATCAGCTGGCCCGGCAATCATCGCTCAACCGTGGTTATC 120
QY 41 PheLeuAlaIleSerPheValGlyValAsnIleValLeuAlaLeuValLeuGlnArgLysPro 60
DB 121 TTCCTGGCGGCTCTTTGCTGGCAACATAGTGGCGCTAGTGTGCGAGCGCAAGCGG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuValThrAspLeuLeuGln 80
DB 181 CAGCTGCTGCAGAGTGACCAACCGTTTATCTTTAACTTCCTGTCACCACTGCTGCAG 240
QY 81 IleSerLeuValAlaProTrpValValAlaThrSerValProLeuPheThrProLeuAsn 100
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DB 361 ACCATTGGTCGTGTGTCAGTGTGCTACTTGTCTCATCATCACCTCTCTCTCAACCG 420
QY 141 SerLysMetThrGlnArgArgGlyTyrLeuLeuLeuTyrGlyThrTriIleValAlaIle 160
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QY 161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlnAlaAlaPheAspGluArgAsnAla 180
DB 481 CTGGAGAGACCTCTCCACTTCAACGGCTGGGCGCAGGCTGCTTTGATAGCGCATGCT 540
QY 181 LeuCysSerMetIleTyrGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200
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QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerSerValValPheCysAlaAlaArg 220
DB 601 ATCGTCATTCCACTGATGTGCATGATGGTCTCTGCTCTGCTGTCAGCGCCGG 660
QY 221 ArgGlnHisAlaLeuLeuTyrAsnValIleValArgHisSerLeuGlnValAlaArgValIleAsp 240
DB 661 AGGAGCAATGCTCTGTGTACAAATGTCAAGAGACACAGCTTGGAACTGGAGTCAAGGAC 720
QY 241 CysValGluAsnGluAspGluGluGlyAlaGluValLeuValLeuGluGluPheGlnAspGluSer 260
DB 721 TGTGTGGAATGAGAGATGAAGAGGAGCAGAGAAAGAGAGAGAGTTCAGAGATGAGAGT 780
QY 261 GluPheAspArgGlnHisGluGluGlyValValIleValGluGluGlyValArgMetGluAlaLys 280
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QY 301 ArgGlySerGluGluValArgGluSerSerThrValAlaSerAspGluSerMetGluGly 320
DB 901 AGGGCAGCGAGAGGTGAGAGAGAGAGCAGCGGGTGGCAGCAGAGCGCATGGAGGCT 960
QY 321 LysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
DB 961 AAGGAAGCAGCAGCAAAAGTTGAGGAGAAACAGCATGAAGGACAGCAAGGTCGACAG 1020
QY 341 ValAsnGlnCysSerTyrAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
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DB 1141 CGTAACACCAACAGCAACCTCTCTGCCAGGTGCTTCAAGTGAAGAGCTGTAAGTGT 1200
QY 401 IlePheIleIleIlePheSerTyrValLeuSerLeuGlyProTyrCysPheLeuAlaVal 420
DB 1201 ATCTTCATCATCATTTTCTCTTATGTGCTATCCCTGGGGCCCTTCTCTTTTATGCAATC 1260
QY 421 LeuAlaValTyrPvalAspValGluThrGlnValProGlnTyrPvalIleThrIleIleIle 440
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QY 461 IleLysLysGluIleGlnAspMetLeuLysAspPheCysLysGluLysProProLys 480
DB 1381 ATTAAGAAAGAAATCCAGACATGCTGAAGAAATTTCTTCCAGAAAGAAACCCCGAAA 1440
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyTyrThrGluGlyLysIleValPro 500
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QY 501 SerTyrAspSerAlaThrPhePro 508
DB 1501 TCCTACGATTCTGCTACTTTTCT 1524

RESULT 2
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; Sequence 103, Application US/10314048A
; Patent No. 6902902
; GENERAL INFORMATION:
; APPLICANT: Unetel, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Huang T.
; APPLICANT: Choi, Bryan
; APPLICANT: Leonard, James
; APPLICANT: Hakak, Yaron
; APPLICANT: Liaw, Chen
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lerner, Michael
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; FILE REFERENCE: 22 US6 CIP
; CURRENT APPLICATION NUMBER: US/10/314, 048A
; PRIORITY FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/096, 511
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/ PRIOR FILING DATE: 2002-03-12
/ PRIOR APPLICATION NUMBER: 09/995,543
/ PRIOR FILING DATE: 2001-11-27
/ PRIOR APPLICATION NUMBER: 60/399,917
/ PRIOR FILING DATE: 2002-07-29
/ PRIOR APPLICATION NUMBER: 60/404,761
/ PRIOR FILING DATE: 2002-08-19
/ PRIOR APPLICATION NUMBER: 60/410,747
/ PRIOR FILING DATE: 2002-09-13
/ NUMBER OF SEQ ID NOS: 161
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 103
/ LENGTH: 2781
/ TYPE: DNA
/ ORGANISM: Homo Sapiens and Rat
US-10-314-048A-103

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Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
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US-10-712-615-2 (1-508) x US-10-314-048A-103 (1-2781)

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QY 121 ThrIleValLeuValSerValAspArgIleLeuSerIleIleHisProLeuSerIlePro 140
DB 361 ACCATTGTGTGTGTGTCAGTGATGCTACTTGTTCATCATCCACCTCTCTCTCCACCG 420
QY 141 SerIleMetThrGlnArgArgIleIleLeuLeuLeuValIleValIleValIleValIle 160
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QY 161 LeuGlnSerThrProProLeuValIleIleValIleValIleValIleValIleValIle 180
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QY 181 LeuCysSerMetIleIleIleValIleSerProSerIleThrIleLeuSerValIleSerPhe 200
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QY 201 IleValIleProLeuIleValMetIleAlaCysIleSerValIlePheCysAlaIleArg 220
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DB 721 TGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 261 GluPheArgArgGlnHisGluGluValIleValIleValIleValIleValIleValIleVal 280
DB 781 GAGTTTCCGCGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 281 AspGlySerIleuValAlaGlyGluGlySerThrIleValIleSerAspIleSerMetGluGly 300
DB 841 GACGCGAGCTGAAAGCCCAAGAGGACAGGAGGACAGGAGGACAGGAGGAGGAGGAGGAGG 900
QY 301 ArgGlySerGluGluValArgIleSerSerThrValIleSerAspIleSerMetGluGly 320
DB 901 AGGGCGAGCGAGGAGGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY 321 LysGluGlySerThrIleValIleGluIleAsnSerMetIleValIleAspIleValIleArg 340
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QY 361 AsnPheSerGluAspAspValGluIleValIleProGluSerIleuProIleProIlePro 380
DB 1081 AATTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
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DB 1141 CGTACAGCAACAGCAACCTCTCTGCGCAGGTGTACAGTACAGCAACCTGTTAAAGT 1200
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QY 421 LeuAlaValThrValAspValGluThrGlnIleProGlnIleThrIleIleIle 440
DB 1261 CTGGCGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 1320
QY 441 TrpLeuPhePheLeuGlnCysCysIleHisProIleValIleIleValIleValIleVal 460
DB 1321 TGGCTTTCTTCTCTGAGGTGCTGATCCACCTTATGCTATGCTATGCTATGCTATGCT 1380
QY 461 IleLysLysGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysProProLys 480
DB 1381 ATTAAGAAAGAAATCCAGGACATGCTGAAGAAAGTTCTCTGCAAGGAAAGCCCCGAGA 1440
QY 481 GluAspSerHisProAspIleuProGluIleThrGluGluIleValIleValIleValIle 500
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RESULT 3
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/ Sequence 91, Application US/10314048A
/ Patent No. 6902902
/ GENERAL INFORMATION:
/ APPLICANT: Unect, David J.
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Richman, Jeremy
/ APPLICANT: Connolly, Daniel
/ APPLICANT: Dang, Huang T.
/ APPLICANT: Choi, Bryan
/ APPLICANT: Leonard, James
/ APPLICANT: Hakak, Yaron
/ APPLICANT: Liaw, Chen
/ APPLICANT: Lowitz, Kevin P.
```

APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
FILE REFERENCE: 22 US6 CIP
CURRENT APPLICATION NUMBER: US/10/314,048A
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: 10/096,511
PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/995,543
PRIOR FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/399,917
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 60/404,761
PRIOR FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 60/410,747
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 91
LENGTH: 1527
TYPE: DNA
ORGANISM: Homo sapiens
US-10-314-048A-91

Alignment Scores:
Pred. No.: 1,316-277 Length: 1527
Score: 2636.00 Matches: 506
Percent Similarity: 99.80% Conservative: 1
Best Local Similarity: 99.61% Mismatches: 1
Query Match: 99.70% Indels: 0
Gaps: 0

US-10-712-615-2 (1-508) x US-10-314-048A-91 (1-1527)

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QY 21 LeuSerLysMetProG1SerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
Db 61 CTCCTCAAAATGCCATCAGCTGCGCCACGCGCATCATCCGCTCAACCGCTGGTTATC 120
QY 41 PheLeuAlaIaSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLysPro 60
Db 121 TTCCTCGCGCCTTTGGTGGCAACATAGTGGCGCTAGTGGTGCAGCGCAAGCCG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuValThrAspLeuGln 80
Db 181 CAGCTGCTGCAGGTACCAACCGTTTATCTTTAACTCTCTGTCACCGACTGCTGAG 240
QY 81 IleSerLeuValAlaProThrValValAlaThrSerValProLeuPheThrProLeuAsn 100
Db 241 ATTGGCTCGTGGCCCCCTGGGTGGTGGCCACTCTGTGCTCTCTTCTGGCCCCCTCAAC 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
Db 301 AGCCACTCTGCAGCGCCCTGGTTAGCTCAACCCACTGTCGCTTGCCTTGCAGCGTCAAC 360
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Db 361 ACCATTTGCTGGTGTCAAGTGCATCTGTGCATCATCACCCCTCTCTCCACCG 420
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QY 221 ArgGlnHisAlaLeuLeuThrAsnValIlyAsnArgHisSerLeuGlnValArgValIlyAsn 240
Db 661 AGGCAGCATGCTGCTGCTGTACATGTCAGAGACACACCTTGGAAGTCCGAGTCAAGGAC 720
QY 241 CysValGluAsnGluAspGluGluGlyValGluLysValGluGluPheGlnAspGluSer 260
Db 721 TGTGTGAGAAATGAGATGAAGAGGAGACAGAGAAAGAGAGAGTTCAGAGATGAGT 780
QY 261 GluPheArgArgGlnHisGlyGlyValIlyAsnAlaLysGluGlyArgMetGluAlaLys 280
Db 781 GAGTTTCCCGCCAGCAGTGAAGTGAAGTCAAGCCAGAGAGGAGGAGAGATGAAACCAAG 840
QY 281 AspGlySerLeuValAlaLysGluGlySerThrGlyThrSerGluSerSerValGluAla 300
Db 841 GACGCGACCTGAAAGGCCAAGAGAGAGCAGCGGAGCCAGTGAAGTGTAGAGGCC 900
QY 301 ArgGlySerGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGly 320
Db 901 AGGGCAGCAGAGAGGTGAGAGAGAGCAGCGGTGGCAGAGCGCAGCTGGAGGCT 960
QY 321 LysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
Db 961 AAGGAAGCAGACCAAAAGTTGAGAGAAACAGCATGAAGGCGAGCAAGGTCGACAGAG 1020
QY 341 ValAsnGlnCysSerThrAspLeuGlyLysAspAspMetGluPheGlyGluAspAspIle 360
Db 1021 GTCAACCGATGAGATTGACTGGGTGTAACATGACATGAGATTGTTGTAAGACACATC 1080
QY 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProSerArg 380
Db 1081 AATTTCAGTGAAGAGAGTGAAGAGTGAACATCCGAGAGGCTCCACCGCTGCT 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysThrGlnCysValAlaIaLysVal 400
Db 1141 CCTAACACACACAGCAACCTCTCTGCGCAGTGTCTACAGTGCAGAAAGCTAAGAAAGT 1200
QY 401 IlePheIleIleIlePheSerThrValLeuSerLeuGlyProThrCysPheLeuAlaVal 420
Db 1201 ATCTTCATCATCATTTCTCTATGTCTATCCCTGGGGCCCTACTGCTTTTACACATC 1260
QY 421 LeuAlaValITrpValAspValGluThrGlnValProGlnTrpValIleThrIleIleIle 440
Db 1261 CTGGCCGTGTGGTGAATGCAAAACCAAGTACCCAGTGGGTATCAACCTAATATCATC 1320
QY 441 TrpLeuPhePheLeuGlnCysCysIleHisProThrValIlyGlyIlyThrMetHisLysThr 460
Db 1321 TGGCTTTCTCTCTGCAATGCTGCAATCCACCCCTATGTCTATAGGTACATGACAAAGACC 1380
QY 461 IleLysValGluIleGlnAspMetLeuLysLysPhePheCysValGluLysProProLys 480
Db 1381 ATTAAGAAAGAAATCAGAGACATGCTGAAGAAATCTTCTGCAAGAAAGCCCCGAAA 1440
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyIlyThrGluGlyLysIleValPro 500
Db 1441 GAAAGATGACCAACCAAGACCTGCGGAAACAGAGGGGTGGAATGAAAGGCAAGTTGCTCT 1500
QY 501 SerTyrAspSerAlaThrPhePro 508
Db 1501 TCTTACGATTCTGCTACTTTTCT 1524

RESULT 4
US-09-364-425B-22
; Sequence 22, Application US/09364425B
; Patent No. 6653086
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.

APPLICANT: Chalmers, Derek T.
APPLICANT: Lin, Chen W.
APPLICANT: Lin, I-Lin
APPLICANT: Lowitz, Kevin P.
APPLICANT: Chen, Ruoping
TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Receptor
FILE REFERENCE: A60047
CURRENT APPLICATION NUMBER: US/09/364,425B
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/094,879
PRIOR FILING DATE: 1998-07-31
PRIOR APPLICATION NUMBER: 60/106,300
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/110,906
PRIOR FILING DATE: 1998-12-04
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patent version 3.1
SEQ ID NO 22
LENGTH: 1382
TYPE: DNA
ORGANISM: Homo sapiens
US-09-364-425B-22

Alignment Scores:
Pred. No.: 1,586-32 Length: 1382
Score: 391.50 Matches: 113
Percent Similarity: 38.40% Conservative: 69
Best Local Similarity: 23.84% Mismatches: 143
Query Match: 14.81% Indels: 149
DB: 3 Gaps: 13

US-10-712-615-2 (1-508) x US-09-364-425B-22 (1-1382)

QY 9 ThrArgGluSerAsnSerSerHisThrCys---MetProLeuSerLysMetProIleSer 27
DB 58 ACCATGAGCTCAACTCTCCCTCAGCTCGAGAGAGAGCTGATCTCAGCTGAGAG 117
QY 28 LeuAla-----HisGlyIleIleArgSerThrValIleValIlePheLeuAlaIleSer 45
DB 118 GAGGCTGGGAGAGGGGGCTCATCATCACCCAGCTTATCGCCATCTGTGCATCACCANT 177
QY 46 PheVal-----GlyAsnIleValIleValIleValIleValIleValIleValIleVal 63
DB 178 TTGTGTGCTGGGAAACCTGCTCATCGGTGCTCATCTGTGACAAAGAGTCTACCTCTC 237
QY 64 GlnValThrAsnArgPheIlePheAsnLeuValThrAspLeuGlnIleSerLeu 83
DB 238 ACCCTCAGCAACAGTTGCTTCAGCTGACTCTGCCAATCTCTGCTGCTGCTG 297
QY 84 ValAlaProTrpValValAlaThrSerValProLeuPheTrpProLeuAsnSerHisPhe 103
DB 298 GTGCTGCTTTTGTGTGTAAGAGCTCATCCGAGGAAATGATCTTGTGTGTAGTGG 357
QY 104 CysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsnThrIleVal 123
DB 358 TGCATCTCTGCTGCTGCTCTCATCGCTGATCAGCTCTGCGACGATGCTAACCTCGGG 417
QY 124 LeuValSerValAspArgGlyLeuSerIleIleHisProLeuSerLysProSerLysMet 143
DB 418 GTCATTCATCATCAGCTCACTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 477
QY 144 ThrGlnArgArgGlyLeuLeuLeuValGlyThrThrIleValAlaIleLeuGlnSer 163
DB 478 ACGAGGAACCGGCTGTGATGACATTTGTATCATCTGGCTTACTGCTGCTGCTGCTG 537
QY 164 ThrProLeuValGlyLysGlyGlnAlaAlaPheAspGlnArgAsnAlaLeuCysSer 183
DB 538 CTGGCAACCTCTGTTGTGTGTGCTCATCGGTGATTTGACAGAGTTCAAATGAGTGTGG 597
QY 184 MetIleTrpGlyAlaSerProSerLysTrpHisLeuSerValValSerPheIleValIle 203

DB 598 GCTGCTGGACCGGAGGCTGCTACAGGCTCTTGGCAGATCTGTGTGCTCTCTTC 657
QY 204 ProLeuIleValMetIleAlaCysTrpSerValIlePheCysAlaIleArgArgGlnHis 223
DB 658 CCTTTCTGTGCTATGCTGT 708
QY 224 AlaLeuLeuTrpAsnValIleValIleValIleValIleValIleValIleValIleVal 243
DB 709 -----GTCAAGGACAGCAAGTGCAGTGTGCGACAGCTCTCATCTGTGAG 753
QY 244 AsnGluAspGluGluGluValIleGluValIleGluValIleGluValIleGluValIle 263
DB 754 ---GAGGATGCTCAG----- 765
QY 264 ArgGlnHisGluGluValIleValIleValIleValIleValIleValIleValIleVal 283
DB 766 -----AGACCGGAGG----- 777
QY 284 LeuValAlaValGluGluGluSerThrGlyTrpSerGluSerSerValGluAlaArgGlySer 303
DB 778 -----AAGAACTCCAGACACTTCCACCTCTCTTACAGC----- 810
QY 304 GluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGluGluGluGlu 323
DB 810 ----- 810
QY 324 SerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGluValAsnGln 343
DB 810 ----- 810
QY 344 CysSerIleAspLeuGluGluAspAspMetGluPheGlyGluAspAspIleAsnPheSer 363
DB 810 ----- 810
QY 364 GluAspAspValGluAlaValAsnIleProGluSerLeuProProSerArgAsnSer 383
DB 811 -----AGCAGGAGAAATGCC 825
QY 384 -----AsnSerAsnProProLeuProArgCysTrpGlnCysLysAla 397
DB 826 TTTCAGGCTGTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864
QY 398 AlaLysValIlePheIleIleIlePheSerTrpValIleSerLeuGlyProTrp---Cys 416
DB 865 CTCATCAGCATCTGT 924
QY 417 PheLeuAlaValLeuAlaValTrp-----ValAspValGluThrGlnValProGlnTrp 434
DB 925 GTCATGCTCTGAGGCTCTGTGGGGAAGCTCCGCTCTCCCGAGCTGAGACTTGG 984
QY 435 ValIleThrIleIleIleTrpLeuPhePheLeuGlnCysCysAlaIleHisProTrpValTrp 454
DB 985 GCC-----ACATGGCTGTCTTGTGCGAGGCTGTCTGCCACCCCTGATCTA 1032

RESULT 5

US-08-748-485-2
Sequence 2, Application US/08748485

Patent No. 5817480

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice

APPLICANT: Guegler, Karl J.

APPLICANT: Goli, Surya K.

TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 Porter Drive

CITY: Palo Alto

APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITTH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 284:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADNOT06
CLONE: 1722180
US-09-016-434-284
Alignment Scores:
Pred. No.: 3, 71e-32 Length: 1584
Score: 389.00 Matches: 110
Percent Similarity: 38.82% Conservative: 74
Best Local Similarity: 23.21% Mismatches: 142
Query Match: 14.71% Indels: 148
Gaps: 12
DB: 3
US-10-712-615-2 (1-508) x US-09-016-434-284 (1-1584)
QY 9 ThrArgGluSerAsnSerSerHisThrCys--MetProLeuSerLysMetProIleSer 27
DB 164 ACCATGAGCTCAACTCTCCCTCAGCTGCGAGAGAGAGTGAATCTCACTGAGGG 223
QY 28 LeuAla-----HisGlyIleIleIleArgSerThrValLeuValIlePheLeuAlaIleAsp 45
DB 224 GAGGGTGGCGAAGGGGGCGTCATCACTGAGTCACTGCGCATCTGCTGCTGCTGCTG 283
QY 46 PheVal-----GlyAsnIleValLeuAlaLeuValLeuGlnArgLysProGlnLeu 63
DB 284 TTGTGTGCTGCTGGAAACCTGTCATCTGTCATCTGTCATCTGTCATCTGTCATCTG 343
QY 64 GlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuGlnIleSerLeu 83
DB 344 ACCCTAGCAACAAGTCTGCTTCAAGCTGACTCTGCTCAACTTCTGCTGCTGCTG 403
QY 84 ValAlaProThrValValAlaThrSerValProLeuPheThrProLeuAsnSerHisPhe 103
DB 404 GTGCTGCTTTTGTGTGAGACAGCTCCATCGGAGGAAATGATCTTTGTGTGATGTGG 463
QY 104 CysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsnThrIleVal 123

DB 464 TCGAATCTTCTGCTCTCTCTCACTGCTGATCAGCTGCGACAGATGTAACTCCGCG 523
QY 124 LeuValSerValAspArgThrLeuSerIleIleHisProLeuSerLysMet 143
DB 524 GTCATTCGATCGACCGCTACTATGCTGCTCTGATCCATGATGTCATCCCATGAAGATC 583
QY 144 ThrGlnArgArgGlyTyrrLeuLeuLeuTyrrGlyThrTrpIleValAlaIleLeuGlnSer 163
DB 584 ACAGGGAAACGGGCTGTATGACATTCGTCTCATCTGCTTCACTGCTGCTGCTGCTG 643
QY 164 ThrProLeuTyrrGlyTyrrGlyGlnAlaAlaPheAspGlnArgAsnAlaLeuCysSer 183
DB 644 CTGCCACCCCTGTTGGTGTGTCATCCGAGAGTTGAGAGATTCGAATGATGCTGTGG 703
QY 184 MetIleTrpGlyAlaSerProSerTyrrThrIleLeuSerValValSerPheIleValIle 203
DB 704 GCTGCTGGACCGGGAGCTGCTGCTACAGGCTTCTGCAATCTGCTGCTGCTGCTTTC 763
QY 204 ProLeuIleValMetIleAlaCysTyrrSerValAlaPheCysAlaAlaArgArgGlnHis 223
DB 764 CCTTCTGTCATGCTGTGTGTGTGTATGCTTCACTTCTCGGGTGGCCAGG----- 814
QY 224 AlaLeuLeuTyrrAsnValIleArgHisSerLeuGlnValArgValIleAspCysValGlu 243
DB 814 ----- 814
QY 244 AsnGluAspGluGluGlyAlaGluLysLysGluGluPheGlnAspGluSerGluPheArg 263
DB 814 ----- 814
QY 264 ArgGlnHisGluGlyGluValIleValLysAlaLysGluGlyArgMetGluAlaLysAspGlySer 283
DB 815 -----GTCAAGGCACGC----- 826
QY 284 LeuLysAlaLysGluGlySerThrGlyThrSerGluSerSerValGluAlaArgGlySer 303
DB 827 ---AAGTGCACCTGTGACAGTCGTCATCGTCGAGAGAGATGCTCAGACGACCGC--- 880
QY 304 GluGluValArgGluSerSerThrValAlaAspArgLysSerMetClnLysGluGly 323
DB 881 -----GTCCGAAAGAACTCCAGACCTCCACTCTCTTCA----- 916
QY 324 SerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGluValAsnGln 343
DB 916 ----- 916
QY 344 CysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIleAsnPheSer 363
DB 916 ----- 916
QY 364 GluAspAspValGluAlaValAlaIlePheProGluSerLeuProProSerArgArgAsnSer 383
DB 917 -----GGCAGCGAGGAATGCC 934
QY 384 -----AsnSerAsnProProLeuProArgCysTyrrGlnCysLysAla 397
DB 935 TTTCAGGGTGTGCTACTCGGCCAAC-----CAGTCCAAAGCC 973
QY 398 AlaLysValIlePheIleIleIlePheSerTyrrValLeuSerLeuGlyProTyrr---Cys 416
DB 974 CTCATCAGCATCTGTGTGTGCTCGGTCCTTCATGTCATGTCATGTCATGTCATGTCAT 1033
QY 417 PheLeuAlaValLeuAlaValTrp-----ValAspValGluThrGlnValProGlnTrp 434
DB 1034 GTCATGCTCTGTGAGGCTCTGCGGGAAGACTCCGTCTCCCGAGGCTGAGACTTGG 1093
QY 435 ValIleThrIleIleIleThrLeuPhePheLeuGlnCysCysIleHisProTyrrValTyrr 454
DB 1094 GCC-----ACATGCTGTCTTTCGACAGGCTGTCTGCCACCCCTGATCTAT 1141
QY 455 GlyTyrrMetHisLeuThrIleLysLysGluIleGlnAspMet 468

QY 389 LeuProArgCysTyrGlnCysValAlaAlaValIlePheIleIleIlePheSerTyr 408
DB 893 -----CAGTGCMAAGCCCTCATCATCATCTGGTGTCTCGTCCGCTTC 937
QY 409 ValLeuSerLeuGlyProTyr---CysPheLeuAlaValLeuAlaValTP-----Val 425
DB 938 ATGGTACCTGGGGCCCTACATGTTGTCATGCTGTGAGGCCCTGTGGGGGAAAGC 997
QY 426 AspValGluThrGlnValProGlnTPValIleThrIleIleIleTPLeuPheLeu 445
DB 998 TCGGTCTCCCGAGCCTGGAGACTTGGGC-----ACATGGCTGTCTTGGC 1045
QY 446 GlnCysCysIleHisProTyrValTyrGlyTyrMetHisLeuThrIleuSylsGluIle 465
DB 1046 AGCGCTGTCTGGACCCCTGATCTATGACTGTGGAACAGACAGTTCGCAAGAAGCTA 1105
QY 466 GlnAspMet 468
DB 1106 CTGGGCATG 1114
RESULT 10
US-08-334-698-5
Sequence 5, Application US/08334698
Patent No. 5556753
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
TITLE OF INVENTION: Receptors and Uses Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,698
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/952,798
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 376901
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYROTHERICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 126..1523
OTHER INFORMATION:
US-08-334-698-5
Alignment Scores:
Pred. No.: 1..29e-26 Length: 1639

Score: 338.50 Matches: 108
Percent Similarity: 37.15% Conservative: 80
Best Local Similarity: 21.34% Mismatches: 167
Query Match: 12.80% Indels: 131
DB: 2 Gaps: 11
US-10-712-615-2 (1-508) x US-08-334-698-5 (1-1639)
QY 8 SerThrArgGluSerAsnSerSerHisThrCysMetProLeuSerTyrMetProIleSer 27
DB 138 TCGGAAAGAGCTTCGCAAGACTTCGAAGTCCAGCCCAAGCC-----CCGGACCGGTGAAC 191
QY 28 LeuAlaHisGlyIleIleLeuArgSerThrValLeuValIlePheLeuAlaIleAspPheVal 47
DB 192 ATTTCGAAGGCAATTCCTGCGGGGTAGTCTTGGGGGGGCTGATCTTCTTGGGGGTGCTG 251
QY 48 GlyAsnIleValLeuAlaLeuValLeuGlnArgIleGlySerProGlnLeuGlnValThrAsn 67
DB 252 GGTAACTCTAGTAGTCTCTCCGAGCCTGTCAACCGACCTGCATCACTCAAGCAGC 311
QY 68 ArgPheIlePheAsnLeuLeuValThrAspLeuLeuGlnIleSerLeuValAlaProTyr 87
DB 312 TACTACATGCTAACTGGCGGTGGCCGACCTCTGCTCACTCCACGGTCTGCTTC 371
QY 88 ValValAlaThrSerValProLeuPheTyrProLeuAsnSerHisAspCysThrAlaLeu 107
DB 372 TCGGCATGTTGAGAGTCTTAGGCTAGTGGCTTCGGCAGGCTTCTTCCAAACATCTGG 431
QY 108 ValSerLeuThrHisLeuPheAlaPheAlaSerValIleThrIleValLeuValSerVal 127
DB 432 GCGGAGTGTAGTGTGTGTGTGACACCGGCTCATCATGAGGCTGTGATCATCTTCATC 491
QY 128 AspArgTyrLeuSerIleIleHisProLeuSerTyrProSerTyrMetThrGlnArgArg 147
DB 492 GACCGCTACATGCGCGGTAGCTACCGCTGCCCTACCAACATGCTCCACGAGAG 551
QY 148 GlyTyrLeuLeuLeuTyrGlyThrTyrPleValAlaIleLeuGlnSerThrProProLeu 167
DB 552 GGTCTCATGCTGT 611
QY 168 TyrGlyTyrGlyGlnAlaAlaPheAspGluAspAsnAlaLeuCysSerMetIleTyrGly 187
DB 612 TTCGGCTGAGGACGCGGCC---CCCGAGGACGAGACCATCTGCCAGATC-----AAC 662
QY 188 AlaSerProSerTyrThrIleLeuSerValIleAspPheIleValIleProLeuIleVal 207
DB 663 GAGGAGCGGGCTAGCTGCTCTTCTCAGCGCTGGGCTCTTCTTACCTCTGAGCCATC 722
QY 208 MetIleAlaCysTyrSerValValPheCysAlaAlaArgArgGlnHisAlaLeuLeuTyr 227
DB 723 ATCTGCTCATGATGATGCGCGGCTTACGTCGTGGCCAAAGG----- 764
QY 228 AsnValIlyAspArgHisSerLeuGlnValAlaArgValIlyAspCysValGluAsnGluAspGlu 247
DB 765 -----GAGAGCGGGGCTC 779
QY 248 GluGluAlaGluIlyLeuGluIlyLeuPheGlnAspGluSerGluPheArgArgGlnHisGlu 267
DB 780 AAGTGTGCGCTCAAGACGCAAGTCGAGCTGCGAGCAGTAGACCTCCGATCCATCCG 839
QY 268 GlyGluValIlyLeuAlaLeuGluIlyArgMetGluAlaIlyAspGlySerLeuIlyAlaIlyAs 287
DB 840 AAAAAGCGCCCGCA----- 854
QY 288 GluGlySerThrGlyThrSerGluSerSerValGluAlaArgGlySerGluIlyValArg 307
DB 855 ---GGAGGAGCGGATGCGCAGCGCAAGACCAAGACCACTTCTCACTGAGGCTC--- 908
QY 308 GluSerSerThrValAlaSerAspGlySerMetGluIlyGlyGluIlySerThrIlyVal 327
DB 908 ----- 908
QY 328 GluGluAsnSerMetCysAlaAspIlyGlyArgThrGluValAsnGlnCysSerIleAsp 347

Db 908 ----- 908
Qy 348 LeuGIyAaPAspMetGluPheGlyLubAepAeIleAenPheSerGluAaPAspVal 367
Db 909 -----CTCAAGTTCTCCCGGAGAG---- 929
Qy 368 GluAlaValAenIleProGluSerLeuProPAspArgAAsnSerAAsnSerAAsnPro 387
Db 929 ----- 929
Qy 388 ProLeuProArgCysTyrgInCysAlaValAlaValIlePheIleIleIlePheSer 407
Db 930 -----AAAGCGGCAAAAGCGTGGCATGCTGCTGCGCTGC 965
Qy 408 TyrValLeuSerLeuGlyProTyrCysPheLeuAlaValIlePheIleIleIlePheVal 427
Db 966 TTCGTCCTCTGCTGCTGCTGCTTTT---TTCTTAAGTCATGCCATTTGGCTTTCTTCCT 1022
Qy 428 GluThrGlnValProGlnTTrpValIleThrIleIleIleIleIleIlePhePheLeuGlnCys 447
Db 1023 GATTTCAGCCCTCGAAACAGTTTAAATAGATTTTGGCTCGATATCTAAACAGC 1082
Qy 448 CysIleLeuProTyrValTyrGlyTyrIleThrIleIleIleIleIleIleIleIleIleIle 467
Db 1083 TGCATCAACCCCATATATACCATGCTCCAGCCAAAGAGTTCAAAAGCCTTTTCAGAT 1142
Qy 468 MetLeuLys---LysPhePheCysAlaValLysProPheLysLys-----Asp 482
Db 1143 GCTTTGAGAAATCCATGCTCTGCAAGAAAGCAGTCTCCAAACATGCCCTGGGCTACAC 1202
Qy 483 SerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyLysIle---ValProSer 501
Db 1203 CTGCACCGCCGACGAGCGCTGGAAGGCAACAGACATGATGCGCATCCCGCG 1262
Qy 502 TyrAspSerAlaThrPhe 507
Db 1263 GGATCAAGAGAGACCTTC 1280
RESULT 11
US-08-228-932-5
; Sequence 5, Application US/08228932
; Patent No. 5578611
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
; APPLICANT: Theresa A. Branche, John M. Weizel and Paul R. Harris
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
; TITILE OF INVENTION: PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,932
; FILING DATE: 13-APR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-B/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: (212) 422523 COOP UI

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1639 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 126..1523
; OTHER INFORMATION:
; US-08-228-932-5

Alignment Scores:
Pred. No.: 1,29e-26 Length: 1639
Score: 338.50 Matches: 108
Percent Similarity: 37.15% Conservative: 80
Best Local Similarity: 21.34% Mismatches: 187
Query Match: 12.80% Indels: 131
DB: 2 Gaps: 11

US-10-712-615-2 (1-508) x US-08-228-932-5 (1-1639)
Qy 8 SerThrArgGluSerAAsnSerSerHisThrCysMetProLeuSerLysMetProIleSer 27
Db 138 TCGGGAATAGCTTCGACAGCTCCACACTGCACCCACCG-----CCGACACCGGTGAC 191
Qy 28 LeuAlaHisGlyIleIleArgSerThrValLeuValIlePheLeuAlaIleSerPheVal 47
Db 192 ATTTCAGAGCCATCTGCTGCGGATATCTTGGGGGCGCTCATCTTTTGGGGTGCTG 251
Qy 48 GlyAenIleValIleAlaLeuValLeuGlnArgLysProGlnLeuLeuGlnValThrAAsn 67
Db 252 GGTAAACATCTTAGATCTCTCCGTACCCCTGCACACACCTGCACCTAGTACGAC 311
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Qy 108 ValSerLeuThrHisLeuPheAlaPheAlaSerValAenThrIleValIleValSerVal 127
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Db 552 GGTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 611
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Db 612 TTCGCTGAGAGACCGCGC-----CCGAGACGAGACCATCTGCCAATC-----AAC 662
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Db 663 GAGGACCGGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 722
Qy 208 MetIleAlaCysTyrSerValValPheCysAlaAlaArgGlnHisAlaLeuLeuTyr 227
Db 723 ATCCGTGATGATGATGCGCGGTCTACGCTGCGCAAGG----- 764
Qy 228 AenValLysArgHisSerLeuGluValArgValLysAspCysValGluAAsnGluAspGlu 247
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Qy      208 MetIleAlaCytyrSerValIalPheCyValAlaIarGargIlnIleAlaIeuLeuTy 227
Db      723 ATCTGCTGATGATGATGCTGCGCGCTACGTCGTCGCGCAAGAG- 764
Qy      228 AenValIySargHisSerIleuGluValIarGValIySarpCyValIgluAnGluAerGlu 247
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Qy      248 GluGluAlaGluIyLeuGluIupheGluAerGluSerGluPheArgGlnIleGlu 267
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Qy      268 GlyGluValIySAlaIySgluGluIyArgMetGluAlaIySapGlySerIleuIySAlaIy 287
Db      840 AAAAAGCGCCCGCA----- 854
Qy      288 GluGlySerThrGlyThrSerGluSerSerValIgluAlaArgIySerGluIuValArg 307
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; Sequence 5, Application US/08406855A
; Patent No. 5861309
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08406, 855A
; FILING DATE: 21-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28, 678
; REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1639 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 126..1523
; OTHER INFORMATION:
; US-08-406-855A-5
;
Alignment Scores:
Pred. No.: 1,29e-26 Length: 1639
Score: 338.50 Matches: 108
Percent Similarity: 37.15% Conservative: 80
Best Local Similarity: 21.34% Mismatches: 187
Query Match: 12.80% Indels: 131
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Qy      68 ArgPheIlePheAenIleuValItrAerPheIleuGlnIleSerIeuValAlaProTrp 87
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RESULT 14
US-08-722-190-5
; Sequence 5, Application US/08722190
; Patent No. 5990128
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, Carlos C. Forray, George
; APPLICANT: Chiu, Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
; TREAT BENIGN PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; FILING DATE: 4-Apr-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-D-PCT/JPW/AGL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1639 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEtical: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 126..1523
; OTHER INFORMATION:
US-08-722-190-5
Alignment Scores:
Pred. No.: 1,29e-26 Length: 1639
Score: 338.50 Matches: 108
Percent Similarity: 37.15% Conservative: 80
Best Local Similarity: 21.34% Mismatches: 187
Query Match: 12.80% Indels: 131
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US-10-712-615-2 (1-508) x US-08-722-190-5 (1-1639)
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Patent No. 6015819

GENERAL INFORMATION:

APPLICANT: Charles Gluchowski, et al.

TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO

TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSER: COOPER & DUNHAM LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/244,354

FILING DATE: April 1, 1997

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28, 678

REFERENCE/DOCKET NUMBER: 41878-D-PCT-US/JPM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1639 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

HYPOTHEICAL: N

ANTI-SENSE: N

FEATURE:

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

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Total number of hits satisfying chosen parameters: 19587084

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Maximum Match 100%
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8	2641	99.9	1527	3	US-09-791-932-52

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10	2641	99.9	1527	5	US-10-094-417-5	Sequence 5, App11
11	2641	99.9	1527	5	US-10-225-567A-582	Sequence 582, App
12	2641	99.9	1527	6	US-10-345-332-1	Sequence 1, App11
13	2641	99.9	1527	6	US-10-321-807-15	Sequence 15, App1
14	2641	99.9	1527	6	US-10-276-242-2	Sequence 2, App11
15	2641	99.9	1527	7	US-10-436-715-13	Sequence 13, App1
16	2641	99.9	1527	7	US-10-343-650A-89	Sequence 89, App1
17	2641	99.9	1527	7	US-10-321-807-15	Sequence 15, App1
18	2641	99.9	1527	7	US-10-314-048A-15	Sequence 15, App1
19	2641	99.9	1527	8	US-10-712-615-45	Sequence 45, App1
20	2641	99.9	1527	8	US-10-897-815-15	Sequence 15, App1
21	2641	99.9	1527	9	US-10-930-662-15	Sequence 15, App1
22	2641	99.9	1527	10	US-11-086-846-5	Sequence 15, App1
23	2641	99.9	1588	6	US-10-292-798-925	Sequence 925, App
24	2641	99.9	1920	6	US-10-276-243-1	Sequence 1, App11
25	2641	99.9	2781	6	US-10-321-807-103	Sequence 103, App
26	2641	99.9	2781	7	US-10-321-807-103	Sequence 103, App
27	2641	99.9	2781	7	US-10-314-048A-103	Sequence 103, App
28	2641	99.9	2781	8	US-10-897-815-103	Sequence 103, App
29	2641	99.9	2781	9	US-10-930-662-103	Sequence 103, App
30	2641	99.9	3024	6	US-10-017-161-1087	Sequence 1087, Ap
31	2641	99.9	7524	6	US-10-345-332-3	Sequence 3, App11
32	2637	99.7	1659	3	US-09-892-238-44	Sequence 44, App1
33	2637	99.7	1659	8	US-10-608-990-1	Sequence 1, App11
34	2637	99.7	1659	8	US-10-712-615-44	Sequence 44, App1
35	2636	99.7	1527	3	US-09-992-238-46	Sequence 46, App1
36	2636	99.7	1527	6	US-10-321-807-91	Sequence 91, App1
37	2636	99.7	1527	7	US-10-321-807-91	Sequence 91, App1
38	2636	99.7	1527	7	US-10-314-048A-91	Sequence 91, App1
39	2636	99.7	1527	8	US-10-712-615-46	Sequence 46, App1
40	2636	99.7	1527	8	US-10-897-815-91	Sequence 91, App1
41	2636	99.7	1527	9	US-10-930-662-91	Sequence 91, App1
42	2628	99.4	1527	3	US-09-992-238-48	Sequence 48, App1
43	2628	99.4	1527	8	US-10-712-615-48	Sequence 48, App1
44	2619	99.1	1527	3	US-09-971-269-1	Sequence 5, App11
45	2619	99.1	1704	3	US-09-971-269-1	Sequence 1, App11

ALIGNMENTS

RESULT 1
US-09-992-238-1
; Sequence 1, Application US/09992238
; Publication No. US2003005444A1
; GENERAL INFORMATION:
; APPLICANT: BATTAGLINO, PETER
; APPLICANT: FEDER, JOHN N
; APPLICANT: MINTIER, GABE
; APPLICANT: NELSON, THOMAS C
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: WESTPHAL, RYAN
; APPLICANT: CACACE, ANGELA
; APPLICANT: BARBER, LAUREN
; APPLICANT: HAWKEN, DONALD R
; APPLICANT: KORNACKER, MICHAEL G
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGFRAVY8,
; FILE REFERENCE: D0047NP
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/317166
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/308285
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/268581
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/248285
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1527

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-992-238-1

```

Alignment Scores:

Pred. No.:	3.82e-284	length:	1522
Score:	2644.00	Matches:	508
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-712-615-2 (1-508) x US-09-992-238-1 (1-1527)

QY	1	MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro	20
DB	1	ATGAGCTCCACCTGCACCAACAGCAGCGCGGAGATGACAGCAGCCACAGCTGATGCC	60
QY	21	LeuSerLysMetProLieserLeuAlaHisGlyIleIleArgSerThrValLeuValIle	40
DB	61	CTCTCCAAATATGCCCATCAGCTGAGCCCAAGCATATCCGCTCAACCCGCTGATTATC	120
QY	41	PheLeuAlaAlaSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgGlyPro	60
DB	121	TTCTCTGCGCGCTCTTTGCTGCGCAATAGTCTGAGCTATGTTGACGCCCAAGCCG	180
QY	61	GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeuGln	80
DB	181	CAGCTGCTCAGGTGACCAACGGTTTATCTTAACTCTCTGTCACCGACTGCTGACG	240
QY	81	IleSerLeuValAlaProTyrValValAlaIleThrSerValProLeuPheTyrProLeuAsn	100
DB	241	ATTTCGTGCTGTGAGCCCCCTGGGGTGGGCACTCTGTGCTCTCTCTGGCCCCCTCAC	300
QY	101	SerHisPheCysThrLalaLeuValSerLeuThrHisIleLeuPheAlaPheAlaSerValAsn	120
DB	301	AGCCACTTTCGACGGCCCTGTTAGCTTACCTCACCCACTGTTCCGCTTGGCAGCGTAC	360
QY	121	ThrIleValIleLeuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro	140
DB	361	ACCATATGCTTGGTGTCACTGATCCGCTACTTGTTCATATCCACCTCTCTCTCACCCG	420
QY	141	SerLysMetThrGlnArgArgGlyTyrIleLeuLeuLeuTyrGlyThrTrpIleValAlaIle	160
DB	421	TCCAAAGATACCAAGCGCGCGGTATCTGCTCTCTATGCACTCGATATTGGCCATC	480
QY	161	LeuGlnSerThrProProLeuTyrGlyTyrIleGlyAlaAlaPheAspGluArgAsnAla	180
DB	481	CTGCAGAGACATCTCTCACTCTACGCGGTGGGCAAGGCTCTTTGATGAGCCCAATGCT	540
QY	181	LeuCysSerMetLileTrpGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe	200
DB	541	CTCTCTCCATATATCTGGGGGGGCAAGCCCCAGGTACATATTTCAAGCGGTGCTCTTC	600
QY	201	IleValIleProLeuIleValMetIleAlaCysTyrSerSerValAlaPheCysAlaAlaArg	220
DB	601	ATCGTCATTCACATGATGTGTCATGATTGCTCTGCTACTCCCTGGTGTCTGTGCAGCCGG	660
QY	221	ArgGlnHisAlaLeuLeuTyrAsnValIleValArgHisSerLeuGlnValaArgValIleAsp	240
DB	661	AGCGCAGCATGCTCTGCTGTACATGTCCAGAGACACACAGCTTGGAGAGCGCAGTCAAGAC	720
QY	241	CysValIleGluAsnGluAspGluGluGlyValaGluIleLysGluGluIlePheGlnAspGlySer	260
DB	721	TGTGTGGAAATATGAGATGAGGGAGGACGAGAAGAGAGAGAGATTCCAGATGAGAGT	780
QY	261	GluPheArgArgGlnHisGluGluGlyGluValIleValaLysGluGlyArgMetGluAlaLys	280
DB	781	GAGTTTCGCCCGCAGCATGAGGTGAGGTCAAGGCCCAAGAGGCGCAGATGGAAGCCAG	840
QY	281	AspGlySerLeuLeuValaLysGluGlySerThrGlyThrSerGluSerSerValGluAla	300
DB	841	GACGGCAGGCTTAAGGCCCAAGGAAGACAGGGGACAGTGAAGATATGATGAGAGCC	900

[illegible]

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6 Gaps: 0

US-10-712-615-2 (1-508) x US-10-088-726-26 (1-1527)

QY 1 MetThSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
DB 1 ATGACGTCACCTGACCAACAGACGCGAGAGTAAAGCAGCCACGTCGATGCC 60
QY 21 LeuSerIysMetProIleSerLeuAlaHisGlyIleIleArgSerThrValIleValIle 40
DB 61 CTCCTCAAAATGCGCATCAGCTGGCCACGCGCATCATCCGCTCAACCGCTGATTATC 120
QY 41 PheLeuAlaIleAspPheValGlyAsnIleValIleValIleValIleValIleValIle 60
DB 121 TTCCTGCGCCCTCTTTCGTGGCAACATAGTGTGGCTAGGTGTGACGCGCAAGCCG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeuGln 80
DB 181 CAGCTGCTGACGGTGAACCAACCGTTTATCTTTAACTCTCTGTCACCGACTGCTGACG 240
QY 81 IleSerLeuValAlaProIlePValValAlaThrSerValProLeuPheTrpProLeuAsn 100
DB 241 ATTTCGCTCGTGGCCCCCTGGGTGGTGGCCACCTCTGTGCTCTCTTCTGGCCCTCAAC 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisIlePheAlaPheAlaSerValAsn 120
DB 301 AGCCACTTCTGACGCGCCCTGGTGAAGCTCAACCACTGTTGCGCTTGGCAGCGTCAAC 360
QY 121 ThrIleValIleValSerValAspArgIleLeuSerIleIleHisProLeuSerIlePro 140
DB 361 ACCATTGTCTTGGTGTGATGAGATCGTACTTGTCCATCATCACTCTCTCTCAACCG 420
QY 141 SerIysMetThrGlnArgArgIleYrLeuLeuLeuIleYrThrTrpIleValAlaIle 160
DB 421 TCCAAATGACCCAGCGCCGCGGTACTCTCTCTATGACCACTGATTTGGCCATC 480
QY 161 LeuGlnSerThrProProLeuIleYrTrpGlyGlnAlaIlePheAspGluAspAla 180
DB 481 CTGCAAGACACTCTCTCACTCACTGAGGTGGGCGGAGCTCTTGTGATGAGCGCAATGCT 540
QY 181 LeuCysSerMetIleTrpGlyAlaSerProSerIleThrIleLeuSerValIleSerPhe 200
DB 541 CTCCTGCTCATGATCTGGGGGCGCAGCCCAAGCTACACTTCTCAGCGGTGCTCTTC 600
QY 201 IleValIleProLeuIleValMetIleAlaCysIleSerValIlePheCysAlaAlaArg 220
DB 601 ATCGTCATTCACATGATTCATGATGCTGCTACTCGTGGTGTCTGTGACGCGCG 660
QY 221 ArgGlnHisIleAlaLeuLeuIleYrAsnValIleArgHisSerLeuGluValAlaGValIleAsp 240
DB 661 AGGCAGATGCTCTGCTGTACATGTCMAAGACACAGCTTGGAAAGTGCACAGTCAAGAC 720
QY 241 CysValGluAsnArgIleAspGluGluValIleGluValIleValIleValIleValIleValIle 260
DB 721 TGTGTGAGAAATGAGATGAGAGGAGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 780
QY 261 GluPheArgArgGlnHisGluGluValIleValIleValIleValIleValIleValIleValIle 280
DB 781 GAGTTTCGCGCCAGCATGAGGTGAGGTCAAGCCCAAGAGAGGCAAAATGGAAGCCAG 840
QY 281 AspGlySerLeuIleValIleGluGlySerThrGlyThrSerGluSerSerValGluVal 300
DB 841 GACGGCGAGCTGAGAGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCC 900
QY 301 ArgGlySerGluGluValIleArgIleSerSerThrValIleSerAspGlySerMetGluGly 320
DB 901 AGGGGCGAGGT 960
QY 321 IysGluGlySerThrIleValIleGluGluAsnSerMetIleValIleValIleValIleValIle 340

DB 961 AAGAAAGCAGACCAAAAGTTGAGAGAAACAGCATGAAAGGACAGCAAGGCTCCACAG 1020
QY 341 ValAsnGlnCysSerIleLeuPheGluGlyGluAspAspMetGluPheGlyGluAspAspIle 360
DB 1021 GTCAACCACTGACAGCATTTGACTTGGGTGAAGATGATGAGATTTGGTGAAGACGATC 1080
QY 361 AsnPheSerGluAspAspValGluAlaValAlaAsnIleProGluSerLeuProProSerArg 380
DB 1081 AATTTCAGTAGAGATGACGTGAGGAGCATGAAATCATCCCGAGAGCTCCCAACCAATCGT 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysIleGlyGlnCysAlaValAlaVal 400
DB 1141 CGTAAACAGAAACAGCAACCTCTCTGCGAGGTGTACAGTGAAGAGCTGTAAAGTG 1200
QY 401 IlePheIleIleIlePheSerIleValIleSerLeuGlyProIleCysPheLeuAlaVal 420
DB 1201 ATCTTATCATCTATTTTCTCTATGAGTATCCCTGGGCGCTACTGCTTTTAAAGATC 1260
QY 421 LeuAlaValTrpValAspValGluTrpGlnValProGlnTrpValIleThrIleIleIle 440
DB 1261 CTGGCGGTGGGTGATGATGCAAAACCAAGTACCCCAAGTGGGTGATCAACATATCATC 1320
QY 441 TrpLeuPhePheLeuGlnCysCysIleIleProIleValIleIleIleIleIleIleIle 460
DB 1321 TGGCTTTCTCTCTGACAGCTGTCATCAACCCCTATGTCTATGTGCTAATGCAAGACC 1380
QY 461 IleIleValGluIleGlnAspMetLeuIleValIlePheCysIleValGluIleValProIle 480
DB 1381 ATTAAGAGAGAAATCCAGGACATGTGAAGATTTCTTGCAAGAAAGCCCGGAA 1440
QY 481 GluAspSerHisProAspLeuProGlyTrpGluGlyGlyIleThrGluGlyIleValPro 500
DB 1441 GAGATAGACCAACCAACCTGCGCGGAGACAGAGGGTGGAGCTGAAGCAAGATTGCTCT 1500
QY 501 SerIleAspSerAlaThrPhePro 508
DB 1501 TCTTACGATTCCTGCTACTTTTCTCT 1524

RESULT 3

US-10-712-615-1
; Sequence 1, Application US/10712615
; Publication No. US20040214317A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPGRMYB, EXPRESSED
; TITLE OF INVENTION: HIGHLY IN BRAIN
; FILE REFERENCE: D0047A-CIP
; CURRENT APPLICATION NUMBER: US/10/712,615
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: U.S. 09/992,238
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: U.S. 60/248,285
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: U.S. 60/268,581
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/308,285
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: U.S. 60/317,166
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-712-615-1

Alignment Scores:

Pred. No.: 3,82e-284 Length: 1527
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-712-615-2 (1-508) x US-09-992-238-47 (1-1580)

QY 1 MetThSerThCyethrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
DB 32 ATGAGCTCACTGACCAACCAAGCAGCCGAGAGTAACAGACGACACGTCATGCC 91
QY 21 LeuSerLysMetProLLeuSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
DB 92 CTCTCAAAATGCCATCAGCTGGGCCACGGCATCATCCGCTCAACCGCTGGTTATC 151
QY 41 PheLeuAlaAlaSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLysPro 60
DB 152 TTCCTGCGCGCTCTTTCGTCGCAACATAGTGGCTGGCTAGTGTTCAGCGCAAGCCG 211
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuValThrAspLeuGln 80
DB 212 CAGCTGCTGACAGTACCAACCGTTTATCTTAACCTCTGTCACCGACTGCTGACG 271
QY 81 IleSerLeuValAlaProTrpValValAlaIleThrSerValProLeuPheTrpProLeuAsn 100
DB 272 ATTTGGCTGTGGCCCCCTGGGTGGGTGGCCACTGCTGCTCTTCTGGCCCCCTCAAC 331
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValIle 120
DB 332 ACCCACTTCTGACCGCCCTGTGTAGCCCTACCCACCTGTGGCTTCCGCCAGCGTCAC 391
QY 121 ThrIleValLeuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTrpPro 140
DB 332 ACCATTTGTTGATGTCAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 451
QY 141 SerLysMetThrGlnArgArgLysTyrLeuLeuLeuValGlyThrTrpIleValAlaIle 160
DB 452 TCCAAAGATACCCAGGCGCGGCTTACCTGCTCTTAAGGACCGTGATGGGCTGCTG 511
QY 161 LeuGlnSerThrProProLeuValTyrGlyGlnAlaAlaPheAspGluArgAsnAla 180
DB 512 CTGCAAGACACTCTCCACTTCAACGCTGGGCGACGGCTGCTTGTATAGCGCAATGCT 571
QY 181 LeuCysSerMetIleTrpGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200
DB 572 CTCTGCTCATATCTGCGGGGCGAGCCCAAGCTACATATCTCAAGCTGGTCTTCT 631
QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerValValPheCysAlaAlaArg 220
DB 632 ATCGTCATTCACACTGATTTGTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 691
QY 221 ArgGlnHisAlaLeuLeuTyrAsnValIlySerGHisSerLeuGlnValArgValIlyAsp 240
DB 692 AGGCGAGCATGCTCTGCTGTCATGATGTCACAGACACAGCTTGGAGTGGAGTCAAGGAC 751
QY 241 CysValIleGluAsnGluAspGluGluGlyAlaGlyIlyValGlyGluGlnPheGlnAspGluSer 260
DB 752 TGTGTGAAATGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 811
QY 261 GluPheArgArgGlnHisGluGlyGluValIlyAlaGlyGluValArgMetGluAlaLys 280
DB 812 GAGTTTCCGCGCAGATGAGTGAAGTCAAGGCCAAGAGGCGCAATGAGAGCGAAG 871
QY 281 AspGlySerLeuLysAlaLysGluGlySerThrGlyThrSerGluSerSerValGluAla 300
DB 872 GACGGCAGGCTCAAGGCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 931
QY 301 ArgGlySerGluGluValAlaArgLysSerThrValAlaSerAspGlySerMetGluGly 320
DB 932 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 991
QY 321 LysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340

DB 992 AAGGAAGGAGAGCAAAAGTTGAGAGAGAAACAGCAAGAGGCGAGACAGGCTGCACAGAG 1051
QY 341 ValAsnGlnCysSerIleAspLeuGlyGluAspMetGluPheGlyGluAspAspIle 360
DB 1052 GTCAACCGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1111
QY 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProProSerArg 380
DB 1112 AATTCAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1171
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysLysAlaAlaLysVal 400
DB 1172 CGTAACAGCAAGCAAGCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1231
QY 401 IlePheIleIleIlePheSerTyrValLeuSerLeuGlyProTyrCysPheLeuAlaVal 420
DB 1232 ATCTTCATCATATTTCTCTCATATGCTATCTCGGGGCTCTACTGCTTTTATCAGTTC 1291
QY 421 LeuAlaValAlaTrpValAspValGluThrGlnValProGlnTrpValIleThrIleIle 440
DB 1292 CTGGCCGTGTGGGTGATGTCAAAACCAAGTACCCAGTGGTATCACCATATCATTC 1351
QY 441 TrpLeuPhePheLeuGlnCysCysIleHisProTyrValTyrGlyTyrMetHisLysThr 460
DB 1352 TGGCTTTTCTTCTCAGAGCTGATCAACCCCTATGCTATGCTATGCTATGCTATGCT 1411
QY 461 IleLysLysGluIleGluAspMetLeuLysLysPhePheCysValGluLysProProLys 480
DB 1412 ATTAAGAAAGAAATCAGAGACATGCTGAAGAAATCTTCTTGCAAGAAAGCCCGGAA 1471
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyIlyValIleValPro 500
DB 1472 GAAGATAGCCACCAAGCAAGCTGCCCCGAAACAGAGGAGTGGAGTGAAGGCAAGTTGCT 1531
QY 501 SerTyrAspSerAlaThrPhePro 508
DB 1532 TCCTACGATTCGTACTTTTCT 1555

RESULT 5
US-10-712-615-47
; Sequence 47, Application US/10712615
; Publication No. US20040214317A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBM78, EXPRESSED
; FILE REFERENCE: D0047A-CIP
; CURRENT APPLICATION NUMBER: US/10/712,615
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: U.S. 09/992,238
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: U.S. 60/248,285
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: U.S. 60/268,581
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/308,285
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: U.S. 60/317,166
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 1580
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-712-615-47

Alignment Scores:
Pred. No.: 4,04e-284 Length: 1580
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0


```

QY 21 LeuSerIleMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
DB 61 CTCTCCAAATGCGCCATCATCGCTGGCCCAAGCATCATCGCTCAACCGCTGGATTATC 120
QY 41 PheLeuAlaIleSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgIlePro 60
DB 121 TTCCTGCGCGCTTTTCGTGGCAACATAGTGTGGCTGCTAGTGTGGAGCCCAAGCCG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuValThrAspLeuLeuGln 80
DB 181 CAGCTCTCAGAGTGACCAACCTTTATCTTTAACTCTCTGTCACCAACCTGCTGCGAG 240
QY 81 ILeSerLeuValAlaProTyrValValAlaIleThrSerValProLeuPheTyrProLeuAsn 100
DB 241 ATTTGCTGCTGGGCCCCCTGGGGTGGCCACTCTGTGCTCTTCTTGGCCCCCTCAAC 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
DB 301 AGCCACTTTCAGACGGCCCTGTGTACCTCACCCACCTGTTCCTTCGCCACCGTCAAC 360
QY 121 ThrIleValLeuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
DB 361 ACCATTGCTTGTGGTCACTGATGATCGCTACTGTTCATCATCATCACTCTCTCTAACC 420
QY 141 SerIleMetThrGlnArgArgIlyTyrLeuLeuLeuTyrGlyThrTyrIleValAlaIle 160
DB 421 TCCAGATGATCCAGCGCGCGGTTACCTGCTCTCTATGGACCTGGATTGGGCCATC 480
QY 161 LeuGlnSerThrProProLeuTyrGlyTyrTyrGlyGlnAlaAlaPheAspGluArgAsnAla 180
DB 481 CTGCGAGAGACTCTCTCACTCACTACGCTGGGGCCAGCGCTCCCTTATGAGCCCAATGCT 540
QY 181 LeuCysSerMetIleTyrGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200
DB 541 CTCTGCTCATGATCTGGGGGGCCAGCCCAAGCTCACTATCTCAAGCGGGTCTCTC 600
QY 201 ILeValIleProLeuIleValMetIleAlaCysTyrSerValValPheCysAlaAlaArg 220
DB 601 ATCGTCACTTCCACTGATTCATGATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 221 ArgGlnHisAlaLeuLeuTyrAsnValIleValArgHisSerLeuGluValArgValIleAsp 240
DB 661 AGCGACATGCTCTGCTGATCAATGTCACAGAGACACAGCTGGAGAGTGCAGAGTCAAG 720
QY 241 CysValGluAsnGluAspGluGluGluValAlaGluLeuValGluGluIleAspGluSer 260
DB 721 TGTGTGGAATGAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
QY 261 GluPheArgArgGlnHisGluGluValIleValAlaValGluGluIleArgMetGluAlaIle 280
DB 781 GAGTTCCGCCCGCAGATGAGGTGAGTCAAGGCCAAGAGGGCAGAGTGAAGCCAG 840
QY 281 AspGlySerLeuValAlaValGluGlySerThrGlyThrSerGluSerSerValGluAla 300
DB 841 GACGCGAGCTGAGAGCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
QY 301 ArgGlySerGluGluValArgIleSerSerThrValAlaSerAspGlySerMetGluGly 320
DB 901 AGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
QY 321 LysGluGlySerThrIleValGluGluAsnSerMetIleValAlaAspLysGlyArgTyrGlu 340
DB 961 AAGGAAGCAGACCAAAAGTTGAGAGAACAGATGAGGAGGAGGAGGAGGAGGAGGAGG 1020
QY 341 ValAsnGlnCysSerIleAspLeuGlyIleAspAspMetGluPheGlyIleAspAspIle 360
DB 1021 GTCGAACAGTGCAGCACTTGGCTGGAAGATGATGAGAGTTGGTGAAGACGACATC 1080
QY 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProProSerArg 380
DB 1081 AATTTAGTGAAGATACGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysLysAlaIleVal 400

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DB 1141 CGTAACAGCAAGCAACCTCTCTGCGCAGAGTGTACAGTGCACCAACCTGTAAAGTG 1200
QY 401 ILePheIleIleIlePheSerTyrValLeuSerLeuGlyProTyrCysPheLeuAlaVal 420
DB 1201 ATCTTCATCATCATATTTCTCTATGATGCTATCCCTGGGCCCCCTACTGCTTTTAAAGATC 1260
QY 421 LeuAlaValTyrValAspValGluThrGluValProGlnTyrValIleThrIleIleIle 440
DB 1261 CTGGCGGTGGGTGGATGTGCAAAACCAAGTACCCAGTGGGTATGACCAATATCATC 1320
QY 441 TyrLeuPhePheLeuGlnCysCysIleHisProTyrValTyrGlyTyrMetHisLysThr 460
DB 1321 TGGCTTTTCTCTGAGAGTGTGATCCACCCCTATGTCTATAGGCTACATGCAAGACCC 1380
QY 461 ILeLysLysGluIleGlnAspMetLeuLysLysPheCysValGluLysProProLys 480
DB 1381 ATTAAGAAAGAAATCCAGACATGCTGAAGAGTTCTTGTGAAGGAAAGCCCGGAAA 1440
QY 481 GluAspSerHisProAspLeuProGlyTyrGluGlyGlyTyrGluGlyLysIleValPro 500
DB 1441 GAAGATAGCCACCCAGACCTGCCCCGGAACAGAGGTGGAGCTGAAGCAAGATTGCTCT 1500
QY 501 SerTyrAspSerAlaThrPhePro 508
DB 1501 TCTAGATTCTGTACTTTTCTCT 1524

RESULT 7
US-10-293-983-8
; Sequence 8, Application US/10293983
; Publication No. US2003014998A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Blatcher, Maria
; APPLICANT: Paulsen, Janet
; APPLICANT: Bates, Brian G
; TITLE OF INVENTION: Genes Encoding G Protein Coupled Receptors and Uses Therefor
; FILE REFERENCE: AM100476
; CURRENT APPLICATION NUMBER: US/10/293,983
; CURRENT FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 4718
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (332)..(1858)
; OTHER INFORMATION:
US-10-293-983-8

Alignment Scores:
Pred. No.: 2,43e-283 Length: 4718
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-712-615-2 (1-508) x US-10-293-983-8 (1-4718)
QY 1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
DB 332 ATGACGCTCACTGACCAACAGACAGCGCGAGATMAAGAGGACACACGTCAGTCC 391
QY 21 LeuSerIleMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
DB 392 CTCTCCAAATGCGCCATCATCGCTGGCCCAAGCATCATCGCTCAACCGCTGGATTATC 451
QY 41 PheLeuAlaIleSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgIlePro 60
DB 452 TTCCTGCGCGCTTTTCGTGGCAACATAGTGTGGCTGCTAGTGTGGAGCCCAAGCCG 511

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Oy	61	GlneuleuEngIvAla1ThAsnArpHe1IephAenleuVAla1ThAspLeuEngI	80
Db	512	CAGCTGCTGCAGGAGACCAACCGTTTATCTTTAACTCTCTGCACCGACTGTCAG	571
Oy	81	IleSerIeuValAla1ProTrpValValAla1ThSerVal1ProLeuPheTrpProLeuAsn	100
Db	572	ATTTCGCTCGTGGCCCCCTGGGTGGTGGCCACTGTGGCTCTCTTCTGGACCCCTCAAC	631
Oy	101	SerHisPheCyethAla1LeuValSerIeuThrHisLeuPheAla1PheAlaSerValAsn	120
Db	632	AGCCACTTCTGCAGCGCCCTGGTTAGCTCAACCACTGTTGCTTGCCAGCGCTCAAC	691
Oy	121	ThrIleValLeuValSerValAspArgTrpLeuSerIleIleHisProLeuSerTrpPro	140
Db	692	ACCAATTGCTTGATGTGACTGAGTGGATCGCTACTTGTCAATCAATCCACCTCTCTCTCAACCG	751
Oy	141	SerIysMetThrGlnArgArgIyTrpLeuLeuLeuTrpGlyIleHisAla1Ile	160
Db	752	TCCAAAGATGACCCACGCGCGGGTAACTCGCTCTCTGTGGCACTGGATTGTGGCCATC	811
Oy	161	LeuGlnSerThrProProLeuTrpGlyTrpGlyGlnAla1PheAspGluArgAsnAla	180
Db	812	CTGCAGAGCATCTCTCCACTCTACGGCTGGGGCCAGGCTGCTTTGATGAGCGCAATCT	871
Oy	181	LeuCySerMetIleTrpGlyAlaSerProSerTrpThrIleLeuSerValIaSerPhe	200
Db	872	CTCTGCTCCATGATCTGGGGGGCCAGCCCAAGCTCACTAATCTCAGCGTGGTGTCTTC	931
Oy	201	IleValIleProLeuIleValMetIleAlaCyTrpSerSerValValPheCysAlaAlaArg	220
Db	932	ATCGCATTCCTCATATGTCTAGTATGCTGCTACTCTCGATGGTGTCTGTGGACCCGG	991
Oy	221	ArgGlnHisAlaLeuLeuTrpAsnValIysArgHisSerLeuGluValArgValIysAsp	240
Db	992	AGGCAGCATGCTCTGCTGTAACAATGTCAAGAAGACACACGCTTGGAAATGCGAGTCAAGAC	1051
Oy	241	CysValIGluEngIuAspGluGluGluValAGluValysGluGluuPheGlnAspGluSer	260
Db	1052	TGTGTGGAAATGAGAGATGAAGAGGAGACAGAGAAAGAGAGAAATTCACAGATGAAGT	1111
Oy	261	GluPheArgArgGlnHisGluGlyValuValIysAlaValysGluGlyArgMetGluAlaIys	280
Db	1112	GAGTTTCCCCCGCCAGCATGAAGTGAAGTCAAGGCCCAAGAGCGCAATGGAACCCAA	1171
Oy	281	AspGlySerLeuValAlaValysGluGlySerThrGlyIleHisSerGluSerSerValGluAla	300
Db	1172	GACGGCACCTCTGAAGGCCAAGAAAGAAAGACACGGGGACAGATGAAGTATGTAGAGGCC	1231
Oy	301	ArgGlySerGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGly	320
Db	1232	AGGGGACACGAGAGAGTCAAGAAAGACAGACAGGTGGCCAGGACGACGATGGAGGCT	1291
Oy	321	LysGluGlySerThrIysValIGluGluuAsnSerMetLysAlaAspLysGlyArgThrGlu	340
Db	1292	AAGGAAGCAGACCAAAAGTTGAGGAGAACAAGCATGAAGGACGACAAAGGTGCAACAAG	1351
Oy	341	ValAlaGlnIleCysSerIleAspLeuGlyGluuAspAspMetGluPheGlyGluuAspAspIle	360
Db	1352	GTCAACCAAGTGCAGATGATGACTTGGGTGAAGTGCATGGAATTTGGTGAAGACCAACATC	1411
Oy	361	AsnPheSerGluAspAspValIGluAlaValAsnIleProGluSerLeuProProSerArg	380
Db	1412	AATTTCAATGAGAGATGACGTGAGGCAATGAACAATCCGGAGAGGCTCCCAACCCAGTGT	1471
Oy	381	ArgAsnSerAsnSerAsnProProLeuProArgCysTrpGlnCysLeuValAlaIysVal	400
Db	1472	CGTAAACACCAACAGCAACCTCTCTCTGCCCCAGGTCTCAACGTGCAAAAGCTGTAAAGTG	1531
Oy	401	IlePheIleIleIlePheSerTrpValIleuSerLeuGlyProTrpCysPheLeuAlaVal	420
Db	1532	ATCTTCATCATCATTTTCTCTATATGCTATCCCTGGGGCCCTTACTGCTTTTACAGCT	1591

Protein	Accession	Position	Sequence	Position
Oy	421	440	LeuLlaValTrpValAspValGluThrGlnValProGlnTrpValIleThrIleIle	440
Db	1592	1655	CTGGCCGTrGGGTrGAGTrGTGAACCACGGTACCACCGTGGGTGATCACCATTATC	1655
Oy	441	460	TrpLeuPhePheLeuGlnCysCysAlaIleHisProGlyValTyrGlyTyrMetHisIysThr	460
Db	1652	1715	TGGCTTTTCTTCCCTGCAGCTGCTGCATCCACCCCATGTCTTGGCTATCATGCACAAGACC	1715
Oy	461	480	IleIysIysGluIleGlnAspMetLeuLysIysPhePheCysIysGluLysProProIys	480
Db	1712	1775	ATTAGAAGAGGAATCCAGGACATGCTGAAGAAGTTCTTCTCAAGAGAAAGCCCGGAAA	1775
Oy	481	500	GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyLysIleValPro	500
Db	1772	1835	GAAATATGCCACCCAGACCTGCCCGGAAACAAGGGGTGGAGCTGAAGGCAAGATTGTCCCT	1835
Oy	501	508	SerTyrAspSerAlaIleThrPhePro	508
Db	1832	1855	TCTTACGATTTCTGCTACTTTTCTCT	1855

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RESULT 8
US-09-791-932-52
? Sequence 52, Application US/09791932
? Publication No. US20030003451A1
? GENERAL INFORMATION:
? APPLICANT: Vogeli, Gabriel
? APPLICANT: Parodi, Luis A.
? APPLICANT: Hiebsch, Ronald R.
? APPLICANT: Lind, Peter
? APPLICANT: Kaytes, Paul S.
? APPLICANT: Ruff, Valerie
? APPLICANT: Hulf, Rita M.
? APPLICANT: Wood, Linda S.
? TITLE OF INVENTION: No. US20030003451a1el G Protein-Coupled Receptors Cross-Referen
? FILE REFERENCE: 00325 US1
? CURRENT APPLICATION NUMBER: US/09/791.932
? CURRENT FILING DATE: 2001-02-23
? PRIOR APPLICATION NUMBER: 60/184,305
? PRIOR FILING DATE: 2000-02-23
? PRIOR APPLICATION NUMBER: 60/184,304
? PRIOR FILING DATE: 2000-02-23
? PRIOR APPLICATION NUMBER: 60/184,303
? PRIOR FILING DATE: 2000-02-23
? PRIOR APPLICATION NUMBER: 60/184,397
? PRIOR FILING DATE: 2000-02-23
? PRIOR APPLICATION NUMBER: 60/184,247
? PRIOR FILING DATE: 2000-02-23
? PRIOR APPLICATION NUMBER: 60/188,880
? PRIOR FILING DATE: 2000-03-13
? PRIOR APPLICATION NUMBER: 60/217,369
? PRIOR FILING DATE: 2000-07-11
? PRIOR APPLICATION NUMBER: 60/217,370
? PRIOR FILING DATE: 2000-07-11
? PRIOR APPLICATION NUMBER: 60/218,492
? PRIOR FILING DATE: 2000-07-20
? PRIOR APPLICATION NUMBER: 60/186,810
? PRIOR FILING DATE: 2000-03-03
? PRIOR APPLICATION NUMBER: 60/188,064
? PRIOR FILING DATE: 2000-03-09
? PRIOR APPLICATION NUMBER: 60/186,457
? PRIOR FILING DATE: 2000-03-02
? PRIOR APPLICATION NUMBER: 60/213,861
? PRIOR FILING DATE: 2000-06-23
? PRIOR APPLICATION NUMBER: 60/194,344
? PRIOR FILING DATE: 2000-04-03
? PRIOR APPLICATION NUMBER: 60/218,337
? PRIOR FILING DATE: 2000-07-14
? NUMBER OF SEQ ID NOS: 184
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 52
? LENGTH: 1527
? TYPE: DNA
? ORGANISM: Homo sapiens

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US-09-791-932-52

Alignment Scores:

Pred. No.: 8,266-284 Length: 1527
 Score: 2641.00 Matches: 507
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.80% Mismatches: 0
 Query Match: 99.89% Indels: 0
 DB: 3 Gaps: 0

US-10-712-615-2 (1-508) x US-09-791-932-52 (1-1527)

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QY 1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
DB 1 ATGACCTGCACCTGCACCAACAGCAGCGAGAGTAACAGCAGCCACAGCTCATGCCC 60
QY 21 LeuSerLysMetProLLeuSerLeuAlaHisGlyTlleIleArgSerThrValLeuValIle 40
DB 61 CTCTCCAAATATGCCATCAGCCTGGGCCACGGCATCATCGCTCAACCGTGTGTATATC 120
QY 41 PheLeuAlaAlaSerPheValGlyAsnIleValIleuValaleuValleuGlnArgLysPro 60
DB 121 TTCCTGCGCGCCCTTTTCGTGCGCAACATAGTCTGGCTAGTGTGCGCAGCCAGCCG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeuGln 80
DB 181 CAGCTGCTGAGGTGACCAACCGTTTATCTTAACCTCCTCGTCAACCGACTGTGACG 240
QY 81 ILeuSerLeuValAlaProTTPValValAlaThrSerValProLeuPheTTPProLeuAsn 100
DB 241 ATTTCCCTGCTGCGCCCTGCTGGGTGGTGGCCACTGTGTGCTCTCTTGGCCCTTCAC 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisGluPheAlaPheAlaSerValAsn 120
DB 301 AGCCACTTGTGCACGCGCCCTGGTTAGCTTACACCACTGCTTCCCTTCCGCAAGCTCAC 360
QY 121 ThrIleValIleuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
DB 361 ACCATTGTGCTGTGTCAGTGGATCGCTACTTGTTCATCATCAACCTCTCTCTACCCG 420
QY 141 SerLysMetThrGlnArgArgTyrTyrLeuLeuLeuTyrGlyThrTPIleValAlaIle 160
DB 421 TCCAAATATGACCGACGCGCGGTATCCTGCTCTATGCGCACCTGGAGTTGTGGCCATC 480
QY 161 LeuGlnSerThrProProLeuTyrGlyTTPGlyGlyAlaAlaPheAspGluAspAsnAla 180
DB 481 CTGCAAGACCTCTCTCACTTACGCGCTGGGCGCAGGCTGCTTTATATGAGCCAAATGCT 540
QY 181 LeuCysSerMetIleTTPGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200
DB 541 CTCTGCTCATATGATCGGGGGGCGACGCCCATGCTATCTCAGCGTGTGTCTTCTC 600
QY 201 ILeuValIleProLeuIleValIleMetIleAlaCysTyrSerValValPheCysAlaAlaArg 220
DB 601 ATCGTCAATTCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 221 ArgGlnHisAlaLeuLeuTyrAsnValLysArgHisSerLeuGlnValAlaArgValLysAsp 240
DB 661 AGGACACATGCTTGTCTGTAACATGTCACAGACACAGCTTGGAGAGTGCAGACGACGAC 720
QY 241 CysValGluAsnGluAspGluGluGlyAlaGluLysGluGluLysPheGlnAspGluSer 260
DB 721 TGTGTGAGATATGAGATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 261 GluPheArgArgGlnHisGluGlyGluValLysAlaLysGluGlyArgMetGluAlaLys 280
DB 781 GAGTTTCGCGCGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 281 AspGlySerLeuLysAlaLysGluGlySerThrGlyThrSerGluSerSerValGluAla 300
DB 841 GACGGCAGCCTGAGAGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
QY 301 ArgGlySerGluGluValArgLysSerSerThrValAlaSerAspGlySerMetGluGly 320
  
```

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DB 901 AGGGCGAGCAGAGAGGTTCAGAGAGAGCAGCAGCGTGGCCAGCGACGAGCATGAGGGGT 960
QY 321 LysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
DB 961 AAGGAAGGACGACCAAGATGAGGAGACAGCATGATGAAGGACAGACAGGCTCCACAGAG 1020
QY 341 ValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
DB 1021 GTCAACCAATGACAGCATTTGATGAGTGAAGATGATGATGATGATGATGATGATGATG 1080
QY 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProProSerArg 380
DB 1081 AATTCAGTGAAGATGACCTTCAGAGGAGGAGCATCCCGAGAGCCTCCACACGATCGT 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysLysAlaAlaLysVal 400
DB 1141 CGTAACGACAGACGACCACTCTCTGCGCAGAGTGTACAGTGCACAAAGCTCTAAAGTG 1200
QY 401 ILeuPheIleIlePheSerTyrValLeuSerLeuGlyProTyrCysPheLeuAlaVal 420
DB 1201 ATCTTCATCATCATTTTCTCTATGCTATCCCTGGGCGCTTACTGCTTTTACGAGTC 1260
QY 421 LeuAlaValTyrValAspValGluThrGlnValProGlnTyrValIleThrIleIle 440
DB 1261 CTGGCCGTGTGGGTGATGTCCAAACCCAGTACCCCAAGTGGGTATCACCATTAATCATC 1320
QY 441 TrrPhePhePheLeuGlnCysCysIleHisProTyrValTyrGlyTyrMetHisLysThr 460
DB 1321 TGGCTTTTCTTCTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
QY 461 ILeuLysGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysProProLys 480
DB 1381 ATTAAGAAAGAAATCCAGACATGCTGAAGAACTTCTTGCAGAGAAAAGCCCGGAAA 1440
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyLysIleValPro 500
DB 1441 GAAGATAGCCACCCAGACCTGCCCGGAAACAGAGGGTGAATGAAGCAAGATTGTCCCT 1500
QY 501 SerTyrAspSerAlaThrPhePro 508
DB 1501 TCTTACGATTCGTACTTCTTCTTCT 1524

RESULT 9
US-09-992-238-45
; Sequence 45, Application US/09992238
; Publication No. US2003005444A1
; GENERAL INFORMATION:
; APPLICANT: BATTAOLINO, PETER
; APPLICANT: FEDER, JOHN N
; APPLICANT: MINTIER, GABE
; APPLICANT: NELSON, THOMAS C
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: WESTPHAL, RYAN
; APPLICANT: CACACE, ANGELA
; APPLICANT: BARBER, LAUREN
; APPLICANT: HAWKEN, DONALD R
; APPLICANT: KORNAKNER, MICHAEL G
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY8,
; FILE REFERENCES: D0047NP
; CURRENT APPLICATION NUMBER: US/09/992,238
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/317166
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/308285
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/268581
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/248285
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patentin Ver. 2.1
  
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; SEQ ID NO 45
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-992-238-45

Alignment Scores:
Pred. No.:      8, 266-284      Length:      1527
Score:          2641.00        Matches:      507
Percent Similarity: 100.00%    Conserved:    1
Best Local Similarity: 99.80%   Mismatches:  0
Query Match:    99.89%        Indels:      0
DB:             3              Gaps:        0

US-10-712-615-2 (1-508) x US-09-992-238-45 (1-1527)

QY      1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
DB      1 ATGAGCGTCCACCTGCACCAACAGCAGCGCGGAGAGTAAACAGACGACGTCATGCC 60
QY      21 LeuSerLysMetProIleSerLeuAlaHisGlyIleIleArgSerThrValIleValIle 40
DB      61 CTCCTCAAAATGCCATACGCTGCGCCACGGGCATCATCCGCTCAACCTGCTGGTTATC 120
QY      41 PheLeuAlaAlaSerPheValGlyAsnIleValIleValIleValIleValIleValIle 60
DB      121 TTCCTCGCGCGCTCTTTCGTGCGCAACATAGTGTGGCGCTAGTGTTCGACGCGCAAG 180
QY      61 GluLeuLeuGlnValThrAsnArgPheIlePheAsnLeuValThrAspLeuGln 80
DB      181 CAGCTGCTGCAGGTGACCAACGGTTTATCTTAACTCTCGTACCGACCTGCTGCAG 240
QY      81 IleSerLeuValAlaProTyrValAlaAlaThrSerValProLeuPheTyrProLeuAsn 100
DB      241 ATTTGGCTCGTGGCCCCCGTGGGTGGTGCACCTCTGCTCTCTTCTGGCCCCCTCAAC 300
QY      101 SerHisPheCysThrAlaLeuValSerLeuThrHisIlePheAlaPheAlaSerValAsn 120
DB      301 AGCCACTTCTGCACGCGCTGTGTAGCCCTCACCCACTGTTCGCCCTTCCGCGCGTCAAC 360
QY      121 ThrIleValIleValSerValAsnArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
DB      361 ACCATTGTGCTGTGTCAGTGAATGCTACTGTTCATCATCACTCTCTCTCTCAACCCG 420
QY      141 SerLysMetThrGlnArgArgGlyTyrIleLeuLeuLeuTyrGlyThrTyrIleValAlaIle 160
DB      421 TCCAAAGATGACCAAGCGCGGGGTTACCTGCTCTTAAGGACCTGGATTGGGCATC 480
QY      161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlnAlaAlaPheAspGluArgAsnAla 180
DB      481 CTGCAGAGCACTCTCCACTCTTACGCGCTGGGGCCAGGCTGCTTGTATGAGCGCAATGCT 540
QY      181 LeuCysSerMetIleTyrGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200
DB      541 CTCTGCTCATATCTGGGGGGCGAGCCCAAGCTACATATCTCAAGCTGGTGTCTTC 600
QY      201 IleValIleProLeuIleValMetIleAlaCysTyrSerValValPheCysAlaAlaArg 220
DB      601 ATCGCATTTCCACTGATTTCTCATGATGCTGCTGCTACTCGGTGTCTCTGTCAGCCGG 660
QY      221 ArgGlnHisAlaLeuLeuTyrAsnValIleValArgHisSerLeuGlnValArgValIleAsp 240
DB      661 AGGCGAGCATGCTCTCTGTACAAATGTCAAGAGACACAGCTTGAAGTGGAGTCAAGGAC 720
QY      241 CysValGluAsnGluAspGluGluGlyAlaGluValIleValIleValIleValIleVal 260
DB      721 TGTGTGGAATGAGAGTAAAGAGGAGAGCAAGAAAGAGAGAGTTCAGAGATGAGAT 780
QY      261 GluPheArgArgGlnHisGluGlyGluValIleValIleValIleValIleValIleVal 280
DB      781 GAGTTTCCGCGCGCAGCATATGAAGTGAAGTCAAGGCCAAGAGAGGCGAATGGAAGCCAG 840
QY      281 AspGlySerLeuValAlaGluGlySerThrGlyThrSerGluSerSerValGluAla 300
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DB      841 GACGCGACCTGAGAGCCAGAGAGAGCAACGCGGAGACAGTGAAGATGTATAGCGCC 900
QY      301 ArgGlySerGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGly 320
DB      901 AGGGCAGCAGAGAGTTCAGAGAGAGCAGCAGCGTGGCCAGCGACGCAATGAGAGGT 960
QY      321 LysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
DB      961 AAGGAAGCAGACCAAAAGTTGAGGAACAAGCATGAAGGCAAGACAGAGGTGCACAG 1020
QY      341 ValIleGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
DB      1021 GTCAACCAAGTGCAGATTCAGTGGGTGAAGTGCATGATGAGTTTGGAAGACACATC 1080
QY      361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProSerArg 380
DB      1081 AATTTCAAGTGAAGATGAGTGAAGGACAGTGAACATCCCGAGAGCTTCCACCCAGTGT 1140
QY      381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysLysAlaAlaLysVal 400
DB      1141 CGTAAACAGCAACAGCAACCTCTCTGCGCAGGTGCTCAAGTGCAGAAAGCTGCTAAAGT 1200
QY      401 IlePheIleIleIlePheSerTyrValLeuSerLeuGlyProTyrCysPheLeuAlaVal 420
DB      1201 ATCTTCATCATCATTTTCTCTATGTGTATCCCTGGGGGCCCTTACTGCTTTTTCAGATC 1260
QY      421 LeuAlaValITrpValAspValGluThrGlnValProGlnTyrValIleThrIleIleIle 440
DB      1261 CTGGCCGTGTGGTGGATGTAAGTGAACCAAGGTAACCCAGTGGGTATATCACTAATC 1320
QY      441 TrpLeuPhePheLeuGlnCysCysIleHisProTyrValITyrGlyTyrMetHisLysThr 460
DB      1321 TGGCTTTTCTCTCTCAGAGTGCATCCACCCCTATGTCTATAGCTATATGCAAGAACC 1380
QY      461 IleLysLysGluIleGluAspMetLeuLysLysPhePheCysLysGluLysProLys 480
DB      1381 ATTAAGAAAGAAATCAGAGACATGTGAAGAAATTTCTCTGCAGAAAGAACCCCGGAA 1440
QY      481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyLysIleValPro 500
DB      1441 GAAATAGCCACCCAGACCTGCCGGAACAGAGGTGGACTGAAGGCAAGATTGTCCCT 1500
QY      501 SerTyrAspSerAlaThrPhePro 508
DB      1501 TCTACGATTTGCTACTTTTCTT 1524

RESULT 10
US-10-094-417-5
; Sequence 5, Application US/10094417
; Publication No. US20030045685A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiaqiang
; APPLICANT: Chen, Jin-long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030045685A1el Receptors
; FILE REFERENCE: 018781-008110US
; CURRENT FILING DATE: 2002-06-10
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/802,803
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR36
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FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1527)
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR36
US-10-094-417-5

Alignment Scores:
Pred. No.: 8,266-284 Length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: 5 Gaps: 0

US-10-712-615-2 (1-508) x US-10-094-417-5 (1-1527)

QY 1 MetThrSerThcCythrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
DB 1 ATGACGCTCACTCGACCAACGACGCGAGAGTAACAGACGACCAACGTCATGCCCC 60
QY 21 LeuSerIyMeCProIleSerLeuAlaHisGlyIleIleArgSerThrValIleuValIle 40
DB 61 CTCTCCAAATGCGCCATCAGCCTCGGCCACGCGATCATCCGTCMAACGTCGCTTATC 120
QY 41 PheLeuAlaIleSerPheValGlyAsnIleValIleuAlaIleuValIleuGlnArgIle 60
DB 121 TTCCTCGCGCCCTCTTCGCGCAACATATGTCGCGCTAGTGTGGACGCGCAAGCCG 180
QY 61 GlnLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAsnLeuGln 80
DB 181 CAGCTGCTCAGGTGACCAACGTTTATCTTTAACCTCTGTCACCACTGTCGACAG 240
QY 81 IleSerLeuValAlaProTrpValValAlaThrSerValProLeuPheTrpProLeuAsn 100
DB 241 ATTTCGCTGTGGCCCCCTGGGTGGTGGCCACTCTGTGCTCTTCTTGCCCCCTCAAC 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAan 120
DB 301 ACCCACTTGTGACGCGCCCTGTGATCCTCACCCACTGTTCCCTTCCGCGCAAGCTCAAC 360
QY 121 ThrIleValLeuValSerValAspArgTrpLeuSerIleIleHisProLeuSerTrpPro 140
DB 361 ACCATGTGTGTGTGTCAGTGTGATCGCTACTGTTCATCATCATCACTCTCTCAACCG 420
QY 141 SerIyMeCThrGlnArgArgIlyTrpLeuLeuLeuTrpGlyThrTrpIleValIle 160
DB 421 TCCAGATATACCCAGGCGCGGCTTACCTGCTCTCTATGCGACCTGGATTGGCGCATC 480
QY 161 LeuGlnSerThrProProLeuTrpGlyTrpGlyGlnAlaAlaPheAsnGluArgAsnAla 180
DB 481 CTGCAGAGACATCTCTCCACTCTACGCGCTGGGGCCAGGCTGCTTGTATGAGCGCATGT 540
QY 181 LeuCySerSerMetIleTrpGlyValAsnProSerTrpThrIleLeuSerValValSerPhe 200
DB 541 CTCTGTCTCATATCTGGGGGGGCGACCCCAAGTACATATCTCAGCGTGGTCTCTTC 600
QY 201 IleValIleProLeuIleValMetIleAlaCysTrpSerValValPheCysAlaIleArg 220
DB 601 ATCGCATTCCTCACTATTTCTATGATTCCTGCTCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 221 ArgGlnHisAlaLeuLeuTrpAsnValIlyAsnHisSerLeuGluValAlaArgValIlyAsp 240
DB 661 AGCGAGCATGCTCTGCTGTACAAATGTCAAGAGACACAGCTTGGAACTGGCAAGTCAAGAC 720
QY 241 CysValGluAsnGluAsnGluGluGluValIleGluIlyLysGluIleuPheGlnAsnGluSer 260
DB 721 TGTGTGAAATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 780
QY 261 GluPheArgArgGlnHisGluGluGluValIlyAlaIlyGlyGluIlyArgMetGluAlaIly 280
DB 781 GACTTTCGCGCGCACAGATGAGAGTGAAGTCAAGGCCAAGAGAGGAGGAGAGATGAGAGC 840
QY 281 AspGlySerLeuValIlyGluGluGluSerThrGlyThrSerGluSerSerValGluAla 300
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DB 841 GACGCGAGCTTGAAGGCCAAGAGAGAACACGCGGACCAAGTAGTGTAGAGGCC 900
QY 301 ArgGlySerGluGluValAlaArgIleSerThrValAlaSerAspIlySerMetGluGly 320
DB 901 AGGGCGACGAGAGAGGTTCAGAGAGACACACGCTGGCCACGCGACGACATGAGAGGT 960
QY 321 IySGluGlySerThrIlyValGluGluAsnSerMetIlyAlaAspIlyGlyArgTrpGlu 340
DB 961 AAGGAAGCAGCACCAAGTGTGAGGAACAGCATGAAGCAGAGACAAAGAGGTCCGACAGAG 1020
QY 341 ValAsnGlnCysSerIleAsnLeuGlyGluAsnAspMetGluPheGlyGluAsnAspIle 360
DB 1021 GTCAACACAGTGCAGCTTGTACTTGGGTGAAGATGACATGAGATGTGTGAAGCGCATC 1080
QY 361 AsnPheSerGluAsnAspValGluAlaValAlaAsnIleProGluSerLeuProProSerArg 380
DB 1081 AATTCAGTGAAGATGACCTCGAGCGATGAAACATCCGAGAGCTTCCACCCAGTCTGT 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTrpGlnCysIlyAlaIlyVal 400
DB 1141 CGTAACAGCAACAGCAACCTCTCTGCCAGGTGCTACCAATGCAAACTGCTAAAGTG 1200
QY 401 IlePheIleIleIlePheSerTrpValIleuSerLeuGlyProTrpCysPheLeuAlaVal 420
DB 1201 ATCTTCATCATATTTTCTCTATGTGTATGCTGCGGCGCTTACTGCTTTTATGACATC 1260
QY 421 LeuAlaValTrpValAspValGluTrpGlnValProGlnTrpValIleThrIleIle 440
DB 1261 CTGGCCGTGTGGTGTATGTCAAAACCAAGTACCCCACTGGGTGTATCCCAATATCATC 1320
QY 441 TrpLeuPhePheLeuGlnCysCysIleHisProTrpValTrpGlyTrpMetHisIlyThr 460
DB 1321 TGGCTTTTCTTCTCTGAGTGTGCATCCACCCCTATGTCTATGCGTACATGCAAGACC 1380
QY 461 IleIlyIlyGlnIleGlnAsnMetLeuIlyIlyPhePheCysIlyGluIlySerProIly 480
DB 1381 ATTAAGAAAGAAATCCAGGACATGTGAAGAGTCTTCTGCAAGAGAAAGCCCGGAAA 1440
QY 481 GluAsnSerHisProAsnLeuProGlyTrpGluGlyValThrGluGlyIlyValIlePro 500
DB 1441 GAAGATAGCACCAACCACTGCGCGGACAGAGGGTGGAGTGAAGGCAAGATTGTCCCT 1500
QY 501 SerTrpAspSerAlaThrPhePro 508
DB 1501 TCTTAGATTCTGTACTTCTTCT 1524

RESULT 11
US-10-225-567A-582
; Sequence 582, Application US/10225567A
; Publication No. US20030113798A1
GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Gleena C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 582
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-582

Alignment Scores:
Pred. No.: 8,266-284 Length: 1527
Score: 2641.00 Matches: 507
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Percent Similarity: 100.00%
Best Local Similarity: 99.80%
Query Match: 59.89%
DB: 5
Conservative: 1
Matches: 0
Indels: 0
Gaps: 0

US-10-712-615-2 (1-508) x US-10-225-567A-582 (1-1527)

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QY 1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
Db 1 ATGAGTGCACCTGCACCAACAGCAGCGCGAGAGTAACAGACAGCAGCAGCTGATGCC 60
QY 21 LeuSerIleMetProIleSerIleuAlaHisGlyIleIleArgSerThrValIleuValIle 40
Db 61 CTCTCAAAATGCTCATGACCTGGCCCAAGGACATCTCCGTCAACCGTGTGATATC 120
QY 41 PheLeuAlaAlaSerPheValGlyAsnIleValIleuAlaLeuValIleuGlnArgIlePro 60
Db 121 TTCCTCGCCGCTCTTTCGTGCGCAACATAGTGTGGCCCTAGTGTTCAGCGCAGCCG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspIleuGln 80
Db 181 CAGCTGTGACGAGTGACCAACCGTTTATCTTAACCTCTCGTCAACCGATGCTGAG 240
QY 81 ILeSerIleuValAlaProThrValAlaAlaThrSerValProLeuPheThrProLeuAsn 100
Db 241 ATTGCTGCTGCGCCCTGGGTGGTGGCCACTGTGTGCTCTCTTCTGCGCCCTCAAC 300
QY 101 SerHisPheCysThrAlaLeuValSerIleuThrHisLeuPheAlaPheAlaSerValAsn 120
Db 301 AGCCACTTGTGACGCGCCCTGTGTAGCTCAACCACTGTTGCGCTTCCGCGCCCTCAAC 360
QY 121 ThrIleValIleuValSerValAsnArgIleuSerIleIleHisProLeuSerIlePro 140
Db 361 ACCATTGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 141 SerIleMetThrGlnArgArgIleuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 160
Db 421 TCCAGATGACCCAGCGCGCGGTACCTGCTCTCTTAAGGACCTGAGTGTGCGCCATC 480
QY 161 LeuGlnSerThrProProLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 180
Db 481 CTGCGAGACACTCTCTCACTCAAGGCTGGCGCCAGCGCTTTGATGAGCGCATGCT 540
QY 181 LeuCysSerMetIleIleProGlyValAsnProSerIleuIleuLeuSerValIleSerPhe 200
Db 541 CTCTCTCATGATCTGTGGGCGCCAGCCCACTCACTATCTCAAGCTGTGTGCTCTC 600
QY 201 ILeValIleProLeuIleValMetIleAlaCysIleuSerValValPheValAlaAlaArg 220
Db 601 ATCGCATTCACCTGATGTCATGATGCTGCTCACTCCGTGTGTCTGTGTCACCCGG 660
QY 221 ArgGlnHisAlaLeuLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 240
Db 661 AGCGAGCATGCTCTCTCTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 720
QY 241 CysValGluAsnGluAsnGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 260
Db 721 TGTGTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 261 GluPheArgArgGlnHisGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 280
Db 781 GAGTTTCCCGCCAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 281 AspGlySerIleuValAlaValGluGluGluGluGluGluGluGluGluGluGluGluGlu 300
Db 841 GACGCGACGCTCAAGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 301 ArgGlySerGluGluValArgIleuSerThrValAlaSerAspGlySerMetGluGly 320
Db 901 AGGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 321 LysGluGlySerThrIleValGluGluGluGluGluGluGluGluGluGluGluGluGlu 340
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Db 961 AAGGAGGACAGCACCAAGTTGAGAGAAACGATGAAGGCGAGACAGGTCACAGAG 1020
QY 341 ValAsnGlnCysSerIleAspLeuGlyGluAsnAspMetGluPheGlyGluAspAspIle 360
Db 1021 GTCAACCAAGTCAGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 361 AsnPheSerGluAspAspValGluValAlaAsnIleProGluSerIleuProProSerArg 380
Db 1081 AATTCACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysIleuGlnCysIleuValAlaVal 400
Db 1141 GCTAACACCAACAGCAACCTCTCTGCGCGAGTGTCTTCCAGTGTCAAAAGCTGTAAAGTG 1200
QY 401 ILePheIleIleIlePheSerThrValIleuSerIleuGlyProIleCysPheLeuAlaVal 420
Db 1201 ATCTTCATCATCATTTCTCTTATGTGTATCCCTGGGGGCTTACTGCTTTTATGCACTC 1260
QY 421 LeuAlaValIleProValAspValGluThrGlnValProGlnIleProValIleThrIleIle 440
Db 1261 CTGGCCGTGTGGTGTGATGTGAAACCCAGGTACCCCGAGTGTGATCATCATATATCATC 1320
QY 441 ThrLeuPhePheLeuGlnCysCysIleHisProIleuValIleuIleuIleuIleuIleu 460
Db 1321 TGCTTTCTCTCTGCACTGCTGATCCACCTCTATGCTATGCTATGCTATGCTATGCTATG 1380
QY 461 ILeuIleuGluIleGlnAsnMetLeuIleuIleuIleuIleuIleuIleuIleuIleuIleu 480
Db 1381 ATTAAGAAGAAATCCAGACATGCTGAAAGAAATTTCTTCTCAAGAAACCCCGGAAA 1440
QY 481 GluAspSerHisProAspLeuProGlyIleuGluGlyIleuIleuIleuIleuIleuIleu 500
Db 1441 GAAGATACCAACCAAGACCTTCCCGGAAACAGAGGTGTGATGATGATGATGATGATG 1500
QY 501 SerIleAspSerAlaThrPhePro 508
Db 1501 TCTTACGATTTCTGCTACTTTTCT 1524
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RESULT 12

US-10-345-332-1

/ Sequence 1, Application US/10345332

/ Publication No. US20030129705A1

/ GENERAL INFORMATION:

/ APPLICANT: Li et al.

/ TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

/ TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR

/ TITLE OF INVENTION: PROTEINS, AND USES THEREOF

/ FILE REFERENCE: C1000754CON

/ CURRENT APPLICATION NUMBER: US/10/345,332

/ PRIOR FILING DATE: 2003-01-16

/ PRIOR APPLICATION NUMBER: 09/769,741

/ PRIOR FILING DATE: 2001-01-26

/ PRIOR APPLICATION NUMBER: 60/205,166

/ PRIOR FILING DATE: 2000-05-18

/ PRIOR APPLICATION NUMBER: 09/638,018

/ PRIOR FILING DATE: 2000-04-14

/ NUMBER OF SEQ ID NOS: 7

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 1

/ LENGTH: 1527

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-10-345-332-1

Alignment Scores:

Pred. No.: 8,266-284 Length: 1527

Score: 2641.00 Matches: 507

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 99.80% Matches: 0

Query Match: 99.89% Indels: 0

DB: 6 Gaps: 0

US-10-712-615-2 (1-508) x US-10-345-332-1 (1-1527)

QY 1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
Db 1 ATGAGCTCCACCGCGACCAACGCGGAGAGTAAAGAGCCACGTCAGTCCG 60
QY 21 LeuSerLysMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
Db 61 CTCTCCAAATGCGCATCAGCTCGGCCCGGCATCATCGCTCAACCGGTGGTTATC 120
QY 41 PheLeuAlaIleSerPheValIleGlyAsnIleValLeuAlaLeuValLeuGlnArgLysPro 60
Db 121 TTCTGCGCGCTCTTTCGTGGCAACATAGTCTGCGTACGTGTGACGCCCAAGCCG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeuGln 80
Db 181 CAGCTGCTGAGGTGACCAACGTTTATCTTTTAACTCTCTGTCACCGACCTGCTGAG 240
QY 81 IleSerLeuValAlaProTrpValValAlaThrSerValProLeuPheTrpProLeuAsn 100
Db 241 ATTTCCGCTGTGCGCCCTGGTGGTGGCCACCTCTGCTCTCTTCTGGCCCTCAAC 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
Db 301 AGCCACTTCTGACGCGCCCTGTAGCTTACCCACCTGTTGCTTCCGACCGTCAAC 360
QY 121 ThrIleValIleLeuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
Db 361 ACCATTGTGTGTGTGTGAGTATCGCTACTTCTCATCATCACTCTCTCTCTCAACCG 420
QY 141 SerLysMetThrGlnArgArgIlyTyrLeuLeuLeuTyrGlyThrTrpIleValAlaIle 160
Db 421 TCCAAAGATGACCCAGCGCGCGGTACCTGCTCTCATGAGCACTGAGATTGGGCATC 480
QY 161 LeuGlnSerThrProProLeuTyrGlyTyrTrpGlyGlnAlaAlaPheAspGluAsnGlnAla 180
Db 481 CTGCACAGACCTCTCACTCACTAGCGCTGGGCGCAGCGCTGCTTTATGAGCCCAATGCT 540
QY 181 LeuCysSerMetIleTrpGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200
Db 541 CTCTGCTCATGATCTGGGGGGCGACGCCACGCTACATCTTCAACGCGTGTCTTC 600
QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerValValPheCysAlaAlaArg 220
Db 601 ATCGTCAATTCACATGATTCATGATGCTGCTGCTACCTCGGTGTCTGTGACGCCGG 660
QY 221 ArgGlnHisAlaLeuLeuTyrAsnValLysArgHisSerLeuGlnValArgValLysAsp 240
Db 661 AGGCACACATGCTTGTGTAACAATGTCACAGACACAGCTTGAAGTCAAGACGAC 720
QY 241 CysValGluAsnGluAspGluGluGlyAlaGluLysLysGluLysPheGlnAspGluSer 260
Db 721 TGTGTGAAGATAGATGAGAGGAGGACGACGACGACGACGAGAGGAGGAGTCCGAGTGAAGT 780
QY 261 GluPheArgArgGlnHisGluGlyGluValLysAlaLysGluLysArgMetGluAlaLys 280
Db 781 GAGTTTCCGCGCAGCATGAGGTGAGTCAAGGCCAAGGAGGAGGAGGAGGAGGAGGAG 840
QY 281 AspGlySerLeuLysAlaLysGluGlySerThrGlyThrSerGluSerSerValGluAla 300
Db 841 GAGGAGAGCTGAGAGCCAGAGAGAGACGAGGAGCAGTGAAGTGAAGAGGCC 900
QY 301 ArgGluSerGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGly 320
Db 901 AGGGGACGACGAGAGGTCAAGAGACGACGACGAGTCCGACGACGACGACGAGGAGT 960
QY 321 LysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
Db 961 AAGGAGGAGGAGCAACAAGTTGAGAGACAGCATGAGGACAGCAAGGTTCCACAGAG 1020
QY 341 ValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
Db 1021 GTCAACCAAGTGAAGCATTAAGTGGGTGAAGATGACATGAGTTGTGTAAGACGACATC 1080

QY 361 AsnPheSerGluAspAspValGluValAlaAlaIleProGluSerLeuProProSerArg 380
Db 1081 AATTTCAGTGAAGATGACCTGAGGACGATGAGACATCCCGAGAGGCTCCACCACTCGT 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProAlaGlyGlyTrpGlnCysLysValAlaLysVal 400
Db 1141 CGTAACAGACAGCAACCTCTCTGCGCAGAGTGTACAGATGCAACCTCTAAAGTG 1200
QY 401 IlePheIleIleIlePheSerTyrValIleSerLeuGlyProTyrCysPheLeuAlaVal 420
Db 1201 ATCTTCATCATCATTTTCTCTATGTGCTATGCTCTGAGGACCTTACTGCTTTTATGACATC 1260
QY 421 LeuAlaValTrpValAspValGluThrGlnValProGlnTrpValIleThrIleIleIle 440
Db 1261 CTGGCCGTGTGGGTGATGTCCAAACCCAGTACCACCACTGGGTATCACTAATATCATC 1320
QY 441 TrpLeuPhePheLeuGlnCysCysIleHisProTyrValTyrGlyTyrMetHisLysThr 460
Db 1321 TGGCTTTTCTCTGAGTGTGATCCACCTCTATGTCTATGCTTACATGACAAAGACC 1380
QY 461 IleLysLysGluIleGluAspMetLeuLysLysPhePheCysLysGluLysProProLys 480
Db 1381 ATTAGACAGAAATCCAGACATGCTGAGAAAGTTCTTCTGACAGAAAGCCCGGAA 1440
QY 481 GluAspSerHisProAspPheProGlyThrGluGlyGlyThrGluGlyLysIleValPro 500
Db 1441 GAAAGATAGCCACCAAGACCTGCGCGGAAACAGAGGGGTGGAGCTGAAGGCAAGATTGTCCCT 1500
QY 501 SerTyrAspSerAlaThrPhePro 508
Db 1501 TCTACGATTCGTACTTTCCT 1524

RESULT 13
US-10-321-807-15
; Sequence 15, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Rungong
; APPLICANT: Dang, Hong T.
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; PRIORITY FILING DATE: 2002-12-15
; PRIOR APPLICATION NUMBER: US/09/714,008
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 15
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-321-807-15

US-10-712-615-2 (1-508) x US-10-276-243-2 (1-1527)

QY 1 MetThSerThrCythraSensThraArgLuserAsnSerSerHisThrCysMetPro 20
Db 1 ATGACGTCACCTCGACCAACAGACGCGGAGAGTAAAGCAACGACGACGATGCCCC 60

QY 21 LeuSerLyMetProIleSerLeuAlaHisGlyIleIleArgSerThrValIleValIle 40
Db 61 CTCCTCAAAATGCGCATCAGCTCGGCCACGGCATCATCCGCTCAACCGCTGGTTATC 120

QY 41 PheLeuAlaIleSerPheValGlyAsnIleValIleValIleValIleValIleValIle 60
Db 121 TTCCTGCGCGCTCTTTCGTCGCAACATAGTCTGCGCTAGGTTGTCAGCCCAAGCCG 180

QY 61 GluLeuLeuGlnValThrAsnArgPheIlePheAsnLeuValThrAspLeuLeuGln 80
Db 181 CAGCTGCTGCAAGGTGACCAACGTTTATCTTTAACTCTCGTACCGACCTGCTGCGAG 240

QY 81 IleSerLeuValAlaProTTPValValAlaIleThrSerValProLeuPheTTPProLeuAsn 100
Db 241 ATTTCCGTCGTGCGCCCTGCTGGTGGTGGCCACCTCTGCTGCTCTTCTGCGCCCTCAAC 300

QY 101 SerHisPheCythraIleLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
Db 301 AGCAGCTTCTGACGCGCCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360

QY 121 ThrIleValIleValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
Db 361 ACCATTGCTGTGTGTCAGTGGATCGCTACTTGTCCATCATCACTCTCTCTCTTACCCG 420

QY 141 SerLyMetThrGlnArgArgIlyTyrLeuLeuLeuTyrGlyThrTTPIleValAlaIle 160
Db 421 TCCAAAGATGACCCAGCGCGCGGTGTAAGTCTCTCTCTATGACGACCTGGATTTGGCCATC 480

QY 161 LeuGlnSerThrProProLeuTyrGlyTTPGlyGlnAlaIlePheAspGlnAsnAla 180
Db 481 CTGCAAGACATCTCTCACTCTCACTGCGGTGGGCGCGGTGGTGGTGGTGGTGGTGGTGG 540

QY 181 LeuCySerMetIleTTPGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200
Db 541 CTCGCTCCATGATCTGGGGGGCCAGCCCAAGCTACCTATTTCTCAGCGTGGTGGTGGTGG 600

QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerValIlePheCysAlaIleArg 220
Db 601 ATCGTCACTTCACTGATGTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

QY 221 ArgGlnHisAlaLeuLeuTyrAsnValIleArgHisSerLeuGlnValIleArgValIleAsp 240
Db 661 AGGCACATGCTCTGCTGTAACAATGTCMAAGACACACGCTTGGAAAGTGCAGATCAAGGAC 720

QY 241 CysValGluAsnGluAspGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 260
Db 721 TGTGTGAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAG 780

QY 261 GluPheArgArgGlnHisGluGluGluValIleAlaIleArgGluGluValIleArgMetGluAlaIle 280
Db 781 GAGTTTCGCGCCAGCATGAGATGAGTCAAGGCCAAGAGGCGCAAGATGAGAACCAAGCAAG 840

QY 281 AspGlySerLeuValAlaIleGluGluGluGluGluGluGluGluGluGluGluGluGlu 300
Db 841 GACGCGAGCTCTGAAGGCAAG 900

QY 301 ArgGlySerGluGluValIleArgGluGluGluGluGluGluGluGluGluGluGluGluGlu 320
Db 901 AGGGGAGCGAGAGAGGTCAG 960

QY 321 LySGluGlySerThrLySValIleGluGluAsnSerMetLySAlaAspLySGlyArgThrGlu 340
Db 961 AAGGAAGGAGAGCAAAAGTTTGAAGAGACAGCATGAGAGAGAGAGAGAGAGAGAGAGAG 1020

QY 341 ValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
Db 1021 GTCAACCAAGTGCAGCATGACTTGGGTGAAGATGACATGAGATTGGTGAAGACGACATC 1080

QY 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProProSerArg 380
Db 1081 AATTTCAGTAGAGATACGTCAGAGCAGTAGAACATCCCGAAGAGCTCCCAACCAAGTCGT 1140

QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysAlaIleValIleVal 400
Db 1141 CGTAAACAGAACAGCAACCTCTCTGCGCAGGTGTACAGTGAAGACGCTGTAAGAGT 1200

QY 401 IlePheIleIleIlePheSerTyrValIleSerLeuGlyProTyrCysPheLeuAlaVal 420
Db 1201 ATCTTATATCATTTTCTCTATGTGCTATCCCTGGGCCCTTACTGCTTTTAAAGAGTC 1260

QY 421 LeuAlaValTTPValAspValGluThrGlnValProGlnTTPValIleThrIleIleIle 440
Db 1261 CTGGCGGTGTGGTGGATGTCCGAACCCAGTACCCCAATGGGTATACCAATATCATC 1320

QY 441 TTPLeuPhePheLeuGlnCysCysIleHisProTyrValIleTyrGlyTyrMetHisLyThr 460
Db 1321 TGGCTTTTCTTCTCTGACGTGTGCATCCACCCCTATGTCTATGGCTAATGACAAAGACC 1380

QY 461 IleLyLyGluIleGlnAspMetLeuLySerPhePheCysGlyGluLySProProLyS 480
Db 1381 ATTAAAGAGAAATCCAGACATGTGAAGAAATTCTTGTCAAGGAAAGCCCGGAAA 1440

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Db 1441 GAAGATAGCACCAACCAACCTGCCGGAACAGAGGTGGAGATGAAAGCAAGATTGCCCT 1500

QY 501 SerTyrAspSerAlaThrPhePro 508
Db 1501 TCCTACGATTCGCTACTTTTCT 1524

RESULT 15
US-10-436-715-13
; Sequence 13, Application US/10436715
; Publication No. US20040018976A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,
; TITLE OF INVENTION: AND SPLICER VARIANTS THEREOF
; FILE REFERENCE: D0262 NP
; CURRENT APPLICATION NUMBER: US/10/436, 715
; CURRENT FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: U.S. 60/380, 336
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; LOCATION: (1)..(1524)
US-10-436-715-13

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US-10-712-615-2 (1-508) x US-10-436-715-13 (1-1527)

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 Qy 41 PheLeuAlaIaIaSerPheValGlyAsnIleValIleuAlaLeuValIleuGlnArgIysPro 60
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 Qy 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuValThrAspLeuGln 80
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 Qy 201 IleValIleProLeuIleValMetIleAlaCysTyrSerSerValIlePheCysAlaAlaArg 220
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 Qy 241 CysValGlnAsnGlnAspGlnGlnGlyAlaGlnIlyIlyIlyIlyIlyIlyIlyIlyIly 260
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 Qy 341 ValAsnGlnCysSerIleAspLeuGlyIlyAspAspMetGlnPheGlyIlyAspAspIle 360
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 Qy 481 GluAspSerHisProAspLeuProGlyThrGlnGlnIlyIlyIlyIlyIlyIlyIlyIlyIly 500
 Db 1441 GAAGATAGCCACCCAGACCTGCCGGAACAGAGGTGGAGCTGAAGGCAAGATTTGCTCT 1500
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 Db 1501 TCTTACGATTCGCTACTTTTCT 1524

Search completed: December 10, 2005, 09:27:58
 Job time : 817 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 10, 2005, 07:45:15 ; Search time 150 Seconds
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1266.111 Million cell updates/sec

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Delop 6.0 , Delext 7.0

Searched: 3392430 segs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
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-THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0
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Database : Published Applications NA_New:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	210	7.9	1658	7	US-11-170-153-1
7	210	7.9	1658	7	US-11-170-153-3
8	204.5	7.7	1059	7	US-11-068-686-19

9	202.5	7.7	1410	6	US-10-992-577-1	Sequence 1, Appl1
10	198	7.5	1334	6	US-10-992-577-43	Sequence 43, Appl1
11	197.5	7.5	1260	7	US-11-067-884-7	Sequence 7, Appl1
12	196	7.4	1594	7	US-11-170-153-9	Sequence 9, Appl1
13	196	7.4	1594	7	US-11-170-153-11	Sequence 11, Appl1
14	194.5	7.4	3383	7	US-11-068-686-1	Sequence 1, Appl1
15	190.5	7.2	1977	6	US-10-750-185-35938	Sequence 35938, A
16	186.5	7.1	1915	7	US-11-068-686-3	Sequence 3, Appl1
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19	181	6.8	1685	6	US-10-750-185-36071	Sequence 36071, A
20	180.5	6.8	1435	6	US-10-750-185-26145	Sequence 26145, A
21	175.5	6.6	1293	6	US-10-992-577-7	Sequence 7, Appl1
22	175.5	6.6	1302	6	US-10-992-577-5	Sequence 5, Appl1
23	175.5	6.6	1936	6	US-10-510-018-1	Sequence 1, Appl1
24	175	6.6	1834	6	US-10-627-633-1	Sequence 1, Appl1
25	173	6.5	1376	6	US-10-627-633-3	Sequence 3, Appl1
26	172	6.5	246960	7	US-11-121-086-8	Sequence 8, Appl1
27	171.5	6.5	1225	6	US-10-955-054A-112	Sequence 112, App
28	171.5	6.5	8747	6	US-10-955-054A-141	Sequence 141, App
29	170.5	6.4	1102	6	US-10-955-054A-121	Sequence 121, App
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34	164.5	6.2	1888	7	US-11-080-991-25	Sequence 25, Appl1
35	164	6.2	1965	6	US-10-980-388-57	Sequence 57, Appl1
36	163.5	6.2	1031	6	US-10-980-388-58	Sequence 58, Appl1
37	156	5.9	2146	6	US-10-750-185-35936	Sequence 35936, A
38	154.5	5.8	193084	7	US-11-121-086-82	Sequence 82, Appl1
39	153.5	5.8	653	6	US-10-750-185-39564	Sequence 39564, A
40	148.5	5.6	2613	6	US-10-750-185-39572	Sequence 39572, A
41	148	5.6	987	7	US-11-155-595-1	Sequence 1, Appl1
42	147	5.6	1089	7	US-11-110-274-2	Sequence 2, Appl1
43	146	5.5	1309	6	US-10-750-185-50916	Sequence 50916, A
44	145.5	5.5	857	6	US-10-750-185-35457	Sequence 35457, A
45	144	5.4	1776	6	US-10-851-667A-25	Sequence 25, Appl1

ALIGNMENTS

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US-10-980-388-52
; Sequence 52, Application US/10980388
; Publication No. US20050255450A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325 US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369

;; PRIOR FILING DATE: 2000-07-11
;; PRIOR APPLICATION NUMBER: 60/217,370
;; PRIOR FILING DATE: 2000-07-11
;; PRIOR APPLICATION NUMBER: 60/218,492
;; PRIOR FILING DATE: 2000-07-20
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 184
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO: 52
;; LENGTH: 1527
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-980-388-52

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Pred. No.: 3,886-270 Length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: 6 Gaps: 0

US-10-712-615-2 (1-508) x US-10-980-388-52 (1-1527)

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Db 121 TTCCTCGCGCGCTCTTGTGTCGCAACATAGTGTGGCGCTAGTGTGACGGCAAGCCG 180
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Db 841 GACGCGACCTGAAGGCGCAAGAAAGAGCAACGCGGAGCAAGTGAAGTGTAGAGGCC 900
QY 301 ArgGlySerGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGly 320
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; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayes, Paul S.
; APPLICANT: Rufe, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325, US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; PRIOR FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932


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; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
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; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-980-388-8

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Db 145 ATGACCTCCACCTGACCAACACGCGAGAGTAACGACCAACGTCATGCC 204
QY 21 LeuSerLyMePProIleSerLeuAlaHISGLYIleIleArGSerThrValLeuVal 40
Db 205 CTCTCCAAATGCGCATTCAGCCGCGCCACGCGCATATCGCTCAACCGTGGTTATC 264
QY 41 PheLeuAlaIleSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLysPro 60
Db 265 TTCCTCGCGCGCTCTTTCGTCGCAACATAGTGTGCGCTAGTGTGCGCGCAAGCCG 324
QY 61 GlnLeuGlnValThrAnArgPheIlePheAsnLeuValThrAspLeuGln 80
Db 325 CAGCGCTCAGGTGACCAACCGTTTATCTTTAACTCTCTGTCACCGACCTGTCGAG 384
QY 81 IleSerLeuValAlaProTrpValValAlaThrSerValProLeuPheTrpProLeuAsn 100
Db 385 ATTTCCTGTGTCGCGCGCTGCGGTGCGGACCTCTGTGCTCTTTCGCGCGCTCAAC 444
QY 101 SerHisPheCySerThAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
Db 445 AGCACAATTGTGACGCGCGCTGTTAGCTTACCAACCACTGTTCCCTTCGCGCAAGCTCAAC 504
QY 121 ThrIleValLeuValSerValAspArgTrpLeuSerIleIleHisProLeuSerTrpPro 140
Db 505 ACCATTGTGTGTGTGTCAGTGATGCTACTTGTCCATCATCATCACTCTTCTTACCCG 564
QY 141 SerLyMetThGlnArgArgGlyTrpLeuLeuLeuTrpGlyThrTrpIleVal 158
Db 565 TCCAAATATACCAAGCGCGCGGTACTGCTCTATGACCACTGGATTGG 618

RESULT 3
US-11-170-153-5
; Sequence 5, Application US/1170153
```

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; Publication No. US20050266529A1
; GENERAL INFORMATION:
; APPLICANT: DELERSNIJDER, WILLY
; APPLICANT: WESP, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: LOKEN, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(1299)
; OTHER INFORMATION: IGS4B long version
US-11-170-153-5

Alignment Scores:
Pred. No.: 2.54e-12 Length: 1658
Score: 216.00 Matches: 99
Percent Similarity: 33.73% Conservative: 73
Best Local Similarity: 19.41% Mismatches: 133
Query Match: 8.17% Indels: 206
DB: 7 Gaps: 16

US-10-712-615-2 (1-508) x US-11-170-153-5 (1-1658)

QY 7 AenSerThrArgGlu-----SerAsnSerSerhThrCysMet 19
Db 133 AACAGACCGAGAGATGTCGCTTCTCTGCGACCTGCGGACCACTTCTTCCTC 192
QY 20 ProLeuSerLyMePProIleSerLeuAlaHISGLYIleIleArGSerThrValLeuVal 39
Db 193 CCGGTG-----TCTGTGGTATGTG 213
QY 40 IlePheLeuAlaIleSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLys 59
Db 214 CCAATTTTGTGTGGGGGTGATGCGCAATGTCTGTGCTGTGTATTCGACGAC 273
QY 60 ProGlnLeuGlnValThrAnArgPheIlePheAsnLeuValThrAspLeu 79
Db 274 CAGGCTATGAAGACCGCCCAACATACTACTTCAAGCTGCGGCTGTGACCTCTG 333
QY 80 GlnIle-SerLeuValAlaProTrp-----ValValAlaThrSerValProLe 95
Db 334 GTTCGTCTCTTGGATGCGCTGAGGTCTATGAGATGTGCGCAACTACCTTTC- 392
QY 95 UpheTrpProLeuAnSerhPheCySerThAlaLeuValSerLeuThrHisLeuPheAl 115
Db 393 GTTCGGCGCGGTGCTGTACTTCAAGCGCGCTCTTTGAGACCGTG-----TG 443
QY 115 ApeAlaSerValAsnThrIleValLeuValSerValAspArgTrpLeuSerIleIleH 135
Db 444 CTTCGCTCATCTTCAGCATCACCACGCTGACGCGGTGAGCCCTAGTGGCCATCTACA 503
QY 135 sProLeuSerTrpProSerLyMeThGlnArgArgGlyTrpLeuLeuLeuTrpGlyH 155
Db 504 CCGCTTCGCGCCAAATGTCAGAGACCGCGCGCGCGCTCAGAGATCTCGGACATCGT 563
QY 155 rTrpIleValAlaIleLeuGlnSerThrPro-----ProLeuTrpGly----- 169
Db 564 CTGGGCTTCTCGGTCTTCTTCTCCCTGCGCAACACAGCATCATGATGATCAAGTTCCA 623
QY 170 ----TrpGlyAlaIleAlaPheAspGluArgAsnAlaLeuCySerMetIleTrpGlyAl 188
DB: 11 Indels: 11 Gaps: 11
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Db 624 CTACTTCCCAATGGGTCCCTGGTCCCAAGTTCCGACCTTACGGTCAATC----- 675
Qy 188 aSerProSerTyrrhr-----IleuSerVal1SerPhele-----Val11 203
Db 676 -AAGCCCAATGGTGAATTCATATTCATATTCACAGGACCTCTTCTTATTCATCTCTCT 734
Qy 203 eProleuIleValMetIleValCysTyTserValValPheCysAlaAlaArgGlnHi 223
Db 735 CCCCATGACTGCTCATCAGTCTCTCTAC----- 762
Qy 223 bAlaIleuTyrrAanVal1LyArgHisSerIleuGluValArgVal1LyAAspCysValG1 243
Db 763 -----TACTCTATGGCAGCTCAAGCTTAAG----- 786
Qy 243 uAAspGluAAspGluGluGluVal1GluLysGluGluArgMetGluAlaLyAAspGlySe 263
Db 786 ----- 786
Qy 263 gArgGlnHisGluGluGluVal1LysGluGluArgMetGluAlaLyAAspGlySe 283
Db 787 -----AAAGACAAATC 797
Qy 283 rIleuVal1AlaLyGluGluGluSerThrGlyThrSerGluSerSerVal1GluAlaArgGlySe 303
Db 798 TCTTGAAGGCAATGAAAGGAAT----- 819
Qy 303 rGluGluVal1ArgGluSerSerThrVal1AlaSerAAspGlySerMetGluGlyLyGluG1 323
Db 819 ----- 819
Qy 323 ySerThrLySVal1GluGluAAspSerMetLysAlaAAspLyGlyArgThrGluVal1AAspG1 343
Db 819 ----- 819
Qy 343 nCySerIleAAspLeuGlyGluAAspAAspMetGluPheGlyGluAAspAAspIleAAspPheSe 363
Db 819 ----- 819
Qy 363 rGluAAspAAspVal1GluAlaVal1AAsp1IleProGluSerLeuProProSerArgArgAAspSe 383
Db 820 -----GCAATATATTCAAAGA-----CCCTGAGAAATAATCACT 851
Qy 383 rAAspSerAAspProProleuProArgCysTyTglnCysVal1AlaAlaLySVal1IlePhe11 403
Db 852 CAAC-----AAGATCCTGTTTGT 869
Qy 403 eIleIlePheSerTyrrVal1LeuSerIleuGlyProTyrr-----CysPheLeuAl 419
Db 870 CTGGTCTTAGTGTTCATATCTGTGGGCCCCGTTCCACATTCAGCAGACTCTTCTTCAG 929
Qy 419 aVal1leuAlaVal1TrpVal1AAspVal1GluThrGlnVal1ProGlnTrpVal1IleThrIle11 439
Db 920 CTTCGTGGAGAGCTGAGTGAATCCCTGGCTGCTGTTCAACCTGTCATGATGCTGCTG 989
Qy 439 eIleIlePhePhePheLeuGlnCysCysAl1eHisProTyrrVal1TyrrGlyTyrrMetHisLy 459
Db 990 AGGTCTCTTATTCATCTGAGCTCAGCTGTCAACCCCATTAATCACTACTGCTG 1049
Qy 459 sThrIleLySVal1GluGluAAspMetLysLySVal1PheCysVal1GluLyProBr 479
Db 1050 CCGCTTCCAGGAGCATTCACAAATGATGATCTTCTTTC-----CACAAACAGTG 1100
Qy 479 oLySVal1AAspSerHisProAAspLeuPro 488
Db 1101 GCATCTCCAGCATGACCCACATTCGCA 1128

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RESULT 4

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US-11-170-153-7
; Sequence 7, Application US/11170153
; Publication No. US2005026529A1
; GENERAL INFORMATION:
; APPLICANT: DELERSNIJDER, WILLY
; APPLICANT: WEESP, GUY NYS

```

```

; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: LOKEN, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170.153
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088.744
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO: 7
; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(1299)
; OTHER INFORMATION: IGS4B short version
US-11-170-153-7

```

Alignment Scores:

```

Pred. No.: 2,54e-12 Length: 1658
Score: 216.00 Matches: 99
Percent Similarity: 33.73% Conservative: 73
Best Local Similarity: 19.41% Mismatches: 133
Query Match: 8.17% Indels: 206
DB: 7 Gaps: 16

```

US-10-712-615-2 (1-508) x US-11-170-153-7 (1-1658)

```

Qy 7 AAspSerThrArgGlu-----SerAAspSerHisThrCysMet 19
Db 133 AAACAGCACGAGAGATATCTGACCTTCTGCGAGCTCGCGAGCCAGCCACTTCTCTC 192
Qy 20 ProleuSerLySMetProIleSerIleuAlaHisGlyIleIleAAspSerThrVal1leuVal 39
Db 193 CCCGTG-----TCGTGATGATG 213
Qy 40 IlePheLeuAlaAAspPheVal1GlyAAspIleVal1leuAlaLeuVal1leuGlnArgLyS 59
Db 214 CCAATTTTGTGGTGGGGGTATTCGCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 273
Qy 60 ProGlnLeuGlnVal1ThrAAspArgPheIlePheAAspLeuVal1ThrAAspLeu 79
Db 274 CAGGTATGAGAGAGCCACCAACTACTGCTTCAAGCTGCGGCTGCTGCTGCTGCTGCTG 333
Qy 80 GlnIle-SerIleuVal1AAspTrp-----ValVal1AAspSerVal1Prole 95
Db 334 GTCTGCTCTTGGAAATGCCCTGAGGTCTATGATGATGATGATGATGATGATGATGATG 392
Qy 95 uPheTrpProleuAAspSerHisPheCysThrAlaLeuVal1SerIleuThrHisIleuPheAl 115
Db 393 GTTCGGGCGCTGGGCTCTTCTTCAAGAGCGGCTCTTTCAGACCGTG-----TG 443
Qy 115 aPheAlaSerVal1AAspThrIleVal1leuVal1SerVal1AAspArgTyrrIleuSerIleIle11 135
Db 444 CTTCGCTCTCAATCCATCAGCATCAACCGTACAGGTGAGGCTGACGAGGCTGCTGCA 503
Qy 135 sProleuSerTyrrProSerLySMetThrGlnArgArgGlyTyrrIleuLeuTyrrGlyTh 155
Db 504 CCCGTTCGCGCAAACTGACAGACACCGCGCGCGGCTCCAGAGATCTTCGAGATCGT 563
Qy 155 rTrpIleVal1AlaIleuGlnSerThrPro-----ProleuTyrrGly----- 169
Db 564 CTGGGGCTTCTCGGCTCTTCTCTCCCTGCGCAACACGATTCATGAGCAATCAAGTTCCA 623
Qy 170 -----TrpGlyGlnAlaAAspAAspGluArgAAspAlaLeuCysSerMetIleTrpGlyAl 188
Db 624 CTACTTCCCAATGGGTCCCTGATCCAGGTTCCGAGCTGACCTGATCCGATC----- 675
Qy 188 aSerProSerTyrrhr-----IleuSerVal1SerPhele-----Val11 203

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QY 290 SerThrGlyThrSerGluSerValGluAlaArgGlySerGluGlu---ValArgGlu 308
Db 1383 -----GCTCTGCCCACTCAGGTGATGAAACAATTATGCGAAGA 1421
QY 309 SerSerThrValAlaSerAspGlySerMetGluGlyValGluGlySerThrIysValGlu 328
Db 1422 ACATCCACACATT-----GGGAAAAAG----- 1442
QY 329 GluAsnSerMetCysAlaAspIysGlyArgThrGluValAsnGlnCysSerIleAspLeu 348
Db 1442 ----- 1442
QY 349 GlyIuAspAspMetGluPheGlyGluAspAspIleAsnPheSerGluAspAspValGlu 368
Db 1443 -----TCAGTGGCAG 1451
QY 369 AlaValAsnIleProGluSerLeuProProSerArgAsnSerAsnSerAsnProPro 388
Db 1452 ACCAATT-----TCCACGACACAG----- 1469
QY 389 LeuProArgCysTyrGlnCysIysAlaAlaIysValIlePheIleIlePheSerTyr 408
Db 1470 -----AGAGCTCAAAAGCTCTAGGAGTGTCTTTTCTCTTT 1508
QY 409 ValLeuSerLeuGlyProTyrCysPheLeuAlaValLeuAlaValIleTyrValAspValGlu 428
Db 1509 TTGCTTATGTGGTGTCTCTCTTATTACAAATATATACCTTAGTTTATGTATCTCTGT 1568
QY 429 ThrGluValPro---GlnTyrValIleThrIleIleIleTyrLeuPhePheLeuGlnCys 447
Db 1569 AACCAAACTACTCTCCAAATGCTCTCGAGATATTGTGTGATAGGCTATGTCTCTCA 1628
QY 448 CysIleIleProTyrValTyrGlyTyrMetHisIysThrIleIys 462
Db 1629 GGAGGAAATCCTTTGGTCTACACCCCTTCATTAAGACATTTCGG 1673

RESULT 6
US-11-170-153-1
; Sequence 1, Application US/11170153
; Publication No. US2005026529A1
; GENERAL INFORMATION:
; APPLICANT: DELBERSNIDER, WILLY
; APPLICANT: WESSP, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: LOKEN, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(1299)
; OTHER INFORMATION: IGS4A long version
US-11-170-153-1

Alignment Scores:
Pred. No.: 1,1e-11 Length: 1658
Score: 210.00 Matches: 98
Percent Similarity: 33.53% Conservative: 73
Best Local Similarity: 19.22% Mismatches: 134
Query Match: 7.94% Indels: 206
Db: 7 Gaps: 16

US-10-712-615-2 (1-508) x US-11-170-153-1 (1-1658)

QY 7 AsnSerThrArgGlu-----SerAsnSerSerHisThrCysMet 19
Db 133 AACAGCACCGAAGATATCTGACCTTCTGCGGACCTGCGGACGACCATTTCTCTC 192
QY 20 ProLeuSerIysMetProIleSerLeuAlaHisGlyIleIleIleAspSerThrValLeuVal 39
Db 193 CCGCGT-----TCTGGGTGTATGTG 213
QY 40 IlePheLeuAlaIleSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgIys 59
Db 214 CCAATTTTGTGGTGGGGGTCTATGGCAATGCTCTGCTGCTGCTGCTGCTATTTCTGACGAC 273
QY 60 ProGlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeu 79
Db 274 CAGGCTATGAAGAGCCGACCACTACCTTACGCTGCGGCGGCTGTGACCTCTCG 333
QY 80 GlnIle-SerLeuValAlaProTyr-----ValValAlaThrSerValProIle 95
Db 334 GTCCGTCTCTTGGAAATCCCTCGAGGCTATAGATGTGGCCGACATACCTTTTC-TT 392
QY 95 uPheTyrProLeuAsnSerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAl 115
Db 393 GTTGGGGCCGTGGGCTCTACTTCAAGCGCCCTCTTTAGACCGTG-----TG 443
QY 115 aPheAlaSerValAsnThrIleValLeuValSerValAspArgTyrLeuSerIleIleHis 135
Db 444 CTTCGCTTCATCTCCACATCACCACCGTCAGCGGTGAGCGGCTAGGCGCATCTCA 503
QY 135 aProLeuSerTyrProSerIysMetThrGlnArgArgGlyTyrLeuLeuLeuTyrGlyTh 155
Db 504 CCGGTTCGCGCGCAAACTCCAGAGCACCGGCGCGGCGCCCTCAGAGATCTTGGCATGT 563
QY 155 rTyrIleValAlaIleLeuGlnSerThrPro-----ProLeuTyrGly----- 169
Db 564 CTGGGGCTTCTCCGCTCTTCTCTCCCTGCGCAACGACATCCATGCGCATCAATTCCA 623
QY 170 ---TrrpGlnAlaAlaIleAspGluAspGluAspGluAlaLeuCysSerMetIleTrrpGlyAl 188
Db 624 CTACTTCCCAATGGGTCCTGTCGCGAGGTTGCGCACCTGTAGCGATC----- 675
QY 188 aSerProSerTyrThr-----IleLeuSerValIleSerPheIle-----ValIle 203
Db 676 -AAGCCATGTGGATCTCAATTCATCATCAGGTACCTCTCTTCATTTCTACTCTCT 734
QY 203 aProLeuIleValMetIleAlaCysTyrSerValIlePheCysAlaAlaArgGlnHis 223
Db 735 CCCCATGACTGATCATCAGTCTCTAC----- 762
QY 223 aIleLeuLeuTyrAsnValIysArgHisSerLeuGluValArgValIysAspCysValGlu 243
Db 763 -----TACCATGACCTACAGATCAAG----- 786
QY 243 uAsnGluAspGluGluGlyAlaGluIlyAspGluPheGlnAspGluSerGluPheArg 263
Db 786 ----- 786
QY 263 gArgGlnHisGluGluGluValIlyAspGluGlyArgMetGluAlaIysAspGlySe 283
Db 787 -----AAGACAAATC 797
QY 283 rLeuIysAlaIysGluGlySerThrGlyThrSerGluSerSerValGluAlaArgGlySe 303
Db 798 TCTTAGGCGAGATGAAGGAAT----- 819
QY 303 rGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGlyIysGluGlu 323
Db 819 ----- 819
QY 323 ySerThrIysValGluGluAsnSerMetCysAlaAspIysGlyArgThrGluValAsnGlu 343
Db 819 ----- 819

QY 343 nCySerIleAapLeuGlyGluAapAspMetGluPheGlyGluAapAspIleAsnPhese 363
DB 819 ----- 819
QY 363 rgluaAapValGluAlaValAsnIleProGluSerLeuProProSerArgArgAsnse 383
DB 820 -----GCNAATTTTCAAGA-----CCCTGCAGAAAATCAGT 851
QY 383 rAsnSerAsnProProLeuProArgCysTyrGlnCysLysAlaAlaIleValIlePhe11 403
DB 852 CAAC-----AAGATGCTGTTGT 869
QY 403 eIleIlePheSerTyrValLeuSerLeuGlyProTyr-----CysPheLeuAl 419
DB 870 CTGTGAGAGAGTGTATCTGTGTGGGCCCGCTGCACATTGACCGACTCTTCTTCA 929
QY 419 aValLeuAlaValATrpValAspValGluTrpGlnValProGlnITrpValIleThrIle11 439
DB 930 CTTTGAGAGAGTGTAGTAAATCCCTGCTGCTGTTCMACTGCTCAGTGTGTGTG 989
QY 439 eIleTrpLeuPhePheLeuGlnCysCysIleHisProTyrValTyrGlyTyrMetHis1 459
DB 990 AGGTGCTCTTCTTACTAGCTACGCTCAGCTGCAACCCATTATCTATTACTACTGTCTG 1049
QY 459 sThrIleLysLysGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysProP 479
DB 1050 CCGCTTCCAGGACGACATTCAGATGTGATCTTCTTTC-----CACAAACAGTG 1100
QY 479 oLysGluAapSerHisProAspLeuPro 488
DB 1101 GCACCTCCAGCATGACCCACAGTTGCCA 1128
RESULT 7
US-11-170-153-3
; Sequence 3: Application US/11170153
; Publication No. US20050266529A1
; GENERAL INFORMATION:
; APPLICANT: DELEERSNIJDER, WILLY
; APPLICANT: WEESP, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: LOKEN, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(1299)
; OTHER INFORMATION: IGS4A short version
US-11-170-153-3
Alignment Scores:
Pred. No.: 1,1e-11 Length: 1658
Score: 210.00 Matches: 98
Percent Similarity: 33.53% Conservative: 73
Best Local Similarity: 19.22% Mismatches: 134
Query Match: 7.94% Indels: 206
DB: 7 Gaps: 16
US-10-712-615-2 (1-508) x US-11-170-153-3 (1-1658)
QY 7 AsnSerThrArgGlu-----SerAsnSerSerHisThrCysMet 19
DB 133 AACAGACCGAGAGATATCTGCGCTTCTCTGCGGAGCTTGGCGAGCCACTTCTTCTTC 192

QY 20 ProLeuSerLysMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuVal 39
DB 193 CCGGTG-----TCTGTGGTGATGTG 213
QY 40 IlePheLeuAlaIleAsnSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLys 59
DB 214 CCAATTTTGTGGTGGGGCTCATTTGGCAATGCTCTGTGCTGTGATTTCTGCAGCAC 273
QY 60 ProGlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeu 79
DB 274 CAGGCTATGAAGACGCCCACTACTACTCTTCTGAGCTGCGGCTCTGACTCTTC 333
QY 80 GlnIle-SerLeuValAlaProTrp-----ValAlaAlaThrSerValProLe 95
DB 334 GTTCCGCTCTCTGGAATGCGCCCTGAGAGCTATGAGATGTGGCGCAACTACCTTTC-TT 392
QY 95 uPheTrpProLeuAsnSerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAl 115
DB 393 GTTCCGGGCCCGGCTGCTACTTCAAGACGCCCTCTTGAACCCGTG-----TG 443
QY 115 aPheAlaSerValAsnThrIleValLeuValSerValAspArgTyrLeuSerIleIle11 135
DB 444 CTTCGCTCATCTCTCAGCATCACACGCTCAGCGTGGAGCGCTACGTGAGCATCTTACA 503
QY 135 sProLeuSerTyrProSerLysMetThrGlnArgArgGlyTyrLeuLeuLeuTyrGlyTh 155
DB 504 CCGGTTCCGGCGCAAACTCAGACGACCGGGGCGCGGCTCAGAGATCTGGCGATCGT 563
QY 155 rTrpIleValAlaIleLeuGlnSerThrPro-----ProLeuTyrGly----- 169
DB 564 CTGGGGCTTCTCCGCTCTCTCTCTCCCTGCCCAACACACAGATCATGAGTCAAGTTCCA 623
QY 170 -----TrpGlyGlnAlaIlePheAspGluArgAsnAlaLeuCysSerMetIleTrpGlyAl 188
DB 624 CTACTTCCCAATGGGTCCCTGTGCTCCAGCTTCGGCAGCTGACTGATC----- 675
QY 188 aSerProSerTyrThr-----IleLeuSerValIleSerPheIle-----Val11 203
DB 676 -AAGCCCATGTGATGTACAAATTTGATCATTCAGAGTCACCTCTTCTTACTACCTCGT 734
QY 203 eProLeuIleValMetIleAlaCysTyrSerValValPheCysAlaAlaArgArgGlnHis 223
DB 735 CCCCAGTACTGATCATCAGTGTCTCTAC----- 762
QY 223 sAlaLeuLeuTyrAsnValLysArgHisSerLeuGlnValArgValLysAspCysValG1 243
DB 763 -----TACCTCATGGCACTCAGACTAAAG----- 786
QY 243 uAsnGluAapGluGluGlyAlaGluLysGluGluPheGlnAapGluSerGluPheAr 263
DB 786 ----- 786
QY 263 gArgGlnHisGluGluGluValLysAlaLysGluGlyArgMetGluAlaLysAapGlySe 283
DB 787 -----AAAGACAAATC 797
QY 283 rLeuLysAlaLysGluGlySerThrGlyThrSerGluSerSerValGluAlaArgLysSe 303
DB 798 TCTTGAGCAGATGAAGGAAT----- 819
QY 303 rgluGluValArgGluSerSerThrValAlaSerAapGlySerMetGluGlyLysGluG1 323
DB 819 ----- 819
QY 323 ySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGluValAsnG1 343
DB 819 ----- 819
QY 343 nCySerIleAapLeuGlyGluAapAspMetGluPheGlyGluAapAspIleAsnPhese 363
DB 819 ----- 819

```

QY      363  rgluapaspvAlgluAlaValAsnllleProgluSerleuProProSerArgArgpense 383
Db      820  -----GCAAAATATTCMAAGA-----CCCTCGAGAAATACTGT 851
QY      363  rAsnSerAnpProProleuProArgCysTyrGlnCysylsAlaAlaIleValIlePheIle 403
Db      852  CNAAC-----AAGATCTGTTGTT 869
QY      403  eillelePheSerTyValleuSerleuGlyProTyr-----CysPheleuAl 419
Db      870  CTGTGCTTACGTGTTGCTATCTGTTGGCCGCCGCTTCCACATTGACCGACCTCTTCTGCG 929
QY      419  aValleuAlaValITrpValAspValAlaGlnThrGlnValProGlnITrpValIleThrIleI 439
Db      930  CTCTTGAGAGAGTGAATCCCTGCTGCTGTTCAACCTGTCATGATGCTGTC 989
QY      439  eilleITrpPhePheleuGlnCysSerIleHisProTyValITyrglyTyrMetHisIle 459
Db      990  AGGTGCTCTTCTTACCTGAGCTCAGCTGTCAACCCCATTTATCTATACCTTACTGCTG 1049
QY      459  eThrIleTySylsgIuIleGlnAspMetleuTySylsPhePheCysTySylsIleProBr 479
Db      1050  CCGCTTCAGCAGCATTCACAAATGTATCTCTTCTTCC-----CACAAACAGTG 1100
QY      479  olysegluaspSerHisProAspLeuPro 488
Db      1101  GCACCTCCAGCATGACCCACAGTTGCGCA 1128

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RESULT 8

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US-11-068-686-19
; Sequence 19, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
;
;   Schweickart, Vicky L.
;   Report, Carol J.
;
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068,686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
;
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1059 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1056
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-11-068-686-19

```

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Alignment Scores:
Pred. No.:      2,086-11      Length:      1059
Score:          204.50      Matches:      61
Percent Similarity: 47.41%      Conservative: 49
Best Local Similarity: 26.28%      Mismatches: 103
Query Match:      7.73%      Indels:      19
DB:              Gaps:      7

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US-10-712-615-2 (1-508) x US-11-068-686-19 (1-1059)

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QY      16  HisITrCysMetProleuSerIleMetProIle---SerleuAlaHisGlyIleIleArg 34
Db      43  TATACATCGAACCCTGCCAAATAATCATGTGAACAATCGCGCCGCTCTGCT 102
QY      35  SerITrValleuValIlePheleuAlaIleSerPheValIleGlyAsnIleValleuAla 54
Db      103  CCGCTCTACTACGTGTTCTATC---TTTGTTTGTGGCCACATCTGTCCTCTC 159
QY      55  ValIeuGlnArgIysProGlnIleuGlnValIThrAsnArgPheIlePheAsnIleu 74
Db      160  ATCTGTATAAATCGCAAAAGCTGAAAGCATGATGATGATCTACTCTCACTGACC 219
QY      75  ValITrAspIleuGlnIleSerIleuValAlaProITrpValAlaIleThrSerValPro 94
Db      220  ATCTGTGACCTGCTTCTTCTTACTGTCTCCCTTCTG-----GCTCATTAGCTGCT 273
QY      95  LeuPheITrpProleuAsnSerHisPheCysIThrAlaIleuValSerleuThrHisleuPhe 114
Db      274  GCCCAGTGGACTTGGAAATACATGTGTCTCACTCTTGACAGGCTCTATTTTATGAC 333
QY      115  AlaPheAlaSerValAsnIThrIleValleuValSerValAspArgTyrleuSerIleIle 134
Db      334  TTCTTCTCTGGAATCTTCTTATCATCTCTCGAACAATGATAGTATGATCTGCTATGCG 393
QY      135  HisProleuSerTyrProSerIleMetIThrGlnArgGlyITyrIleuIleuITyrgly 154
Db      394  CATGCTGTGTTGCTTTAAAGCCGAGCAGTCACTTTGGGTGGTGAAGTGTGATC 453
QY      155  ThrITrIleValAlaIleIleuGlnSerIThrProProleuTyrGlyITyrglyIleAla 174
Db      454  ACTTGGTGTGGTGTCTGTGTGGTCTCTCTCCAGAAATCATC---TTTACCGAGATCTGAG 510
QY      175  PheAspGluArgAsnAlaIleuCysSer-----MetIleITrp 186
Db      511  AGAGAAGGCTTCATTACACCTGACGCTCTATTTCATACAGTCAGATCAATTCATG 570
QY      187  GlyAlaSerProSerTyrIThrIleleuSerValAlaSerPheIleIleValIleProleuIle 206
Db      571  -----AAGAAITTTTCAGACATTAAGAATGTCATCTGGGGCTGCTCGCTGCTT 624
QY      207  ValMetIleAlaCysTyrSerValValPheCysAlaIleAlaArgArgGlnHisAlaIleu 226
Db      625  GTCATGTGTCATGTCTACTCTGGGAATCTCGAAATCTGCTTGG-----TGT 672
QY      227  TyrAsnValIysArgHisSerleuGlnValArgVal 238
Db      673  CGAAACGAGAAGAAAGACAGCAGGCTGTGAGGCTT 708

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RESULT 9

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US-10-992-577-1
; Sequence 1, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 57155-D/UPW
; CURRENT APPLICATION NUMBER: US/10/992,577

```



```

/ APPLICANT: Bonini, James A.
/ APPLICANT: Borowsky, Beth E.
/ APPLICANT: Craig, Douglas A.
/ TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FR (NPFF) Receptors
/ TITLE OF INVENTION: And Uses Thereof
/ FILE REFERENCE: 57155-D/JPM
/ CURRENT APPLICATION NUMBER: US/10/992,577
/ CURRENT FILING DATE: 2004-11-18
/ PRIOR APPLICATION NUMBER: US/09/538,036
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: 09/405,558
/ PRIOR FILING DATE: 1999-09-24
/ PRIOR APPLICATION NUMBER: 09/255,368
/ PRIOR FILING DATE: 1999-02-22
/ PRIOR APPLICATION NUMBER: 09/161,113
/ PRIOR FILING DATE: 1998-09-25
/ NUMBER OF SEQ ID NOS: 71
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 43
/ LENGTH: 1334
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-10-992-577-43

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Alignment Scores:
Pred. No.: 1.47e-10 Length: 1334
Score: 198.00 Matches: 82
Percent Similarity: 31.9% Conservative: 69
Best Local Similarity: 17.3% Mismatches: 141
Query Match: 7.49% Indels: 180
DB: 6 Gaps: 12

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US-10-712-615-2 (1-508) x US-10-992-577-43 (1-1334)

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QY 33 ILEAGSERThValLeuValIlePheLeuAlaIleSerPheValGlyAsnIleValLeu 52
DB 170 ATTAGCTCTACTTCTCTGATCTTCTTCTGTC-----ATGGTGGAAACACTGTCGT 223
QY 53 ALALEuValLeuGlnArgLysProGlnLeuLeuGlnValThrAsnArgPheIlePheAsn 72
DB 224 TCGTTGTGTGTAATAAGAAATAGTCATGCACACGTCATTAATTTCTTCACTTCAAC 283
QY 73 LeuLeuValThrAspLeuLeuGlnIleSerLeuValAlaProTrpValAlaThrSer 92
DB 284 CTCGCAATAGTACTTACTGCTGGATATTCTGCATCTCATCTGTCGACAAAC 343
QY 93 ValProLeuPheTrpProLeuAsnSerHisPheCysThrAlaLeuValSerLeuThrHis 112
DB 344 ATCATAGCAGATGCCGTTTGGAGCAGCATGTGCAGATGACGCGGCTGTGCAAGG 403
QY 113 LeuPheAlaPheAlaSerValAsnThrIleValIleValSerValAspArgTrpLeuSer 132
DB 404 AATATCGGTCGCGCTTCTCTTCTTCTGTTGCGATGACCGTACAGATTCGCGT 463
QY 133 ILEIleHisProLeuSerTrpProSerLysMetThrGlnArgArgGlyTrpLeuLeu 152
DB 464 GTGCTCTACCCC-----TTTAAGCCCAAGCTCATCTGTCAGACACCTTTGTCATGATC 517
QY 153 TyrGlyThrTrpIleValAlaIleLeuGlnSerThrProProLeuTrp----- 168
DB 518 GTGATCATCTGGGCGCTGGCCATACCATATTGACCCCTGTCATCATGTTACATGTA 577
QY 169 -----GlyTrpGlyGlnAlaAlaPheAspGlyArgAsnAlaLeuCysSerMetIle 185
DB 578 CAGGAAGAAATATCTACCTGTGAGGCTCAGCTCCACATAAACCAGACACAGCTAC 637
QY 186 TrpGlyAlaSer-----ProSer-----TyrThrIleLeuSerVal 197
DB 638 TGTGTGCGGAGGATTTGCCAAACCGAAGATGAGAGATCTACACACCGGCTCTT 697
QY 198 ValSerPheIleValIleProLeuIleValMetIleAlaCysTrpSerValValPheCys 217
DB 698 GCCACTATCTACTGCTGCACACTCTCTCATTTGTTATCATGATATCA----- 745

```

```

QY 218 ALAAlaArgArgGlnHisAlaLeuLeuTrpAsnValLysArgHisSerLeuGluValArg 237
DB 746 -----AGGATTGGGCTTCCCTTCAAGACCTGACACACAGC----- 784
QY 238 ValLysAspCysValGluAsnGluAspGluGlyAlaGluLysLysGluGluPheGln 257
DB 785 -----ACAGTAAGCAGCCCTGACACAGTGG--- 811
QY 258 AspGluSerGluPheArgArgGlnHisGluGlyValLysAlaLysGluGlyArgMet 277
DB 812 -----CATGTATCCAAAGAAACAG----- 832
QY 278 GluAlaLysAspGlySerLeuLysAlaLysGluGlySerThrGlyThrSerGluSerSer 297
DB 832 ----- 832
QY 298 ValGluAlaArgGlySerGluGluValArgGluSerSerThrValAlaSerAspGlySer 317
DB 832 ----- 832
QY 318 MetGluGlyLysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGly 337
DB 832 ----- 832
QY 338 ArgThrGluValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGlu 357
DB 832 ----- 832
QY 358 AspAspIleAsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuPro 377
DB 832 ----- 832
QY 378 ProSerArgArgAsnSerAsnSerAsnProLeuProArgCysTrpGlnCysLysAla 397
DB 833 -----AAGTC 838
QY 398 ALALysValIlePheIleIlePheSerTrpValLeuSerLeuGlyProTrpCysAsp 417
DB 839 ATCAAGATGCTGCTGACGTGGCCCTCTTTCATCTTCTGCTGCTCCCTGGTGGACT 898
QY 418 LeuAlaValLeuAlaValTrpValAspValGluThrGlnValProGlnTrpValIleThr 437
DB 899 CTGATGATGCTCTGACATATGCTGACCTGCACCTTAACAATACGT--GTCAATCAT 955
QY 438 ILEIleIle-----TrpLeuPheLeuGlnCysCysIleHisProTrp 452
DB 956 ATTTATGCTTACCTTTTGGCCATGCTGCTGCTTCTGCAATGACAGTCAACCCCATC 1015
QY 453 ValTrpGlyTrpMetHisLysThrIleLysLysGluIleGlnAspMetLeuLysAspHe 472
DB 1016 ATTATGGTTCTTTAATGAATAATTTGCGAGTGTTCCTCAAGATGCTTTCAG----- 1069
QY 473 PheCysLysGluLysProProLysGluAspSerHis 484
DB 1070 TTCTGCAAAAGAAAGTCAAAACCCAGAGAAGCTTAT 1105

```

RESULT 11

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/ Sequence 7, Application US/11067884
/ Publication No. US20050261252A1
/ GENERAL INFORMATION:
/ APPLICANT: Miller, Duane D.
/ APPLICANT: Tigyil, Gabor
/ APPLICANT: Dalton, James T.
/ APPLICANT: Sarda, Vaneet M.
/ APPLICANT: Elrod, Don B.
/ APPLICANT: Xu, Huiping
/ APPLICANT: Baker, Daniel L.
/ APPLICANT: Wang, Dean
/ APPLICANT: Lillom, Karoly
/ APPLICANT: Fischer, David J.
/ APPLICANT: Vireg, Tamas

```



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; PRIOR APPLICATION NUMBER: US/10/088,744
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(942)
; OTHER INFORMATION: IGS4A truncated DNA long version
US-11-170-153-9

Alignment Scores:
Pred. No.: 3,19e-10 Length: 1594
Score: 196.00 Matches: 68
Percent Similarity: 47.74% Conservative: 48
Best Local Similarity: 27.98% Mismatches: 84
Query Match: 7,41% Indels: 44
DB: Gaps: 9

US-10-712-615-2 (1-508) x US-11-170-153-9 (1-1594)

QY 7 AensertHrArgGlu-----SerAnsSerSerHieThrcYsmet 19
   |||||
Db 133 AACACACCGAGAGATATCTGGCTCTCTCGGACCTCGGCGAGCCACTTCTTCCCTC 192
QY 20 ProLeusertYmerProIleSerLeuAlaHieGlyIleIleArgSerThrValLeuVal 39
   |||||
Db 193 CCCGTG-----TCTGTGTGTATGTG 213
QY 40 IlePheLeuAlaIleSerPheValGlyAnsIleValLeuAlaLeuValLeuGlnArgLyS 59
   |||||
Db 214 CCAATTTTGTGTGGGGGTATCTGGCAATGTCCTGTGCTGTGATTCGAGCAGAC 273
QY 60 ProGlnLeuLeuGlnValThrAsnArgPheIlePheAnsLeuLeuValThrAspLeu 79
   |||||
Db 274 CAGGCTATGAGACGCCCACTACTTCAAGCGCTGAGCGGTCTGACCTCCG 333
QY 80 GlnIle-SerLeuValAlaProTrp-----ValValAlaThrSerValProle 95
   |||||
Db 334 GTCCTGCTCTTGGAAATGCCCTGAGAGTCTATGAGATGTGGCGCACTACCTTTC-TT 392
QY 95 uPheTrpProLeuAnsSerHiePheCysThrAlaLeuValSerLeuThrHieLeuPheAl 115
   |||||
Db 393 GTTCGGGCCGTGGGCTGCTACTTCAAGACGCCCTCTTGAGACCGTG-----TG 443
QY 115 aPheAlaSerValAnsThrIleValLeuValSerValAspArgTyTrLeuSerIleIleHie 135
   |||||
Db 444 CTTGCCCTTCATCTCCAGCATCACCACCGTCAGCGTGAGCGCTACGTCGTCATCTACA 503
QY 135 aProLeuSerTyTrProSerTymerThrgInArgArgGlyTyTrLeuLeuLeuTyGlyTh 155
   |||||
Db 504 CCCGTTCCGCCCAACTGACAGACGCCGGCGCGCCCTCAGAGATCTTGCGCATCGT 563
QY 155 rTrpIleValAlaIleLeuGlnSerThrPro-----ProLeuTyGly----- 169
   |||||
Db 564 CTGGGGCTTCTCCGTCCTCTTCCCTGCCCAACACAGCATCAGATCAGATCAAGTTCA 623
QY 170 ----TrpGlyGlnAlaIlePheAspGlyArgAsnAlaLeuCySerMetIleTrpGlyAl 188
   |||||
Db 624 CTACTTCGCCCAATGGGCTCGTCCAGAGTTCCGGCACCTTGACCGTATC----- 675
QY 188 aSerProSerTyTrThr-----IleLeuSerValIleSerPheIle-----ValI 203
   |||||
Db 676 -AAGCCCATGTGATTTACAAATTTCAATCCAGGTCACCTCTTCTCTTCACTCTCT 734
QY 203 eProLeuIleValMetIleAlaCysTyTrSerValValPheCysAlaAlaArgArgGlnHie 223
   |||||
Db 735 CCCCATGATGTGTATGATGTCCTCTACTACTCATGAGCATCAGACTAAAGAAACAA 794
QY 223 aAlaLeu 225
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Db 795 ATCTCTT 801
RESULT 13
US-11-170-153-11
; Sequence 11, Application US/11170153
; Publication NO. US20050266529A1
; GENERAL INFORMATION:
; APPLICANT: DELEBRSNIDER, WILLY
; APPLICANT: WEBER, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: LOKEN, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 11
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(942)
; OTHER INFORMATION: IGS4A truncated DNA short version
US-11-170-153-11

Alignment Scores:
Pred. No.: 3,19e-10 Length: 1594
Score: 196.00 Matches: 68
Percent Similarity: 47.74% Conservative: 48
Best Local Similarity: 27.98% Mismatches: 84
Query Match: 7,41% Indels: 44
DB: Gaps: 9

US-10-712-615-2 (1-508) x US-11-170-153-11 (1-1594)

QY 7 AensertHrArgGlu-----SerAnsSerSerHieThrcYsmet 19
   |||||
Db 133 AACACACCGAGAGATATCTGGCTCTCTCGGACCTCGGCGAGCCACTTCTTCCCTC 192
QY 20 ProLeusertYmerProIleSerLeuAlaHieGlyIleIleArgSerThrValLeuVal 39
   |||||
Db 193 CCCGTG-----TCTGTGTGTATGTG 213
QY 40 IlePheLeuAlaIleSerPheValGlyAnsIleValLeuAlaLeuValLeuGlnArgLyS 59
   |||||
Db 214 CCAATTTTGTGTGGGGGTATCTGGCAATGTCCTGTGCTGTGATTCGAGCAGAC 273
QY 60 ProGlnLeuLeuGlnValThrAsnArgPheIlePheAnsLeuLeuValThrAspLeu 79
   |||||
Db 274 CAGGCTATGAGACGCCCACTACTTCAAGCGCTGAGCGGTCTGACCTCCG 333
QY 80 GlnIle-SerLeuValAlaProTrp-----ValValAlaThrSerValProle 95
   |||||
Db 334 GTCCTGCTCTTGGAAATGCCCTGAGAGTCTATGAGATGTGGCGCACTACCTTTC-TT 392
QY 95 uPheTrpProLeuAnsSerHiePheCysThrAlaLeuValSerLeuThrHieLeuPheAl 115
   |||||
Db 393 GTTCGGGCCGTGGGCTGCTACTTCAAGACGCCCTCTTGAGACCGTG-----TG 443
QY 115 aPheAlaSerValAnsThrIleValLeuValSerValAspArgTyTrLeuSerIleIleHie 135
   |||||
Db 444 CTTGCCCTTCATCTCCAGCATCACCACCGTCAGCGTGAGCGCTACGTCGTCATCTACA 503
QY 135 aProLeuSerTyTrProSerTymerThrgInArgArgGlyTyTrLeuLeuLeuTyGlyTh 155
   |||||
Db 504 CCCGTTCCGCCCAACTGACAGACGCCGGCGCGCCCTCAGAGATCTTGCGCATCGT 563
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 10, 2005, 04:47:54 ; Search time 3866 Seconds
(without alignments)
6147.915 Million cell updates/sec

Title: US-10-712-615-2

Perfect score: 2644

Sequence: 1 MTSTCTNSTRESNSHTCMP.....GTEGTEKIVPSYDSTAFP 508

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-g=/cgn2.1/USPTO_spool/US10712615/runat_02122005_103722_24072/app_query.fasta_1.647
-DB=EST -Qfmt=fastap -SUFFIX=first -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10712615 @CGN 1.1 4015 @runat_02122005_103722_24072 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEOUTER -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOC
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hlc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	640	24.2	655	1	BB179791 BB179791
2	569	21.5	644	5	BY723772 BY723772
3	544	20.6	646	11	AL280651 Tetradodon
4	492	18.6	1064	11	CNS03V11 AL282450 Tetradodon
5	467	17.7	772	8	DR860076 JGI-CABG4
6	435	16.5	641	8	CX254611 CX254611 1307373 N
7	391	14.8	1587	10	AY421262 Mus muscu

8	391	14.8	1590	10	AY421260	AY421260 Homo sapi
9	391	14.8	1590	10	AY421261	AY421261 Pan trogl
10	366	13.8	620	5	BY724046	BY724046 BY724046
11	341	12.9	1401	10	AY399428	AY399428 Mus muscu
12	341	12.9	4124	4	AK085653	AK085653 Mus muscu
13	341	12.9	4135	4	AK079597	AK079597 Mus muscu
14	340.5	12.9	1269	10	AY402237	AY402237 Homo sapi
15	338.5	12.8	1401	10	AY399426	AY399426 Homo sapi
16	331.5	12.5	1269	10	AY402239	AY402239 Mus muscu
17	331.5	12.5	3113	4	AK043668	AK043668 Mus muscu
18	331.5	12.5	3888	4	AK049814	AK049814 Mus muscu
19	331.5	12.5	4356	4	AK049884	AK049884 Mus muscu
20	330.5	12.5	3533	4	AK034017	AK034017 Mus muscu
21	328	12.4	821	8	CX956538	CX956538 JGI CA08
22	322	12.2	832	8	CX491699	CX491699 JGI XZG38
23	319.5	12.1	1213	10	AY402238	AY402238 Pan trogl
24	318	12.0	798	8	CX914631	CX914631 JGI CA04
25	312	11.8	818	8	CX915108	CX915108 JGI CA04
26	311	11.8	797	8	CX419536	CX419536 JGI XZG14
27	311	11.8	801	8	CX907462	CX907462 JGI CA03
28	311	11.8	865	8	CX400009	CX400009 JGI XZT41
29	308	11.6	802	8	CX843215	CX843215 JGI CA01
30	306	11.6	816	8	CX815278	CX815278 JGI CA01
31	294	11.1	1440	10	AY404934	AY404934 Homo sapi
32	290.5	11.0	722	6	CF147810	CF147810 AGENCOURT
33	290.5	11.0	1397	10	AY399427	AY399427 Pan trogl
34	290	11.0	1440	10	AY404935	AY404935 Pan trogl
35	287	10.9	1401	11	DO029898	DO029898 Homo sapi
36	287	10.9	2342	4	AK042759	AK042759 Mus muscu
37	285.5	10.8	1474	4	AK039291	AK039291 Mus muscu
38	284	10.7	1072	10	AY398880	AY398880 Homo sapi
39	283	10.7	1440	10	AY404936	AY404936 Mus muscu
40	283	10.7	1764	4	BC018330	BC018330 Mus muscu
41	283	10.7	2611	4	AK004891	AK004891 Mus muscu
42	283	10.7	3050	4	AK043877	AK043877 Mus muscu
43	280.5	10.6	729	8	DR003001	DR003001 T1108456
44	279	10.6	1722	10	AY398881	AY398881 Pan trogl
45	275.5	10.4	3649	4	AK050183	AK050183 Mus muscu

ALIGNMENTS

RESULT 1
LOCUS BB179791 655 bp mRNA linear EST 19-OCT-2001
DEFINITION BB179791 RIKEN full-length enriched, adult male hypothalamus Mus musculus cDNA clone A230080N06 3', mRNA sequence.

ACCESSION BB179791.2 GI:16269966
VERSION BB179791
KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 655)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Komoto,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

TITLE Unpublished (2001)

JOURNAL On Jun 29, 2000 this sequence version replaced gi:8838874.

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216


```

Qy 227 TTYAenVallyArghisSerLeuGluValArgVallyAspCysValGluangluAap 246
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Db 308 CACCCATACAGACGCAATCTTAC----- 331
Qy 247 GUGUGUGlyAlaGluUlysluGluGluPheGluAspGluSerGluPheArgGlnHis 266
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Db 332 ---TCCCA-GCCCGCCACACAGGACTTCAGAGGACCGAGCTCGACGCCCGAG--- 384
Qy 267 GUGUGlyVallyAlaVallysluGluArgMetGluAlaLysAspGluSerLeuLysAla 286
    ::::: |||
Db 385 -----CAGGCCAGTTCCCGCATGCGCTTTATTCGGCG 417
Qy 287 LysGluGlySerThrGlyThrSerGluSerSerValGluAlaArgGlySerGluGluVal 306
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Db 418 -----ACGGG----- 423
Qy 307 ArgGluSerSerThrValAlaSerAspGlySerMetGluGlyLysGluGlySerThrLys 326
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Db 423 ----- 423
Qy 327 ValGluGluAsnSerMetLysAlaAspLysGlyArgThrGluValaAngGlnCysSerIle 346
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Db 423 ----- 423
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Db 423 ----- 423
Qy 367 ValGluAlaValaAsnIleProGluSerLeuProProSerArgArgAsnSerAsnSerAn 386
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Db 424 -----TACCCGCTCAGAGCTTCGACAGCGTTTTCAC 456
Qy 387 ProProLeuProArgCysArgGlnCysLysAlaAlaLysValIlePheIleIlePhe 406
    ||| |||
Db 457 -----TACCACTGCAGAGCGCGCTGCTTTTTCATCATGAGCA 498
Qy 407 SerTyrValLeuSerLeuGlyProTyrCysPheLeuAlaValLeuAlaValTyrValAsp 426
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Db 499 TGTGATATCTCAGCATGAGGCGCTTACAGCGCTCTAATACGTATCT-----ATGAGT 552
Qy 427 ValGluThrGluValProGlnTyrValIleThrIleIleIleTyrLeuPhePheLeuGln 446
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Qy 447 CysCValIleHisProTyrValTyrGlyTyrMetHisIleThrIleLysLysGluIleGln 466
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Qy 467 AspMetLeuLysPhePheCysLysGluLysProProLysGluAspSerHisProAsp 486
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Db 673 GCTTGCTCTCGCGGCTGTTTTCAGACAGAGCGGCCCGCCAGACGCTCGCGGCTTGAG 732
Qy 487 -----LeuProGlyThrGluGlyGlyThrGluGlyLysIleValProSerTyrAspSer 504
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Qy 505 AlaThrPhePro 508
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Db 775 GCCACCTGCCCA 786

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REFERENCE
1 (bases 1 to 772)
AUTHORS
Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C.,
Brokstein, P. and Lindquist, E.A.
TITLE
DOE Joint Genome Institute Xenopus tropicalis EST project
JOURNAL
Unpublished (2004)
COMMENT
Other ESTs: JGI CABG4788.rev
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 226 5600
Fax: 925 226 5710
Email: cdna@jgi-psf.org
http://image.llnl.gov
Tissue Procurement: Robert M. Grainger
CDNA Library Preparation: Bruce Blumberg Laboratory, University of
California, Irvine
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LLNL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Place: CABG 0049 row: n column: 21
High quality sequence stop: 772.
Location/Qualifiers
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/organism="Xenopus tropicalis"
/mol_type="mRNA"
/strain="N6 (Nigerian 6th generation inbred)"
/db_xref="taxon:8364"
/clone="IMAGE:7836743"
/tissue_type="Stomach"
/dev_stage="Adult"
/lab_host="Electromax DH10B TI Phage Resistant cells"
/clone_lib="NIH XGC tropicstol"
/vector="PCSI07; Site 1: EcoRI; Site 2: XhoI; The
library was prepared from 5 ug of poly A+ RNA by oligo-dT
priming
(5'-ACTAGTCGGCGCGGCTGAGCTTCAGATTTTCTTTTCTTTTCTTTT-3') and
Stratascript reverse transcriptase. After ligation of
EcoRI adaptors (5'-AATTCGCGACGAG-3') followed by kinasing
adapters and by XhoI digestion, the cDNA was size selected
by chromatography on Sepharose CL-2B columns and fractions
containing cDNAs larger than 1000 bp were ligated into
EcoRI/XhoI-digested pCSI07. Reference for library
construction: Current Genomes 4, 635-644. Library
constructed by Michelle Tabb and Bruce Blumberg (Dept of
Developmental and Cell Biology, University of California,
Irvine)."
ORIGIN
Alignment Scores:
Prid. No.: 2,61e-38 Length: 772
Score: 467.00 Matches: 91
Percent Similarity: 70.55% Conservative: 24
Best Local Similarity: 55.83% Mismatches: 48
Query Match: 17.66% Indels: 0
DB: 8 Gaps: 0
US-10-712-615-2 (1-508) x DR860076 (1-772)
Qy 8 SerThrArgGluSerAsnSerSerHisThrCysMetProLeuSerLysMetProIleSer 27
    ||| |||
Db 284 AGTGAAGCGAAGGCTACCTGGAACCAATGATCACTTTCAGCTGAGCAAACTTCATCTCT 343
Qy 28 LeuAlaHisGlyIleIleArgSerThrValLeuValIlePheLeuAlaIleAspPheVal 47
    ||| |||
Db 344 ATGCCGACACCATTTCTCAGATTGCGCATCATTTCCCTGCTTGTCTTTATTATT 403
Qy 48 GlyAsnIleValLeuAlaLeuValLeuGlnArgLysProGlnLeuLeuGlnValThrAn 67
    ||| |||
Db 404 GGAACATATATGCTCTGCTGCTTTTTCATCGAAAGCCTCAGCTGCTCCAGGTAGCAAAC 463

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QY 68 ArgPheIlePheAAsnLeuValThrApleuLeuGlnIleSerLeuValAlaProTrp 87
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 QY 88 ValValAlaThrSerValProleuPheTrpProleuAAsnSerHisPheYsThrAlaLeu 107
 DB 524 GTCATTGTTACTCTCCCTCCATATCTGCTGATTAAGTCTTGTGACACAGG 583
 QY 108 ValSerLeuThrHisLeuPheAlaPheAlaSerValAAsnThrIleValLeuValSerVal 127
 DB 584 GTCGCTGCTGATTCATTTATTTGCTATTTGCAGAGTAACACAAATACACACTTCTCTG 643
 QY 128 AsnArgPheIlePheAAsnLeuValThrApleuLeuGlnIleSerLeuValAlaProTrp 147
 DB 644 GACAAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 703
 QY 148 GlyTyrLeuLeuLeuTyrGlyThrTrpIleValAlaIleLeuGlnSerThrProleu 167
 DB 704 GGAACTCTTCTGATTTTGTGACCTTGGATTTCAGTTCCTCCANAGCACCCACCTCTC 763
 QY 168 TyrGlyTyr 170
 DB 764 TATGCTG 772

RESULT 6
 CX254611 641 bp mRNA linear EST 01-MAR-2005
 LOCUS 1307373 NCCCWA 02RT Oncorhynchus mykiss cDNA 5', mRNA sequence.
 ACCESSION CX254611
 VERSION CX254611.1 GI:60371143
 KEYWORDS EST.
 SOURCE Oncorhynchus mykiss (rainbow trout)
 ORGANISM Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Proacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 641)
 Rexroad,C.E., Goupil,A.-S., Guiguen,Y., and Yao,J.
 02RT IUS, NCCCWA/MVU EST Project, Phase II, in collaboration with
 INRA
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rexroad CE
 USDA, ARS, National Center for Cool and Cold Water Aquaculture
 11876 Leeetown Road, Kearneysville, WV 25430, USA
 Tel: 304 724 8340 x2129
 Fax: 304 725 0351
 Email: crexroad@ncccw.ars.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 Placer: 115 row: J column: 8
 Seq primer: ATTTAGTGACACTATAG.
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 /db_xref="taxon:8022"
 /cfeature_type="pooled"
 /lab_host="DH10B"
 /clone_lib="NCCCWA 02RT"
 /note="Vector: pCMV Sport6.0; This library was created by
 A.-S. Goupil and Y. Guiguen who subcloned the NCCCWA 1RT
 library from the INRA multi-tissue library."

ORIGIN
 Alignment Scores:
 Pred. No.: 4.79e-35 Length: 641
 Score: 435.00 Matches: 90
 Percent Similarity: 59.41% Conservative: 30
 Best Local Similarity: 44.55% Mismatches: 40
 Query Match: 16.45% Indels: 42
 DB: 8 Gaps: 3

US-10-712-615-2 (1-508) x CX254611 (1-641)
 QY 9 ThrArgIleSerAAsnSer-----SerHisThrCys--- 18
 DB 35 ACCCGTAGAGCTGGGCTGGAGAACTGGGAGACCTGTGGAGCTACAGCCACATGCTGT 94
 QY 19 -----MetProleuSerIlyMetProIle----- 26
 DB 95 CTCCTCACCCACACAGCCTCAACATGCCCACTTCCGAGGGCCACAGTGGGAGTAAC 154
 QY 26 ----- 26
 DB 155 TCACACACCGCCCTGGGACCTGTCTCTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 214
 QY 27 SerLeuAlaHisGlyIleIleArgSerThrValLeuValIlePheLeuAlaIleSerPhe 46
 DB 215 TCGGTGGCCACAGCATGTGTAAGATGGTGTGATTCACGCAATTTGTGTGTCTCTG 274
 QY 47 ValGlyAAsnIleValIleuAlaLeuValLeuGlnArgIlyProGlnLeuGlnValThr 66
 DB 275 TTTGGTAACTGT 334
 QY 67 AsnArgPheIlePheAAsnLeuValThrApleuLeuGlnIleSerLeuValAlaPro 86
 DB 335 AACCGCTTGGCTGCAACCTCTCTGCGACAGCTGCTGCGAGCCGTGCTGTATGCTG 394
 QY 87 TrpValValAlaThrSerValProleuPheTrpProleuAAsnSerHisPheCysThrAla 106
 DB 395 TTGCGCATCGCTGCACATGATCGCCGCGTGTGCTGCGCCCTGAGACGCCCTGCTG 454
 QY 107 LeuValSerLeuThrHisLeuPheAlaPheAlaSerValAAsnThrIleValLeuValSer 126
 DB 455 CTGGGTGCTGCATGACCTGTTGCTTCTGCGGGGTCAACACCATATATGCTGTGTG 514
 QY 127 ValAsnArgPheIlePheAAsnLeuValThrApleuLeuGlnIleSerLeuValAlaPro 146
 DB 515 GTGACCGCTTACCTGCGCATCATCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 574
 QY 147 ArgGlyTyrLeuLeuLeuTyrGlyThrTrpIleValAlaIleLeuGlnSerThrProleu 166
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 DB 635 CTCTAC 640

RESULT 7
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 LOCUS AY421262
 DEFINITION Mus musculus HCM7498 gene, VIRTTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY421262
 VERSION AY421262.1 GI:39777219
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Mus.
 1 (bases 1 to 1587)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tenenbaum,D.M., Clavello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 JOURNAL
 PUBMED 14671302
 2 (bases 1 to 1587)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tenenbaum,D.M., Clavello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

TITLE Adams, M.D. and Cargill, M.
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 REFERENCE PUBMED 14671302
 AUTHORS 2 (bases 1 to 1590)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tenenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence as made by sequencing genomic exons and ordering them
 based on alignment.
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 ORIGIN
 Alignment Scores:
 Pred. No.: 8,59e-30 Length: 1590
 Score: 391.00 Matches: 106
 Percent Similarity: 38.53% Conservative: 67
 Best Local Similarity: 23.61% Mismatches: 130
 Query Match: 14.79% Indels: 146
 DB: 10 Gaps: 11
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 QY 31 GYIIEIIEAAGSERTHVALEUVAIIIEPHELEUAIAIASERPHETAI-----Gly 48
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 QY 49 AenileValleuAlaLeuValleuGlnArgLysProGlnLeuGlnValThrAenArg 68
 DB 133 AACCGTCATGTCGTGTCACCTTGTAACAAGAGTCTCTACCTCTACCTCGACCAAG 192
 QY 69 PheilePheAenLeuValThrAenLeuGlnLysSerLeuValAlaProTrrVal 88
 DB 193 TTCGTCACGCTGACTCTGTCCAACTTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 252
 QY 89 ValAlaThrSerValProLeuPheThrProLeuAenSerHisPheCysThrAlaLeuVal 108
 DB 253 GTGACGACGCTCATCCGACGGAATGATCTTGTGTAGTGTGTGCAACTTCTGCC 312
 QY 109 SerLeuThrHisLeuPheAlaPheAlaSerValAenThrIleValleuValSerValAap 128
 DB 313 CTCCTCTACCTGCTATACGCTCTGCGACGATGCTAACCCTCGGGGTCTTCCATGCAC 372
 QY 129 ArgTyrLeuSerIleIleHisProLeuSerTyrProSerLysMetThrGlnArgArgLys 148
 DB 373 CGCTACTATGCTGCTGTCGACCCATGATGTCACCATGAATGATCAGAGAACGGGCT 432
 QY 149 TyrLeuLeuLeuTyrGlyThrTrrIleValAlaIleLeuGlnSerThrProLeuTyr 168
 DB 433 GTGATGGACCTTGCTTACATCGGCTCTCCTGCTCATCGGCTGCTGCTGCTGCTGCT 492
 QY 169 GlyTrrPglyAlaAlaAlaPheAenPgluArgAenAlaLeuCysSerMetIleTrrPglyAla 188
 DB 493 GGTGGTGTATCCGTGAGAGTTTACAGAGTTCAATGATGATGTGTGTGCTGCTGCTGCTG 552
 QY 189 SerProSerTyrThrIleLeuSerValValSerPheIleValIleProLeuIleValMet 208
 DB 553 GAGCGCTGATACACGCGCTTGGGACGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
 QY 209 IleAlaCysTyrSerValValPheCysValAlaAlaArgArgGlnHisAlaLeuLeuTyrAen 228
 DB 613 CTGGTGTGTATGCTTCACTTCCGCTGCGCAGG----- 648

QY 229 ValIlyArgHisSerLeuGlnValArgValIlyAspCysValIgluAenGluAspGlu 248
 DB 649 GTCAAGGACGACAGAGTCACTGTGCGACAGCTGTCATCGTGAG---GAGAGTCTGAG 705
 QY 249 GlyAlaGluYulYulGluGluPheGlnAspGluSerGluPheArgArgGlnHisGluGly 268
 DB 705 ----- 705
 QY 269 GluValIlyAlaYulGluGlyArgMetGluAlaIlyAspGlySerLeuYulAlaYulGlu 288
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 QY 289 GlySerThrGlyThrSerGluSerSerValGluAlaArgLysSerGluGluValArgGlu 308
 DB 724 TCCAGCACCTCCACCTCTTCCAGC----- 750
 QY 309 SerSerThrValAlaSerAspGlySerMetGluGlyYulGluGlySerThrYulValGlu 328
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 DB 751 -----AGCAGAGAGAAATGCTTCAGGCTGTGTC 780
 QY 384 ---AenSerAenProProLeuProArgCysArgLysCysValAlaIlyValIlePhe 402
 DB 781 TACTCGGCAAC-----CAGTCGAAGCCCTCATACCATCTCG 819
 QY 403 IleIleIlePheSerTyrValleuSerLeuGlyProTyr---CysPheLeuAlaValleu 421
 DB 820 GTGGCTCGGAGCTTCATGATGTCACCTGGGCGCCCTCATGATGTCATGCGCTGAG 879
 QY 422 AlaValTrrP-----ValAspValGluThrGlnValProGlnTrrValIleThrIle 439
 DB 880 GCCCTCTGGGGGAAAGCTCCGCTGCCCGACCTGAGAGACTTGGCC----- 927
 QY 440 IleTrrPLeuPhePheLeuGlnCysCysIleHisProTyrValTyrGlyTyrMetHisLys 459
 DB 928 ACATGGCTGTCTTGGCCAGCGCTGTCTGCCACCCCTGATGATGATGACTCTGGAACAAG 987
 QY 460 ThrIleLysLysGluIleGlnAspMet 468
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 LOCUS AY421261 1590 bp DNA linear GSS 12-DEC-2003
 DEFINITION Pan troglodytes HCM7498 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY421261
 VERSION AY421261.1 GI:39777218
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Pan.
 REFERENCE
 1 (bases 1 to 1590)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tenenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Interfering nonneutral evolution from human-chimp-mouse orthologous
 gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1590)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smirsky,J.C., Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.
 FEATURES
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 1.1590
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
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 /locus_tag="HCM7498"
 gene
 ORIGIN
 Alignment Scores:
 Pred. No.: 8,59e-30 Length: 1590
 Score: 391.00 Matches: 106
 Percent Similarity: 38.53% Conservative: 67
 Best Local Similarity: 23.61% Mismatches: 130
 Query Match: 14.79% Indels: 146
 DB: 10 Gaps: 11
 US-10-712-615-2 (1-508) x AY421261 (1-1590)
 QY 31 GYIlelleArgSerThrValleuValIlePheleuAlaIleSerPheVal)-----GIY 48
 Db 73 GGGCGTATATCATCCAGTTCATCGCCATCATGTGTATCATCACTTTTGTGCTCCGCGGA 132
 QY 49 AenlleValleuAlaLeuValleuGlnArgLySProGlnleuGlnValThrAenArg 68
 Db 133 AACCTGTCATCGTGTCTGACCTGTACAGAAAGTCTTACCTCTCACTCCACCTCAGCAGCAAG 192
 QY 69 PheillePheAenleuValIleThrAenleuGlnIleSerleuValAlaProtpVal 88
 Db 193 TTGCTTTAGCTGACCTGTACCTGTCACTTCTGCTGCTGCTGCTGCTGCTTTTGTG 252
 QY 89 ValAlaIleSerValProleuPheTrpProleuAenSerHisPheCysThrAlaLeuVal 108
 Db 253 GTGACGAGCTTCATCCGACGGAATGATCTTGTGTAGTGTGTCGAATCTTCTGCGC 312
 QY 109 SerleuThrHisleuPheAlaPheAlaSerValAenThrIleValleuValSerValAap 128
 Db 313 CTCCTCTACCTGTATGAGCTGCGCAGCATGCTAACCCTTGCGGTCAATGCGCATCGAC 372
 QY 129 ArgTrpIleuSerIleIleHisProleuSerTrpProSerIleMetThrGlnArgGly 148
 Db 373 CGCTACTATGCTGTCTGTACCCCAAGGTGTACCCCATGAAAGATCAGAGGAACCGGGCT 432
 QY 149 TyrleuLeuLeuTyrGlyThrTrpIleValAlaIleleuGlnSerThrProProleuTyr 168
 Db 433 GTGATGCGACTTGTCTACATCTGGCTTCACTGCTGATGCGCTGCGCCCTGCTGTT 492
 QY 169 GIYTPGIYGIAlaAlaPheAenArgIuArgAenAlaLeuCysSerMetIleTrpGlyAla 188
 Db 493 GGTGTGTATCCGTGAGATTGACGATTCAATGATGATGTGTGCTGCTGCGACCGG 552
 QY 189 SerProSerTrpThrIleleuSerValValSerPheIleValIleProleuIleValMet 208
 Db 553 GAGCCGTGGCTACCGCGCTTGTGCGCAACTGTGTGCTGCTTCCCTTTTGTGTGTG 612
 QY 209 IleAlaCysTrpSerValValPheCysAlaIleArgGlnHisAlaLeuLeuTyrAen 228
 Db 613 CTGGTGTGCTATGGCTTCACTTCCCGGTGCGCAGG----- 648
 QY 229 ValIlyArgHisSerleuGlnValArgValIlyAapCysValGlnuAnGlnuAapGlnu 248
 Db 248

Db 649 GTCAAGGACGCGAAGTGATGTCAGACAGTCTTATCTGTGAG--GAGATGCTCAG 705
 QY 249 GIYAlaGluIlyLeuGluGluIupheGlnAenArgIuPheArgArgGlnHisGluGly 268
 Db 705 ----- 705
 QY 269 GIuValIlyAlaLeuGluGluIyArgMetGluAlaIyAapGlySerleuIyAlaIyGlu 288
 Db 706 -----AGACCGGAGAG-----AAGAAC 723
 QY 289 GlySerThrGlyThrSerGluSerSerValGIuAlaArgGlySerGluGIuValArgGlu 308
 Db 724 TCCAGACCTCCACCTCTCTTCAGC----- 750
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 Db 750 ----- 750
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 Db 750 ----- 750
 QY 369 AlaValAenIleProGluSerIleuProProSerArgArgAenSer----- 383
 Db 751 -----ACGAGAGGAATGCTTTGAGGCTGTGTC 780
 QY 384 ---AenSerAenProProleuProAenArgCysTrpGlnCysAlaAlaIySValIlePhe 402
 Db 781 TACTCGGCCAAC-----CACTGAAAGCCCTCATCAACCATCCG 819
 QY 403 IleIleIlePheSerTrpValleuSerleuGlyProTyr--CysPheleuAlaValleu 421
 Db 820 GTGTCTCTGCGGCTTGTATGTGTACCTGCGGCCCCCTCATGCTGTCTATCCCTGTGAG 879
 QY 422 AlaValIlePhe-----ValAapValGluThrGlnValProGlnIleThrIleIle 439
 Db 880 GCCCTGTGGGGAAGAGCTCCGTCTCCCGGACCTGAGACCTTGAGCC----- 927
 QY 440 IleTrpIlePhePheleuGlnCysCysIleHisIleProTyrValIyGlyTyrMetHisIy 459
 Db 928 ACATGGCTGTCTTTGCCAGGCGCTGTGCGCACCCCTGATGTATGATCTGGAACAG 987
 QY 460 ThrIleIyLeuGluIleGlnAapMet 468
 Db 988 ACAGTTCGCAAGAACTACTGCGCATG 1014
 RESULT 10
 BY724046
 LOCUS BY724046 620 bp mRNA linear EST 17-DEC-2002
 DEFINITION BY724046 RIKEN full-length enriched, adult male hypothalamus Mus
 accession BY724046
 version BY724046.1 GI:27137163
 keywords
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Murioidea; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS
 1 (bases 1 to 620)
 Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
 Nikaido,I., Oshio,N., Saito,R., Suzuki,H., Yamanaoka,I.,
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Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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RESULT 12
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LOCUS AK085653
DEFINITION Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched
library, clone: D63005.0N06 product: adrenergic receptor, alpha 1a,
ALPHA 1A-ADRENOCPTOR, full insert sequence.
ACCESSION AK085653.1 GI:26351716
VERSION AK085653.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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          alpha 1a, ALPHA 1A-ADRENORECEPTOR, full insert sequence.
ACCESSION AK079597
VERSION AK079597.1 GI:26348091
KEYWORDS HTC; CAP trapper.

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SOURCE
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
          Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
          prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
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TITLE RIKEN integrated sequence analysis (RISA) system-384-format
          sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE
AUTHORS THE RIKEN Genome Exploration Research Group Phase II Team and the
          PANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE
AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research
          Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
          of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arikawa,T., Bono,H., Carninci,P.,
          Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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TITLE Direct Submision
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
          Physical and Chemical Research (RIKEN), Laboratory for Genome
          Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
          RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
          Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.jp,
          URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
          Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
          Encyclopedia project of Genome Exploration Research Group in Riken
          Genomic Sciences Center and Genome Science Laboratory in RIKEN.
          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues.
          Please visit our web site for further details.
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Alignment Scores:

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Score: 341.00 Matches: 115  
Percent Similarity: 37.48% Conservative: 75  
Best Local Similarity: 22.68% Mismatches: 183  
Query Match: 12.90% Indels: 134  
D: 4 Gaps: 13
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US-10-712-615-2 (1-508) x AK079597 (1-4135)

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Job time : 3884 secs

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November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2005, 01:51:22 ; Search time 896 Seconds
(without alignments)
14093.014 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 19587084

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1527	100.0	1527	8	US-10-712-615-1
4	1527	100.0	1580	3	US-09-992-238-47
5	1527	100.0	1580	6	US-10-712-615-47
6	1527	100.0	4718	8	US-10-293-983-8
7	1525.4	99.9	1527	3	US-09-992-238-52
8	1525.4	99.9	1527	3	US-09-992-238-45
9	1525.4	99.9	1527	5	US-10-094-417-5
10	1525.4	99.9	1527	5	US-10-225-567A-582
11	1525.4	99.9	1527	6	US-10-345-332-1
12	1525.4	99.9	1527	6	US-10-321-807-15
13	1525.4	99.9	1527	6	US-10-276-243-2
14	1525.4	99.9	1527	7	US-10-436-715-13
15	1525.4	99.9	1527	7	US-10-343-650A-89
16	1525.4	99.9	1527	7	US-10-321-807-15
17	1525.4	99.9	1527	7	US-10-314-048A-15
18	1525.4	99.9	1527	8	US-10-712-615-45
19	1525.4	99.9	1527	8	US-10-897-815-15
20	1525.4	99.9	1527	9	US-10-930-662-15
21	1525.4	99.9	1527	9	US-11-086-846-5
22	1525.4	99.9	1659	3	US-09-992-238-44
23	1525.4	99.9	1659	8	US-10-608-990-1

24	1525.4	99.9	1659	8	US-10-712-615-44	Sequence 44, Appl
25	1525.4	99.9	1858	6	US-10-292-798-925	Sequence 925, App
26	1525.4	99.9	1920	6	US-10-276-243-1	Sequence 1, Appl1
27	1525.4	99.9	3024	6	US-10-017-161-1087	Sequence 1087, Ap
28	1525.4	99.9	7524	6	US-10-345-332-3	Sequence 3, Appl1
29	1524	99.8	2241	9	US-10-505-486-233	Sequence 233, App
30	1522.4	99.7	2781	6	US-10-321-807-103	Sequence 103, App
31	1522.4	99.7	2781	7	US-10-321-807-103	Sequence 103, App
32	1522.4	99.7	2781	7	US-10-314-048A-103	Sequence 103, App
33	1522.4	99.7	2781	8	US-10-897-815-103	Sequence 103, App
34	1522.4	99.7	2781	9	US-10-930-662-103	Sequence 103, App
35	1522	99.7	1527	3	US-09-992-238-48	Sequence 48, Appl
36	1522	99.7	1527	8	US-10-712-615-48	Sequence 48, Appl
37	1520.6	99.6	1527	3	US-09-992-238-46	Sequence 46, Appl
38	1520.6	99.6	1527	6	US-10-321-807-91	Sequence 91, Appl
39	1520.6	99.6	1527	7	US-10-321-807-91	Sequence 91, Appl
40	1520.6	99.6	1527	7	US-10-314-048A-91	Sequence 91, Appl
41	1520.6	99.6	1527	8	US-10-712-615-46	Sequence 46, Appl
42	1520.6	99.6	1527	8	US-10-897-815-91	Sequence 91, Appl
43	1520.6	99.6	1527	9	US-10-930-662-91	Sequence 91, Appl
44	1515.8	99.3	1527	3	US-09-971-269-5	Sequence 5, Appl1
45	1515.8	99.3	1704	3	US-09-971-269-1	Sequence 1, Appl1

ALIGNMENTS

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RESULT 1
US-09-992-238-1
; Sequence 1, Application US/09992238
; Publication No. US2003005444A1
; GENERAL INFORMATION:
; APPLICANT: BATTAGLINO, PETER
; APPLICANT: FEDER, JOHN N
; APPLICANT: MINTIER, GABE
; APPLICANT: NELSON, THOMAS C
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: WESTPHAL, RYAN
; APPLICANT: CACACE, ANGELA
; APPLICANT: BARBER, LAUREN
; APPLICANT: HAWKEN, DONALD R
; APPLICANT: KORNACKER, MICHAEL G
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY8,
; FILE REFERENCE: D0047NP
; CURRENT APPLICATION NUMBER: US/09/992,238
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/317166
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/308285
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/268581
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/248285
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-992-238-1
Query Match 100.0%; Score 1527; DB 3; Length 1527;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGACGTCACCTGCACCAAGCAGCGGAGAGTAACAGCAGCCAGTCATGCC 60
DB 1 ATGACGTCACCTGCACCAAGCAGCGGAGAGTAACAGCAGCCAGTCATGCC 60
QY 61 CTCCTCAAAATGCGCATCAGCCTGCAGCCAGGAGCATCATCCGCTCAACCGTGTGTTATC 120
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Db 61 CTCTCAAAATGCCATCAGCTGGCCACGGCATCATCCGCTCAACCGTGTGTATC 120
Qy 121 TTCTTGCGCGCTTTTGTGTGGCAACATAGTGTGGCGCTAGTGTGGACGGACGG 180
Db 121 TTCTTGCGCGCTTTTGTGTGGCAACATAGTGTGGCGCTAGTGTGGACGGACGG 180
Qy 181 CAGCTGTGAGAGTGAACCGTTTATCTTTAAGCTGTGTGACCGAAGCTGTGTGAG 240
Db 181 CAGCTGTGAGAGTGAACCGTTTATCTTTAAGCTGTGTGACCGAAGCTGTGTGAG 240
Qy 241 ATTTCGCTGTGGCCCTGTGGTGTGGACCTGTGTGCTCTCTTGTGGCCCTCAAC 300
Db 241 ATTTCGCTGTGGCCCTGTGGTGTGGACCTGTGTGCTCTCTTGTGGCCCTCAAC 300
Qy 301 AGCCACTTGTGACCGGCTGTGTAGCTTACCCACCTGTGTGCTGTGGCCAGCTCAAC 360
Db 301 AGCCACTTGTGACCGGCTGTGTAGCTTACCCACCTGTGTGCTGTGGCCAGCTCAAC 360
Qy 361 ACCATTGTGTGTGTGATGTGATGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Db 361 ACCATTGTGTGTGTGATGTGATGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Qy 421 TCCAAAGATGACCGAGCGCGGTTACCTGTCTCTATGGACCTGTGTGTGTGTGTGT 480
Db 421 TCCAAAGATGACCGAGCGCGGTTACCTGTCTCTATGGACCTGTGTGTGTGTGTGT 480
Qy 481 GTGCAAGAGACTCTTCACTCTACCGGCTGTGGGCGAGGCTGTGTGTGTGTGTGTGT 540
Db 481 GTGCAAGAGACTCTTCACTCTACCGGCTGTGGGCGAGGCTGTGTGTGTGTGTGTGT 540
Qy 541 CTCTGTCCATATCTGTGGGGGGCGACCCCAAGTACATATTTCTGAGCTGTGTGTGT 600
Db 541 CTCTGTCCATATCTGTGGGGGGCGACCCCAAGTACATATTTCTGAGCTGTGTGTGT 600
Qy 601 ATCGTCAATTCACCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Db 601 ATCGTCAATTCACCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Qy 661 AGGCAAGCATGCTCTGT 720
Db 661 AGGCAAGCATGCTCTGT 720
Qy 721 TGT 780
Db 721 TGT 780
Qy 781 GAGTTTCGCGCGCAGCATGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db 781 GAGTTTCGCGCGCAGCATGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Qy 841 GACGGGAGCTGT 900
Db 841 GACGGGAGCTGT 900
Qy 901 AGGGGAGGAGAGGT 960
Db 901 AGGGGAGGAGAGGT 960
Qy 961 AAGGAAGGAGAGCAACCAAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
Db 961 AAGGAAGGAGAGCAACCAAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
Qy 1021 GTCAACCAAGT 1080
Db 1021 GTCAACCAAGT 1080
Qy 1081 AATTTTCAAGT 1140
Db 1081 AATTTTCAAGT 1140
Qy 1141 CGTAAACAGAAACGAAACCTCTCTGTGGCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
Db 1141 CGTAAACAGAAACGAAACCTCTCTGTGGCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200

Qy 1201 ATCTTCATCATATTTTCTCTATGTGTGTATTCCTGTGGGCGCTTACTGCTTTTACAGTC 1260
Db 1201 ATCTTCATCATATTTTCTCTATGTGTGTATTCCTGTGGGCGCTTACTGCTTTTACAGTC 1260
Qy 1261 CTGGCGGTGTGGGT 1320
Db 1261 CTGGCGGTGTGGGT 1320
Qy 1321 TGGCTTTTCTTCTGT 1380
Db 1321 TGGCTTTTCTTCTGT 1380
Qy 1381 ATTTAAGAAAGAAATTCAGAGCATGTGTGAAGAGTTCTTGTGCAAGAAAGCCCGGAAA 1440
Db 1381 ATTTAAGAAAGAAATTCAGAGCATGTGTGAAGAGTTCTTGTGCAAGAAAGCCCGGAAA 1440
Qy 1441 GAAGATGACCAACCCAGACCTGCGGGAACAGAGGTGTGGACTGTGAAGGAGATTGTCCCT 1500
Db 1441 GAAGATGACCAACCCAGACCTGCGGGAACAGAGGTGTGGACTGTGAAGGAGATTGTCCCT 1500
Qy 1501 TCCTACGATTCTGTACTTTTCTTGA 1527
Db 1501 TCCTACGATTCTGTACTTTTCTTGA 1527

RESULT 2
US-10-088-726-26
; Sequence 26, Application US/10088726
; Publication No. US2003015758A1
; GENERAL INFORMATION:
; APPLICANT: Matsumoto et al.
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE-BINDING PROTEIN-COUPLED RECEPTORS AND USES THEREOF
; FILE REFERENCE: 62514
; CURRENT APPLICATION NUMBER: US/10/088,726
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: PCT/JP00/09408
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 1999-375152
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: JP 2000-101339
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-088-726-26

Query Match 100.0%; Score 1527; DB 6; Length 1527;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGCTCACCTGTGACCAACAGCAGCGCGAGAGTAACAGACGACACGTCATGCGCC 60
Db 1 ATGAGCTCACCTGTGACCAACAGCAGCGCGAGAGTAACAGACGACACGTCATGCGCC 60
Qy 61 CTCTCAAAATGCCATATAGCTGTGGCCAGGCAATCCGCTCAACCGTGTGTATC 120
Db 61 CTCTCAAAATGCCATATAGCTGTGGCCAGGCAATCCGCTCAACCGTGTGTATC 120
Qy 121 TTCTTGCGCGCTTTTGTGTGGCAACATAGTGTGGCGCTAGTGTGGACGGACGG 180
Db 121 TTCTTGCGCGCTTTTGTGTGGCAACATAGTGTGGCGCTAGTGTGGACGGACGG 180
Qy 181 CAGCTGTGAGAGTGAACCGTTTATCTTTAAGCTGTGTGACCGAAGCTGTGTGAG 240
Db 181 CAGCTGTGAGAGTGAACCGTTTATCTTTAAGCTGTGTGACCGAAGCTGTGTGAG 240
Qy 241 ATTTCGCTGTGGCCCTGTGGTGTGGACCTGTGTGCTCTCTTGTGGCCCTCAAC 300

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Db 241 ATTGCGTCGTGAGCCCGCTGGGTGTGGCACTGTGCTCTCTTCTGGCCCTTCAAC 300
Qy 301 AGGCACTTGTGACGGCCCTGGTTAGCTCAACCACCTGTGGCCTTGGCAAGCTCAAC 360
Db 301 AGGCACTTGTGACGGCCCTGGTTAGCTCAACCACCTGTGGCCTTGGCAAGCTCAAC 360
Qy 361 ACCATTGTCTGTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 420
Db 361 ACCATTGTCTGTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 420
Qy 421 TCCAAAGATGACCCAGCGCCGGTTACCTGTCTCTATGAGCACTGGAATTGTGGCCATC 480
Db 421 TCCAAAGATGACCCAGCGCCGGTTACCTGTCTCTATGAGCACTGGAATTGTGGCCATC 480
Qy 481 CTGCAAGAGACTCTCACTCACTGAGCTGGGCGCAGGCTGCTTGTATGAGGCAATGCT 540
Db 481 CTGCAAGAGACTCTCACTCACTGAGCTGGGCGCAGGCTGCTTGTATGAGGCAATGCT 540
Qy 541 CTCTGCTCATGATCTGGGGGGGCAAGCCAGCTACACTATTTCTCAGCGTGTGCTTC 600
Db 541 CTCTGCTCATGATCTGGGGGGGCAAGCCAGCTACACTATTTCTCAGCGTGTGCTTC 600
Qy 601 ATGCTCATTCACCTGATGTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 ATGCTCATTCACCTGATGTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy 661 AGGCAAGATGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 661 AGGCAAGATGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Qy 721 TGTGTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 780
Db 721 TGTGTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 780
Qy 781 GAGTTTCGCGCCGAGCATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 840
Db 781 GAGTTTCGCGCCGAGCATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 840
Qy 841 GAGCGAGCTGTGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Db 841 GAGCGAGCTGTGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Qy 901 AGGCGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
Db 901 AGGCGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
Qy 961 AAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
Db 961 AAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
Qy 1021 GTCAACCACTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Db 1021 GTCAACCACTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Qy 1081 AATTTTCACTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
Db 1081 AATTTTCACTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
Qy 1141 CGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
Db 1141 CGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
Qy 1201 ATTTTCACTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
Db 1201 ATTTTCACTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
Qy 1261 CTGAGCGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Db 1261 CTGAGCGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Qy 1321 TGGCTTTTCTTCTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Db 1321 TGGCTTTTCTTCTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1380
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Qy 1381 ATTAAGAGAAATCAGAGATGCTGAGAGATTTCTTGTGCAAGAAAAGCCCGAAA 1440
Db 1381 ATTAAGAGAAATCAGAGATGCTGAGAGATTTCTTGTGCAAGAAAAGCCCGAAA 1440
Qy 1441 GAAAGATGACCAACCAAGCTGCTGCGGAAAGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1500
Db 1441 GAAAGATGACCAACCAAGCTGCTGCGGAAAGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1500
Qy 1501 TCTTACGATTTCTGCTACTTTTCTTGA 1527
Db 1501 TCTTACGATTTCTGCTACTTTTCTTGA 1527

RESULT 3
US-10-712-615-1
; Sequence 1, Application US/10712615
; Publication No. US20040214317A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMB6, EXPRESSED
; TITLE OF INVENTION: HIGHLY IN BRAIN
; FILE REFERENCE: D0047A-CIP
; CURRENT FILING DATE: 2003-11-13
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: U.S. 60/248,285
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: U.S. 60/268,581
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/308,285
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: U.S. 60/317,166
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-712-615-1

Query Match 100.0%; Score 1527; DB 8; Length 1527;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGCTCCACCTGCAACCAAGCAAGCGCGAGAGTAAACAGCAGCCACGTCATGCC 60
Db 1 ATGAGCTCCACCTGCAACCAAGCAAGCGCGAGAGTAAACAGCAGCCACGTCATGCC 60
Qy 61 CTCTCCAAATGCCATGAGCTGTGCGCCACGCGATCATCTGCTCAACCGTGTGTTATC 120
Db 61 CTCTCCAAATGCCATGAGCTGTGCGCCACGCGATCATCTGCTCAACCGTGTGTTATC 120
Qy 121 TTCTGCGCGCTTTTGTGTGGAACAATAGTGTGAGCTGTGAGTGTGAGGAGGAGCGCG 180
Db 121 TTCTGCGCGCTTTTGTGTGGAACAATAGTGTGAGCTGTGAGTGTGAGGAGGAGCGCG 180
Qy 181 CAGCTGCTCAGATGACCAACCGTTTATCTTTAACTTCTGTCACCGACCTGTGCAAG 240
Db 181 CAGCTGCTCAGATGACCAACCGTTTATCTTTAACTTCTGTCACCGACCTGTGCAAG 240
Qy 241 ATTTGCTGTGAGCGCTGTGAGTGTGAGCAGCTGTGCTCTTCTTGTGAGCGCTCAAC 300
Db 241 ATTTGCTGTGAGCGCTGTGAGTGTGAGCAGCTGTGCTCTTCTTGTGAGCGCTCAAC 300
Qy 301 AGCACTTGTGACGGCCCTGTGAGTGTGAGCAGCAACCTGTGCGCTTGTGCGAGCGTCAAC 360
Db 301 AGCACTTGTGACGGCCCTGTGAGTGTGAGCAGCAACCTGTGCGCTTGTGCGAGCGTCAAC 360
Qy 361 ACCATTGTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
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Db	361	ACCAATGGCTTGGGTGCAAGTGGATGCGTCACTTGTGCATCATCACAACCCCTCTCTCCAAACCGG	420
Qy	421	TCCAAGATGACCCACAGCGCGCGGTTAACTGCTCTCTCTATGAGCACTTGAAATGTGGCCATC	480
Db	421	TCCAAGATGACCCACAGCGCGCGGTTAACTGCTCTCTCTATGAGCACTTGAAATGTGGCCATC	480
Qy	481	CTGCAGAGACATCTCCATCCATAGGCTGTGGGGGCCAGGGCTGCTTTGATGAGGGCAATGCT	540
Db	481	CTGCAGAGACATCTCCATCCATAGGCTGTGGGGGCCAGGGCTGCTTTGATGAGGGCAATCT	540
Qy	541	CTCTAGCTCCATATGATGTGGGGGGCCAGCCCACTACACTATCTCAGCGTGGTGTCTTC	600
Db	541	CTCTAGCTCCATATCTGCGGGGGGCCAGCCCACTACACTATCTCAGCGTGGTGTCTTC	600
Qy	601	ATCGTCATTTCCATGATATGTCATGATTTGCTGTCTACCTCGTGGTGTCTGTGCAACCCGG	660
Db	601	ATCGTCATTTCCATGATATGTCATGATTTGCTGTCTACCTCGTGGTGTCTGTGCAACCCGG	660
Qy	661	AGGCAGCAATGCTCTGCTGTGACAAATGTCAAAGAACACAGTTTGGAAATGTCAGGTCAAAGAC	720
Db	661	AGGCAGCAATGCTCTGCTGTGACAAATGTCAAAGAACACAGTTTGGAAATGTCAGGTCAAAGAC	720
Qy	721	TGTGTGAGAAATGAGATGTAAGAGGAGCAGAGAAAGAGAGAGATTCCAGATGAGAGT	780
Db	721	TGTGTGAGAAATGAGATGTAAGAGGAGCAGAGAAAGAGAGAGATTCCAGATGAGAGT	780
Qy	781	GAGTTTCGCGCGCCAGCATGAAAGTGAAGTCAAGGCCAAGAGAGGAGCAATGGAACCCAAAG	840
Db	781	GAGTTTCGCGCGCCAGCATGAAAGTGAAGTCAAGGCCAAGAGAGGAGCAATGGAACCCAAAG	840
Qy	841	GACGGCAGCCTGAAGGCCAAGGAAGAGACAGGGGACCACTGAGAAATGTTGTAAGGCC	900
Db	841	GACGGCAGCCTGAAGGCCAAGGAAGAGACAGGGGACCACTGAGAAATGTTGTAAGGCC	900
Qy	901	AGGGCAGCGGAGGAGGTCAAGAGAGCAGCAGGTGGCCAGGAGCGGCAGCATGGAAGGT	960
Db	901	AGGGCAGCGGAGGAGGTCAAGAGAGCAGCAGGTGGCCAGGAGCGGCAGCATGGAAGGT	960
Qy	961	AAGGAAGCGCAGCACCMAAGTTGAGAGAAACAGCATGAAGGCAAGAGGTTGCAACAG	1020
Db	961	AAGGAAGCGCAGCACCMAAGTTGAGAGAAACAGCATGAAGGCAAGAGGTTGCAACAG	1020
Qy	1021	GTCAACCAAGTGCAGCATTTGACTTGGGTGAAGTGAATGCAATGGAATTTGTGTGAACACATC	1080
Db	1021	GTCAACCAAGTGCAGCATTTGACTTGGGTGAAGTGAATGCAATGGAATTTGTGTGAACACATC	1080
Qy	1081	AATTTCAAGTGAAGATGACGTGCAGAGCAGTGAACATCCGCGAGAGGCTCCACCCAGTGT	1140
Db	1081	AATTTCAAGTGAAGATGACGTGCAGAGCAGTGAACATCCGCGAGAGGCTCCACCCAGTGT	1140
Qy	1141	CGTAAACAGCAACGCAACCCCTCTCTGCCCAGGTGTCAACAGTGCMAAGCTGTCTAAAGTG	1200
Db	1141	CGTAAACAGCAACGCAACCCCTCTCTGCCCAGGTGTCAACAGTGCMAAGCTGTCTAAAGTG	1200
Qy	1201	ATCTTCATATCATTTTCTCTATGTGTGCTATCCCTGGGGCCTTACTGCTTTTACAGTC	1260
Db	1201	ATCTTCATATCATTTTCTCTATGTGTGCTATCCCTGGGGCCTTACTGCTTTTACAGTC	1260
Qy	1261	CTGGCCGATGTGGGTGATGTCGAAACCAGGTAAACCCAGTGGGTATCCATTAATCATTC	1320
Db	1261	CTGGCCGATGTGGGTGATGTCGAAACCAGGTAAACCCAGTGGGTATCCATTAATCATTC	1320
Qy	1321	TGGCTTTTCTCTGAGTGTGCAATCCACCCCTATGTCTATAGGCTACATGCAACAAGC	1380
Db	1321	TGGCTTTTCTCTGAGTGTGCAATCCACCCCTATGTCTATAGGCTACATGCAACAAGC	1380
Qy	1381	ATTAAAGAGAAATCCAGACATGCTGAAGAAATTTCTGCAAGGAAAAAGCCCCGAAA	1440
Db	1381	ATTAAAGAGAAATCCAGACATGCTGAAGAAATTTCTGCAAGGAAAAAGCCCCGAAA	1440
Qy	1441	GAAAGTATGCCATCCCAAGCCTGTGCCCGGGAACAGAGGGTGGGACTGMAAGCAAGTTGTCCCT	1500
Db	1441	GAAAGTATGCCATCCCAAGCCTGTGCCCGGGAACAGAGGGTGGGACTGMAAGCAAGTTGTCCCT	1500

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QY 1501 TCCTACGATTCGCTACTTTTCCTTGA 1527
Db 1501 TCCTACGATTCGCTACTTTTCCTTGA 1527

RESULT 4
US-09-992-238-47
/ Sequence 47, Application US/09992238
/ Publication No. US2003054444A1
/ GENERAL INFORMATION:
/ APPLICANT: BATAGLINO, PETER
/ APPLICANT: FEDER, JOHN N
/ APPLICANT: MINTIER, GABE
/ APPLICANT: NELSON, THOMAS C
/ APPLICANT: RAMANATHAN, CHANDRA S
/ APPLICANT: WESTPHAL, RYAN
/ APPLICANT: CACACE, ANGELA
/ APPLICANT: BARBER, LAUREN
/ APPLICANT: HAWKEN, DONALD R
/ APPLICANT: KORBACKER, MICHAEL G
/ TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGRPMY8,
/ TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN
/ FILE REFERENCE: D0047NP
/ CURRENT APPLICATION NUMBER: US/09/992,238
/ CURRENT FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: 60/317166
/ PRIOR FILING DATE: 2001-09-04
/ PRIOR APPLICATION NUMBER: 60/308285
/ PRIOR FILING DATE: 2001-07-27
/ PRIOR APPLICATION NUMBER: 60/266581
/ PRIOR FILING DATE: 2001-02-14
/ PRIOR APPLICATION NUMBER: 60/240285
/ PRIOR FILING DATE: 2000-11-14
/ NUMBER OF SEQ ID NOS: 102
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 47
/ LENGTH: 1580
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-992-238-47

Query Match 100.0%; Score 1527; DB 3; Length 1580;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 ATGAGCTGCACCTGCAACCAACGACGCGCGGAGAGTAACAGACGCCAACGTCATGCC 60
Db 32 ATGAGGTCACACTGCAACCAACGACGCGCGGAGAGTAACAGACGCCAACGTCATGCC 91
QY 61 CTCTCCAAATATGCCCATGACGCTGAGCCACAGGATCATCCGCTCAACGCTGCTATATC 120
Db 92 CTCTCCAAATATGCCCATGACGCTGAGCCACAGGATCATCCGCTCAACGCTGCTATATC 151
QY 121 TTCTCGCCGCTCTTTTGTGGGCAACATAGTGTGGGCTTAGTGTGACGCAAGCCG 180
Db 152 TTCTCGCCGCTCTTTTGTGGGCAACATAGTGTGGGCTTAGTGTGACGCAAGCCG 211
QY 181 CAGCTGCTGCAAGGTACCAACCGTTTATCTTTAACCTTCCTGACCGAAGCTGTGAG 240
Db 212 CAGCTGCTGCAAGGTACCAACCGTTTATCTTTAACCTTCCTGACCGAAGCTGTGAG 271
QY 241 ATTTGCTGCTGAGGCCCCCTGGGTGGTGGCACTGTGAGCTCTCTTGAGCCCTCAAC 300
Db 272 ATTTGCTGCTGAGGCCCCCTGGGTGGTGGCACTGTGAGCTCTCTTGAGCCCTCAAC 331
QY 301 AGCCACTTCTGACGAGGCCCCCTGGTTAGCCTCAACCACTGTTGCTTGCCAGGCTCAAC 360
Db 332 AGCCACTTCTGACGAGGCCCCCTGGTTAGCCTCAACCACTGTTGCTTGCCAGGCTCAAC 391
QY 361 ACCATTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Db 392 ACCATTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 451

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421 TCAGAGATGACCGAGCGCGGTTACCTGCTCTCTATGCACTGTGATGTCGATC 480
452 TCAGAGATGACCGAGCGCGGTTACCTGCTCTCTATGCACTGTGATGTCGATC 511
481 CTGAGAGATGACCGAGCGCGGTTACCTGCTCTCTATGCACTGTGATGTCGATC 540
512 CTGAGAGATGACCGAGCGCGGTTACCTGCTCTCTATGCACTGTGATGTCGATC 571
541 CTGCTCTCATGATCTGAGGAGCGAGCGCGGTTACCTGCTCTCTATGCACTGTGATGTCGATC 600
572 CTGCTCTCATGATCTGAGGAGCGAGCGCGGTTACCTGCTCTCTATGCACTGTGATGTCGATC 631
601 ATGCTATTCATGATCTGAGGAGCGAGCGCGGTTACCTGCTCTCTATGCACTGTGATGTCGATC 660
632 ATGCTATTCATGATCTGAGGAGCGAGCGCGGTTACCTGCTCTCTATGCACTGTGATGTCGATC 691
661 AGGAGATGATCTGCTGTACATGATGCAAGAGACACAGCTTGGAGTGGAGTCAAGAC 720
692 AGGAGATGATCTGCTGTACATGATGCAAGAGACACAGCTTGGAGTGGAGTCAAGAC 751
721 TGTGTGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
752 TGTGTGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 811
781 GAGTTTCGCGCGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
812 GAGTTTCGCGCGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 871
841 GAGCGAGCTTGAAG 900
872 GAGCGAGCTTGAAG 931
901 AGGAG 960
932 AGGAG 991
961 AGGAG 1020
992 AGGAG 1051
1021 GTCAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080
1052 GTCAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1111
1081 AATTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1140
1112 AATTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1171
1141 CGTAAAG 1200
1172 CGTAAAG 1231
1201 ATTCATCATGATCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
1232 ATTCATCATGATCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1291
1261 CTGAG 1320
1292 CTGAG 1351
1321 TGGCTTTTCTCTGAG 1380
1352 TGGCTTTTCTCTGAG 1411
1381 ATTTAAG 1440
1412 ATTTAAG 1471
1441 GAGAGATGAG 1500
1472 GAGAGATGAG 1531

1501 TCCTACGATCTGCTACTTTCTTCTGA 1527
1532 TCCTACGATCTGCTACTTTCTTCTGA 1558
RESULT 5
US-10-712-615-47
; Sequence 47, Application US/10712615
; Publication No. US20040214317A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMT8, EXPRESSED
; FILE REFERENCE: D0047A-CIP
; CURRENT APPLICATION NUMBER: US/10/712,615
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: U.S. 09/992,238
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: U.S. 60/248,285
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: U.S. 60/268,581
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/308,285
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: U.S. 60/317,166
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: Patencin version 3.2
; SEQ ID NO 47
; LENGTH: 1580
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-712-615-47
Query Match 100.0%; Score 1527; DB 8; Length 1580;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGAGTCCACCTGACCAACAGACGCGGAGAGTAACAGAGACAGACAGTGCATGCC 60
32 ATGAGTCCACCTGACCAACAGACGCGGAGAGTAACAGAGACAGACAGTGCATGCC 91
61 CTCTCAAAATGCCATGACGCTGCGCCAGCATCATCCGCTCAACCGTGTGTTATC 120
92 CTCTCAAAATGCCATGACGCTGCGCCAGCATCATCCGCTCAACCGTGTGTTATC 151
121 TTCTCGCGCGCTTTTGTGTGCAACATAGTGTGCGGTAGTGTGAGCGCAAGCGG 180
152 TTCTCGCGCGCTTTTGTGTGCAACATAGTGTGCGGTAGTGTGAGCGCAAGCGG 211
181 GAGCTGACAGAGTGAACCAACGTTTATCTTTAATCTCTGTCAGCAAGAGCTGAG 240
212 GAGCTGACAGTGAACCAACGTTTATCTTTAATCTCTGTCAGCAAGAGCTGAG 271
241 ATTGCTGTCGCGCGCGCTGAGTGTGCAACCTGTCCTCTGTCGCGCGCTCAAC 300
272 ATTGCTGTCGCGCGCGCTGAGTGTGCAACCTGTCCTCTGTCGCGCGCTCAAC 331
301 AGCCTCTGCAAGAGCGCGCTGATGCTCAACCACTGTTGCTGCGCGCGCTCAAC 360
332 AGCCTCTGCAAGAGCGCGCTGATGCTCAACCACTGTTGCTGCGCGCGCTCAAC 391
361 ACCATTTCTGAGTGTGCAAGTGTGCACTTGTGCAATCATCAACCTCTCTACCGG 420
392 ACCATTTCTGAGTGTGCAAGTGTGCACTTGTGCAATCATCAACCTCTCTACCGG 451
421 TCAGAGATGACCGAGCGCGGTTACCTGCTCTCTATGCACTGTGATGTCGATC 480
452 TCAGAGATGACCGAGCGCGGTTACCTGCTCTCTATGCACTGTGATGTCGATC 511
481 CTGAGAGATGACCGAGCGCGGTTACCTGCTCTCTATGCACTGTGATGTCGATC 540
512 CTGAGAGATGACCGAGCGCGGTTACCTGCTCTCTATGCACTGTGATGTCGATC 571

QY	541	TTCTGCTCAAGATCTGGGGGGCCAGCCCAAGCTACAATATTCAGGCTGCTCTC	600
Db	572	CTTGCTTCATGATCTGGGGGGCCAGCCCAAGCTACAATATTCAGGCTGCTCTC	631
QY	601	ATCTCATTCACATGATTTGTCAATGATTTGCTCTACTCCGTGGTGTCTGTGCACGCCGG	660
Db	632	ATCTCATTCACATGATTTGTCAATGATTTGCTCTACTCCGTGGTGTCTGTGCACGCCGG	691
QY	661	AGGCAGCATGCTCTGCTCTGTACAATGTCAAGAGACACACACTTGGAAAGTCCGAGTCAAGAC	720
Db	692	AGGCAGCATGCTCTGCTCTGTACAATGTCAAGAGACACACACTTGGAAAGTCCGAGTCAAGAC	751
QY	721	TGTGTGAAGAAATGAGATGGAAGAGGAGCAGAGAAAGAGAGAGTTCCAGATGAGAGT	780
Db	752	TGTGTGAAGAAATGAGATGGAAGAGGAGCAGAGAAAGAGAGAGTTCCAGATGAGAGT	811
QY	781	GAGTTTCGCCGCCACAGCATGAAGGTGAGTCAAAGCCAAAGAGGCGAGATGGAAGCCAAAG	840
Db	812	GAGTTTCGCCGCCACAGCATGAAGGTGAGTCAAAGCCAAAGAGGCGAGATGGAAGCCAAAG	871
QY	841	GACGGCAGCCTTGAAGGCCCAAGGAAGGACACGGGGACCATGTGAGATGATGTAGAGGCC	900
Db	872	GACGGCAGCCTTGAAGGCCCAAGGAAGGACACGGGGACCATGTGAGATGATGTAGAGGCC	931
QY	901	AGGGGACAGCAGAGAGGTCAAGAGAGCAGCAGGTGGCCAGCGGACGGCAGCATGGAGGTT	960
Db	932	AGGGGACAGCAGAGAGGTCAAGAGAGCAGCAGGTGGCCAGCGGACGGCAGCATGGAGGTT	991
QY	961	AAGGAAGCAGCACCAAAATGTTAGGAGAAACAGCATGAAGGCAAGAGGTTGCGACAGAG	1020
Db	992	AAGGAAGCAGCACCAAAATGTTAGGAGAAACAGCATGAAGGCAAGAGGTTGCGACAGAG	1051
QY	1021	GTCAACCAAGTGACGATTAAGTCTGGGGTAAAGTGCATGAGATTGTGGAAAGCAGCATC	1080
Db	1052	GTCAACCAAGTGACGATTAAGTCTGGGGTAAAGTGCATGAGATTGTGGAAAGCAGCATC	1111
QY	1081	AATTTCAAGTGAAGATGAGCTCGAGGACAGTGAACATCCGGAGAGCCTCCACCCAGTGGT	1140
Db	1112	AATTTCAAGTGAAGATGAGCTCGAGGACAGTGAACATCCGGAGAGCCTCCACCCAGTGGT	1171
QY	1141	CGTAACAGCAACAGCAACCCCTCTCTGCCCAGGTGCTACCAAGTCAAAAGCTGTCTAAAGTG	1200
Db	1172	CGTAACAGCAACAGCAACCCCTCTCTGCCCAGGTGCTACCAAGTCAAAAGCTGTCTAAAGTG	1231
QY	1201	ATCTTCATCATCATTTTCTCCCTATGTGCTATCCCTGGGGGCCCTTACTGTGCTTTTATCAGTCT	1260
Db	1232	ATCTTCATCATCATTTTCTCCCTATGTGCTATCCCTGGGGGCCCTTACTGTGCTTTTATCAGTCT	1291
QY	1261	CTGGCCGTGTGGGTGATGTGCAAAACCCAGGTATCCCAAGTGGGTATCAACATATCATC	1320
Db	1292	CTGGCCGTGTGGGTGATGTGCAAAACCCAGGTATCCCAAGTGGGTATCAACATATCATC	1351
QY	1321	TGGCTTTTCTTCTCTGAGTGTCTGCATCCACCCCTATGTCTATAGGCTACATGCACAAGAC	1380
Db	1352	TGGCTTTTCTTCTCTGAGTGTCTGCATCCACCCCTATGTCTATAGGCTACATGCACAAGAC	1411
QY	1381	ATTAGAAGAGAAATCCAGGACATGTCTGAAGAGTCTTCTGCAAGAAAGAGCCCGCGAAA	1440
Db	1412	ATTAGAAGAGAAATCCAGGACATGTCTGAAGAGTCTTCTGCAAGAAAGAGCCCGCGAAA	1471
QY	1441	GAAGATAGCAACCCAGACCTGCCCCGAAACAGAGGTTGGGACTGAAGGCAAGATTTGCCCT	1500
Db	1472	GAAGATAGCAACCCAGACCTGCCCCGAAACAGAGGTTGGGACTGAAGGCAAGATTTGCCCT	1531
QY	1501	TCCTACGATTCGTCTACTTTTCTCTTGA	1527
Db	1532	TCCTACGATTCGTCTACTTTTCTCTTGA	1558

RESULT 6
US-10-293-983-8
; Sequence 8, Application US/10293983

	Publication No.	US20030149998A1
	GENERAL INFORMATION:	
	APPLICANT:	Wyeth
	APPLICANT:	Blatcher, Maria
	APPLICANT:	Paulsen, Janet
	APPLICANT:	Bates, Brian G
	TITLE OF INVENTION:	Genes Encoding G Protein Coupled Receptors and Uses Therefor
	FILE REFERENCE:	AM100476
	CURRENT APPLICATION NUMBER:	US/10/293,983
	CURRENT FILING DATE:	2002-11-13
	NUMBER OF SEQ ID NOS:	25
	SOFTWARE:	Patentin version 3.1
	SEQ ID NO	8
	LENGTH:	4718
	TYPE:	DNA
	ORGANISM:	Homo sapiens
	FEATURE:	
	NAME/KEY:	exon
	LOCATION:	(332)..(1858)
	OTHER INFORMATION:	
	US-10-293-983-8	
	Query Match	100.0%; Score 1527; DB 6; Length 4718;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 1527; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Oy	1	ATGAGCTCCACTTGACCAACAGCAGCGCGAGAGTAAACAGACGACAGCTGCATGCC 60
Db	332	ATGAGCTCCACTTGACCAACAGCAGCGCGAGAGTAAACAGCAGCGACAGCTGCATGCC 391
Oy	61	CTCTCCAAATGGCCCATACGCGCTGGGCCAGCGCATCATCGCTCAAACGTGCTGTTATTC 120
Db	392	CTCTCCAAATGGCCCATACGCGCTGGGCCAGCGCATCATCGCTCAAACGTGCTGTTATTC 451
Oy	121	TTCTCTCCCGCCTCTTTCGTGCGGAACAATAGTGTGGCGCTAGTGTGGAGCGCAAGCGG 180
Db	452	TTCTCTCCCGCCTCTTTCGTGCGGAACAATAGTGTGGCGCTAGTGTGGAGCGCAAGCGG 511
Oy	181	CAGCTGTGAGGTGACCAACCGTTTTATTCTTTAACCTCTCTGTCACGCACTGCTGCAG 240
Db	512	CAGCTGTGAGGTGACCAACCGTTTTATTCTTTAACCTCTCTGTCACGCACTGCTGCAG 571
Oy	241	ATTTCCGTGCTGGCCCCCTGGGTGGTGGGCACTCTGTGACCCTCTCTTGGGCCCTCAAC 300
Db	572	ATTTCCGTGCTGGCCCCCTGGGTGGTGGGCACTCTGTGACCCTCTCTTGGGCCCTCAAC 631
Oy	301	AGCACCTTTCGACAGGCGCTGTGTTAGCTCACACCACTGTTGGCCTTGGCAGCGTCAAC 360
Db	632	AGCACCTTTCGACAGGCGCTGTGTTAGCTCACACCACTGTTGGCCTTGGCAGCGTCAAC 691
Oy	361	ACCAATGTCTTGGTGTGATGATCGCTAATTGTCCATCATCCACCGCTCTCTTAACCG 420
Db	692	ACCAATGTCTTGGTGTGATGATCGCTAATTGTCCATCATCCACCGCTCTCTTAACCG 751
Oy	421	TCCAAGATGACCAAGCGCGCGGTAACTGTCTCTCTATGGAACCTGGATTGGCCATC 480
Db	752	TCCAAGATGACCAAGCGCGCGGTAACTGTCTCTCTATGGAACCTGGATTGGCCATC 811
Oy	481	CTGAGAGGACCTCTCCACTCTAAGGCTGGGGCAGGCGTCTTGATGAGGGCAATGCT 540
Db	812	CTGAGAGGACCTCTCCACTCTAAGGCTGGGGCAGGCGTCTTGATGAGGGCAATGCT 871
Oy	541	CTTGTCTTCATGATCTGGGGGGCAGAGCCAGGTAACATACTAGCTAGCTGTGCTCTTC 600
Db	872	CTTGTCTTCATGATCTGGGGGGCAGAGCCAGGTAACATACTAGCTAGCTGTGCTCTTC 931
Oy	601	ATGTGTCAATTCACATGATGTTCATGATGCTCTGTACTCCGTGGGTGTTCTGTGACGCCG 660
Db	932	ATGTGTCAATTCACATGATGTTCATGATGCTCTGTACTCCGTGGGTGTTCTGTGACGCCG 991
Oy	661	AGGAGCATGCTCTGCTGTACATGTCAAGAGCACAGCTTGGAGTGGGATCAAGAGC 720
Db	992	AGGAGCATGCTCTGCTGTACATGTCAAGAGCACAGCTTGGAGTGGGATCAAGAGC 1051

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QY 721 TGTGTGGAATGAGATGAAAGAGGAGACAGAAAGAGAGGATTCCAGATGAGAGT 780
DB 1052 TGTGTGGAATGAGATGAAAGAGGAGACAGAAAGAGAGGATTCCAGATGAGAGT 1111
QY 781 GAGTTTCCGCGCCAGATGATGAGTCAAGGCCAAGAGGCGCAATGGAAGCCAG 840
DB 1112 GAGTTTCCGCGCCAGATGATGAGTCAAGGCCAAGAGGCGCAATGGAAGCCAG 1171
QY 841 GACGCGAGCTGAAAGGCCAAGAAAGAGACACGCGGACCAAGTGAAGTATGAGAGCC 900
DB 1172 GACGCGAGCTGAAAGGCCAAGAAAGAGACACGCGGACCAAGTGAAGTATGAGAGCC 1231
QY 901 AAGGAGCAGCGAGAGGTCAAGAGAGACACGCGTGGCCACGACCGGACAGATGAGAGGT 960
DB 1232 AAGGAGCAGCGAGAGGTCAAGAGAGACACGCGTGGCCACGACCGGACAGATGAGAGGT 1291
QY 961 AAGGAAGGAGACCCAAAGTTGAGAGAAACAGATGAAAGCGACAAAGGTCCGACAGAG 1020
DB 1292 AAGGAAGGAGACCCAAAGTTGAGAGAAACAGATGAAAGCGACAAAGGTCCGACAGAG 1351
QY 1021 GTCAACCAAGTGCAGATTGACTTGGGTGAAGATGATGAGAGTTGTGTAAGACGACATC 1080
DB 1352 GTCAACCAAGTGCAGATTGACTTGGGTGAAGATGATGAGAGTTGTGTAAGACGACATC 1411
QY 1081 AATTTCAGTGAAGATGACGTGAGGAGTGAACATCCCGAGAGCCTCCACCCAGTCCGT 1140
DB 1412 AATTTCAGTGAAGATGACGTGAGGAGTGAACATCCCGAGAGCCTCCACCCAGTCCGT 1471
QY 1141 CGTAACAGACAGCAACCTCTCTCTGCCAGGTGCTACCAAGTGCMAAGTCTTAAAGTG 1200
DB 1472 CGTAACAGACAGCAACCTCTCTCTGCCAGGTGCTACCAAGTGCMAAGTCTTAAAGTG 1531
QY 1201 ATCTTCATCATGATTTCTCTATGCTATGCCCTGGGCGCTACTGCTTTTAGAGATC 1260
DB 1532 ATCTTCATCATGATTTCTCTATGCTATGCCCTGGGCGCTACTGCTTTTAGAGATC 1591
QY 1261 CTGGCCGTGTGGGTGATGTCGAAACCCAGGTACCCCAAGTGGGTGATCAACATATATC 1320
DB 1592 CTGGCCGTGTGGGTGATGTCGAAACCCAGGTACCCCAAGTGGGTGATCAACATATATC 1651
QY 1321 TGGCTTTTCTTCTGAGTGTGTCATCAACCCCTATGTCTATGCTTACATGACAAAGACC 1380
DB 1652 TGGCTTTTCTTCTGAGTGTGTCATCAACCCCTATGTCTATGCTTACATGACAAAGACC 1711
QY 1381 ATTTAGAAGGAATCCAGACATGCTGAAGAGTTCTTCTGCAAGGAAAGCCCGGAAA 1440
DB 1712 ATTTAGAAGGAATCCAGACATGCTGAAGAGTTCTTCTGCAAGGAAAGCCCGGAAA 1771
QY 1441 GAAGATAGCCACCCAGACCTGCCCCGAAAGAGAGGTGGAGCTGAAGCAATTTGCCCT 1500
DB 1772 GAAGATAGCCACCCAGACCTGCCCCGAAAGAGAGGTGGAGCTGAAGCAATTTGCCCT 1831
QY 1501 TCTTACGATTTCTGCTACTTTTCTCTTGA 1527
DB 1832 TCTTACGATTTCTGCTACTTTTCTCTTGA 1858

RESULT 7
US-09-791-932-52
; Sequence 52, Application US/09791932
; Publication No. US20030003451A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayles, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030003451A1e1 G Protein-Coupled Receptors Cross-Referen
; FILE REFERENCE: 00325. US1
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; CURRENT APPLICATION NUMBER: US/09/791,932
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/186,810
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/188,064
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/186,457
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/213,861
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/194,344
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/218,337
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 52
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-791-932-52

Query Match      99.9%; Score 1525.4; DB 3; Length 1527;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGCTCCAGCTGACCCCAAGCAAGCGCGGAGAGAAACAGAGCCAGCGATGAGCC 60
DB 1 ATGAGCTCCAGCTGACCCCAAGCAAGCGCGGAGAGAAACAGAGCCAGCGATGAGCC 60
QY 61 CTCTCCAAATGCCATCAGCTGCGCCACGAGCATCATCCGCTCAACCGTGTGTTATC 120
DB 61 CTCTCCAAATGCCATCAGCTGCGCCACGAGCATCATCCGCTCAACCGTGTGTTATC 120
QY 121 TTCTGCGCGCTCTTTTGTGCGCAACATAGTGTGGCGCTAGTGTGAGCGCAAGCCG 180
DB 121 TTCTGCGCGCTCTTTTGTGCGCAACATAGTGTGGCGCTAGTGTGAGCGCAAGCCG 180
QY 181 CAGCTGCGAGGTAGCAACCGTTTAACTTTAACTCTCTGTACCGACCGACCTGCGAG 240
DB 181 CAGCTGCGAGGTAGCAACCGTTTAACTTTAACTCTCTGTACCGACCGACCTGCGAG 240
QY 241 ATTTGCGTGTGGCCCTGAGTGTGGCCACCTGTGCTCTCTTCTGAGCCCTCAAC 300
DB 241 ATTTGCGTGTGGCCCTGAGTGTGGCCACCTGTGCTCTCTTCTGAGCCCTCAAC 300
QY 301 ACCCACTTGTGACGCGCCTGTGTTAGCTGACCCACCTGTGCTTGGCCAGCGTCAAC 360
DB 301 ACCCACTTGTGACGCGCCTGTGTTAGCTGACCCACCTGTGCTTGGCCAGCGTCAAC 360
QY 361 ACCATTTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 361 ACCATTTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 TCCAAGATGACCCAGCGCGCGTTAACTGCTCTCTATGGAACCTGATTTGTGCGCATC 480
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Db 421 TCCTAGATGACCGGCGGTTACCTGCTCTCTATGAGACCTGATGTTGGCCATC 480
Qy 481 CTGAGAGACACTCTCCACTCTAGGGCTGGGGCCAGGCTGCTTTGATAGCGCAATGCT 540
Db 481 CTGAGAGACACTCTCCACTCTAGGGCTGGGGCCAGGCTGCTTTGATAGCGCAATGCT 540
Qy 541 CTGCTCCTCATGATCTGGGGGGCCAGCCCAAGCTACACTATTCTCAGCGTGGTCTTC 600
Db 541 CTGCTCCTCATGATCTGGGGGGCCAGCCCAAGCTACACTATTCTCAGCGTGGTCTTC 600
Qy 601 ATCCGATTTCCACTGATGTCATGATGCTGCTCTCTCCGCTGCTCTCTCTCTCTCTCT 660
Db 601 ATCCGATTTCCACTGATGTCATGATGCTGCTCTCTCCGCTGCTCTCTCTCTCTCTCT 660
Qy 661 AGGCGACATGCTCTCTGTAACAATGTAAGAGACACAGCTTGGAGTGGAGTCAAGGAC 720
Db 661 AGGCGACATGCTCTCTGTAACAATGTAAGAGACACAGCTTGGAGTGGAGTCAAGGAC 720
Qy 721 TGTGTGAGAAATGAGATGAAAGGAGGAGAGAGAAAGAGAGAGTTCAGAGATGAGAT 780
Db 721 TGTGTGAGAAATGAGATGAAAGGAGGAGAGAGAAAGAGAGAGTTCAGAGATGAGAT 780
Qy 781 GAGTTTCCCGCCAGCATGAAAGTGAAGTCAAGGCTCAAGAGAGGCAAGATGGAACCCAG 840
Db 781 GAGTTTCCCGCCAGCATGAAAGTGAAGTCAAGGCTCAAGAGAGGCAAGATGGAACCCAG 840
Qy 841 GACGCGACCTGTAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 GACGCGACCTGTAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Qy 901 AGGGGACGAG 960
Db 901 AGGGGACGAG 960
Qy 961 AAGGAAAGGACAGACCAAGTTGAGAGAAACAGCATGAAAGGAGAGAGAGAGAGAG 1020
Db 961 AAGGAAAGGACAGACCAAGTTGAGAGAAACAGCATGAAAGGAGAGAGAGAGAGAG 1020
Qy 1021 GTCAACAGAGTGCAGATGACTTTGGGTGAAATGACATGAGATTTGGTGAAGCAGATC 1080
Db 1021 GTCAACAGAGTGCAGATGACTTTGGGTGAAATGACATGAGATTTGGTGAAGCAGATC 1080
Qy 1081 AATTTCACTGAGATGACGTCGAGGACAGTGAACATCCCGAGAGGCTCCCAACAGTCT 1140
Db 1081 AATTTCACTGAGATGACGTCGAGGACAGTGAACATCCCGAGAGGCTCCCAACAGTCT 1140
Qy 1141 CGTAACAGCAACAGAACCTCTCTGCGCCAGAGTGTACCAAGTGCMAAGCTCTAAAGT 1200
Db 1141 CGTAACAGCAACAGAACCTCTCTGCGCCAGAGTGTACCAAGTGCMAAGCTCTAAAGT 1200
Qy 1201 ATCTTCATCATGATTTCTCTATGTCATGCTCTGGGGGCTCTACCTGCTTTTAAAGATC 1260
Db 1201 ATCTTCATCATGATTTCTCTATGTCATGCTCTGGGGGCTCTACCTGCTTTTAAAGATC 1260
Qy 1261 CTGGCGCTGTGGGTGATGTGAAAACCCAGGTACCCCACTGGGTGATCATCAATATCATC 1320
Db 1261 CTGGCGCTGTGGGTGATGTGAAAACCCAGGTACCCCACTGGGTGATCATCAATATCATC 1320
Qy 1321 TGGGCTTTTCTCTCTGAGTGTGATCCACCCCTATGTCATGTCATGCAAGAGAC 1380
Db 1321 TGGGCTTTTCTCTCTGAGTGTGATCCACCCCTATGTCATGTCATGCAAGAGAC 1380
Qy 1381 ATTAAGAAGAAATCCAGGACATGCTGAAGAATTTCTTGCAGAGAAAGCCCGGAAA 1440
Db 1381 ATTAAGAAGAAATCCAGGACATGCTGAAGAATTTCTTGCAGAGAAAGCCCGGAAA 1440
Qy 1441 GAAGATAGCCACCAAGCTGCTCGGAGACAGAGGTTGAGAGAGAGAGAGAGATGCTCT 1500
Db 1441 GAAGATAGCCACCAAGCTGCTCGGAGACAGAGGTTGAGAGAGAGAGAGAGATGCTCT 1500
Qy 1501 TCCTAGATTTCTGCTACTTTCTTGA 1527
Db 1501 TCCTAGATTTCTGCTACTTTCTTGA 1527

Db 1501 TCCTAGATTTCTGCTACTTTTCTTGA 1527
RESULT 8
US-09-992-238-45
Sequence 45, Application US/09992238
Publicat ion No. US2003005444A1
GENERAL INFORMATION:
APPLICANT: BATTAGLINO, PETER
APPLICANT: FEDER, JOHN N
APPLICANT: MINTIER, GABE
APPLICANT: NELSON, THOMAS C
APPLICANT: RAMANATHAN, CHANDRA S
APPLICANT: WESTPHAL, RYAN
APPLICANT: CACACE, ANGELA
APPLICANT: BARBER, LAUREN
APPLICANT: HAWKEN, DONALD R
APPLICANT: KORNACKER, MICHAEL G
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBM78,
FILE REFERENCE: D0047NP
CURRENT APPLICATION NUMBER: US/09/992,238
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/317166
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/308285
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/26581
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/248285
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 45
LENGTH: 1527
TYPE: DNA
ORGANISM: Homo sapiens
US-09-992-238-45
Query Match 99.9%; Score 1525.4; DB 3; Length 1527;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGAGTGCACCTGACCAACAGCAGCGCGAGAGTAAACAGAGCCAGCATGTCGCC 60
Db 1 ATGAGTGCACCTGACCAACAGCAGCGCGAGAGTAAACAGAGCCAGCATGTCGCC 60
Qy 61 CTCTCCAAATGCCCATAGCTGTGGCCAGGAGATCATCCGCTCAACCGTGTGTTATC 120
Db 61 CTCTCCAAATGCCCATAGCTGTGGCCAGGAGATCATCCGCTCAACCGTGTGTTATC 120
Qy 121 TTCTCGCGGCTCTTTGCTGCGCAACATAGTGTGGGCTAGTGTGCAAGCGG 180
Db 121 TTCTCGCGGCTCTTTGCTGCGCAACATAGTGTGGGCTAGTGTGCAAGCGG 180
Qy 181 CAGCTGTGACAGTGAACCAACCGTTTATCTTTAACTCTCTGACCGACCTGTGCAG 240
Db 181 CAGCTGTGACAGTGAACCAACCGTTTATCTTTAACTCTCTGACCGACCTGTGCAG 240
Qy 241 ATTTGGCTGTGGGCCCCCTGGGTGTGGCCACCTGTGGCTCTTTCTGGCCCCCTCAAC 300
Db 241 ATTTGGCTGTGGGCCCCCTGGGTGTGGCCACCTGTGGCTCTTTCTGGCCCCCTCAAC 300
Qy 301 AGCCACTTCTGACAGGCTGTTAGCTCAACCCACTGTTGACCTTGGCCAGGCTCAAC 360
Db 301 AGCCACTTCTGACAGGCTGTTAGCTCAACCCACTGTTGACCTTGGCCAGGCTCAAC 360
Qy 361 ACCATTTCTTGTGTGTCAGTGTGATGCTATTGTTCATCATTCACCTCTCTCTACCG 420
Db 361 ACCATTTCTTGTGTGTCAGTGTGATGCTATTGTTCATCATTCACCTCTCTCTACCG 420
Qy 421 TCCTAGATGACCAAGCGCGGTTACTGCTCTCTATGCACTGAGATTTGGGCATC 480
Db 421 TCCTAGATGACCAAGCGCGGTTACTGCTCTCTATGCACTGAGATTTGGGCATC 480

Db 421 TCCAGATGACCGACGGCGGGTTACCTGCTCCTTANGGACCTGGATTGTGCCATC 480
Qy 481 CTGCAGAGCACTCTCCACTCTACGGCTGGGGCCAGGCTCTTTGATGAGCCAAATGCT 540
Db 481 CTGCAGAGCACTCTCCACTCTACGGCTGGGGCCAGGCTCTTTGATGAGCCAAATGCT 540
Qy 541 CTCTGCTCAATGATCTGGGGGGCCAGGCCGCTAACATATTTCTCAGCGTGTGCTTTC 600
Db 541 CTCTGCTCAATGATCTGGGGGGCCAGGCCGCTAACATATTTCTCAGCGTGTGCTTTC 600
Qy 601 ATGCTATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 601 ATGCTATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Qy 661 AGGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 661 AGGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Qy 721 TGTGTGAGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 721 TGTGTGAGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Qy 781 GAGTTTCCGCGCCAGCATGAAAGGTGAGTCAAGGCCAAGAGGCGCAAGATGAAAGCCAG 840
Db 781 GAGTTTCCGCGCCAGCATGAAAGGTGAGTCAAGGCCAAGAGGCGCAAGATGAAAGCCAG 840
Qy 841 GACGGCAGCCTGAAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 GACGGCAGCCTGAAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Qy 901 AGGGGAGCGAGAGAGGTGAG 960
Db 901 AGGGGAGCGAGAGAGGTGAG 960
Qy 961 AAGGAAGCGAGCACCAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 961 AAGGAAGCGAGCACCAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy 1021 GTCAACAGTGGAGCATGCTTGGGGTGAAGATGACATGGAGTTGGTGAAGAGCATC 1080
Db 1021 GTCAACAGTGGAGCATGCTTGGGGTGAAGATGACATGGAGTTGGTGAAGAGCATC 1080
Qy 1081 AATTTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Db 1081 AATTTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Qy 1141 CGTAACAGCAAGCAACCTCTCTGCGCAAGTGTCTACAGTGCAGAAAGTGTCTAAAGTG 1200
Db 1141 CGTAACAGCAAGCAACCTCTCTGCGCAAGTGTCTACAGTGCAGAAAGTGTCTAAAGTG 1200
Qy 1201 ATCTTATCATATTTTCTCTATGCTATCTCTGGGGGCTTACTGCTTTTATGAGATC 1260
Db 1201 ATCTTATCATATTTTCTCTATGCTATCTCTGGGGGCTTACTGCTTTTATGAGATC 1260
Qy 1261 CTGGCGGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Db 1261 CTGGCGGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Qy 1321 TGGCTTTTCTCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
Db 1321 TGGCTTTTCTCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
Qy 1381 ATTAAGAGGAATTCAGAGCATGCTGAAGAAGTTCTTCTGCAAGGAAAGCCCGGAA 1440
Db 1381 ATTAAGAGGAATTCAGAGCATGCTGAAGAAGTTCTTCTGCAAGGAAAGCCCGGAA 1440
Qy 1441 GAAGATAGCCAGCCAGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Db 1441 GAAGATAGCCAGCCAGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Qy 1501 TCTTACGATTTCTGCTACTTTTCTTGA 1527
Db 1501 TCTTACGATTTCTGCTACTTTTCTTGA 1527

RESULT 9
US-10-094-417-5
; Sequence 5, Application US/10094417
; Publication No. US20030043685A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiayang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030045685A1e1 Receptors
; FILE REFERENCE: 018781-008110US
; CURRENT APPLICATION NUMBER: US/10/094,417
; CURRENT FILING DATE: 2002-06-10
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 60/276,649
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR36
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1527)
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR36
US-10-094-417-5
Query Match 99.9%; Score 1525.4; DB 5; Length 1527;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGAGCTCCACCTGACCAACAGCAGCGGAGAGTAAGACAGCAGCCAGTCATGCGCC 60
Db 1 ATGAGCTCCACCTGACCAACAGCAGCGGAGAGTAAGACAGCAGCCAGTCATGCGCC 60
Qy 61 CTCTCAAAATGCGCATGACCTGCGCCACGCGCATCCGCTCAACCGTGTGTTATC 120
Db 61 CTCTCAAAATGCGCATGACCTGCGCCACGCGCATCCGCTCAACCGTGTGTTATC 120
Qy 121 TTCTGCGCGCTCTTTGCTGCGCAACATAGTGTGCGCTAGTGTGCAAGCGG 180
Db 121 TTCTGCGCGCTCTTTGCTGCGCAACATAGTGTGCGCTAGTGTGCAAGCGG 180
Qy 181 CAGCTGCTGAGTGAACCAACGTTTATCTTTAACTCTGTCACGACCTGTGCGAG 240
Db 181 CAGCTGCTGAGTGAACCAACGTTTATCTTTAACTCTGTCACGACCTGTGCGAG 240
Qy 241 ATTGCGTGTGGCCCCCTGGGTGAGGCACTCTGTGCTCTCTTCTGSCCCTCAAC 300
Db 241 ATTGCGTGTGGCCCCCTGGGTGAGGCACTCTGTGCTCTCTTCTGSCCCTCAAC 300
Qy 301 AGCAGCTTGTGACGGGCTGTGTTAGCTACCCACCTGTGCGCTTGGCCAGCGTAC 360
Db 301 AGCAGCTTGTGACGGGCTGTGTTAGCTACCCACCTGTGCGCTTGGCCAGCGTAC 360
Qy 361 ACCATGTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 ACCATGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Qy 421 TCCAGATAGCCAGCGCGGTTACTGCTCTCTATGAGCACTGATGATGAGCATC 480
Db 421 TCCAGATAGCCAGCGCGGTTACTGCTCTCTATGAGCACTGATGATGAGCATC 480
Qy 481 CTGCAGAGCACTCTCCACTCTACGGCTGGGGCCAGGCTGCTTTGATGAGCCAAATGCT 540
Db 481 CTGCAGAGCACTCTCCACTCTACGGCTGGGGCCAGGCTGCTTTGATGAGCCAAATGCT 540

Db	721	TGTGTGGAGTAATGAGATGAAGGAGCAGAGAAAGAGAGATTCAGAGATGAGAGT	780
Qy	781	GAGTTTCGCCCCACGACATGAAGGTGAGGTCAAGGCCAAGAGGCGCAGATGGAAAGCCAAAG	840
Db	781	GAGTTTCGCCCCACGACATGAAGGTGAGGTCAAGGCCAAGAGGCGCAGATGGAAAGCCAAAG	840
Qy	841	GACGGCAGCCCTGAAGGCGCCAGAAAGAAAGCAACGGGGAAACAATGAGAGTGTAGAGGCC	900
Db	841	GACGGCAGCCCTGAAGGCGCCAGAAAGAAAGCAACGGGGAAACAATGAGAGTGTAGAGGCC	900
Qy	901	AGGGGCAAGCGAGAGGTTCAGAGAGAGCAGCAGCGGTGCGCAGCGCAGCATGAGAGGAT	960
Db	901	AGGGGCAAGCGAGAGGTTCAGAGAGAGCAGCAGCGGTGCGCAGCGCAGCATGAGAGGAT	960
Qy	961	AAGGAGGCGACGACCAAAAGTTGAGAGAAACAGCATGAAGGCGACAAGAGGTGCGACAGAG	1020
Db	961	AAGGAGGCGACGACCAAAAGTTGAGAGAAACAGCATGAAGGCGACAAGAGGTGCGACAGAG	1020
Qy	1021	GTCAACCGATGTCAGATTTGACTTTGGGTGTAAATGATCATATGAGATTTGGTGAAGACGATC	1080
Db	1021	GTCAACCGATGTCAGATTTGACTTTGGGTGTAAATGATCATATGAGATTTGGTGAAGACGATC	1080
Qy	1081	AATTTCAAGTGAAGATGACGTGAGGCAATGTAACATCCCGAGAGCCTCCACCGAGTGGT	1140
Db	1081	AATTTCAAGTGAAGATGACGTGAGGCAATGTAACATCCCGAGAGCCTCCACCGAGTGGT	1140
Qy	1141	CGTAAACAGCAACAGCAACCTCTCTGCGCCAGGTGCTAACAGTCAAAAGCTGTAAAGTG	1200
Db	1141	CGTAAACAGCAACAGCAACCTCTCTGCGCCAGGTGCTAACAGTCAAAAGCTGTAAAGTG	1200
Qy	1201	ATCTTCATCATATTTTCTCCTATATGTCTATCCCTGGGGCCCTACCTGCTTTTATGACATG	1260
Db	1201	ATCTTCATCATATTTTCTCCTATATGTCTATCCCTGGGGCCCTACCTGCTTTTATGACATG	1260
Qy	1261	CTGGCCGTGTGGGTGAGATGTGAAACCCAGGTACCCAGGTGGATGATCACATATCATC	1320
Db	1261	CTGGCCGTGTGGGTGAGATGTGAAACCCAGGTACCCAGGTGGATGATCACATATCATC	1320
Qy	1321	TGGCTTTTCTTCTCTGACGTGCTGATCCACCCCTATATGTCTATGCTACATGACACAAGCC	1380
Db	1321	TGGCTTTTCTTCTCTGACGTGCTGATCCACCCCTATATGTCTATGCTACATGACACAAGCC	1380
Qy	1381	ATTAAAGAAAGAAATTCAGAGCAATGCTGAAGAAATTTCTCTCAAGAAAGAAACCCCGAAA	1440
Db	1381	ATTAAAGAAAGAAATTCAGAGCAATGCTGAAGAAATTTCTCTCAAGAAAGAAACCCCGAAA	1440
Qy	1441	GAAATGAGCAACCCAGACCTGCGCGGAAACAGAGGTGGGACTGAAGGCAAAATGTGCCCT	1500
Db	1441	GAAATGAGCAACCCAGACCTGCGCGGAAACAGAGGTGGGACTGAAGGCAAAATGTGCCCT	1500
Qy	1501	TCCTACGATTCGCTACTTTTCTCTTGA	1527
Db	1501	TCCTACGATTCGCTACTTTTCTCTTGA	1527
RESULT 11			
US-10-345-332-1			
; Sequence 1, Application US/10345332			
; Publication No. US20030129705A1			
; GENERAL INFORMATION:			
; APPLICANT: Li et al.			
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED			
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR			
; FILE REFERENCE: CLO00754CON			
; CURRENT APPLICATION NUMBER: US/10/345_332			
; CURRENT FILING DATE: 2003-01-16			
; PRIOR APPLICATION NUMBER: 09/769,741			
; PRIOR FILING DATE: 2001-01-26			
; PRIOR APPLICATION NUMBER: 60/205,166			
; PRIOR FILING DATE: 2000-05-18			
; PRIOR APPLICATION NUMBER: 09/638,018			

PRIOR FILING DATE: 2000-04-14									
NUMBER OF SEQ ID NOS: 7									
SOFTWARE: FastSeq for Windows Version 4.0									
SEQ ID NO 1									
LENGTH: 1527									
TYPE: DNA									
ORGANISM: Homo sapiens									
US-10-345-332-1									
Query Match 99.9%; Score 1525.4; DB 6; Length 1527;									
Best Local Similarity 99.9%; Pred. No. 0;									
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0									
Qy	1	ATGACGCTCCACTTGACACCAACGACGCGGCGAGAGTAACAGCAGCCACACCGTCAGTGGCC	60						
Db	1	ATGACGCTCCACTTGACACCAACGACGCGGCGAGAGTAACAGCAGCCACACCGTCAGTGGCC	60						
Qy	61	CTCTCAAAATAGCCCATCAGCCTGAGCCACGAGCATCATCCGTCAAACCGTGTGTATC	120						
Db	61	CTCTCAAAATAGCCCATCAGCCTGAGCCACGAGCATCATCCGTCAAACCGTGTGTATC	120						
Qy	121	TTCTCTGCGCGCTCTTTGTGTGGCAACATAGTGTGGCGCTAAGTGTGACGGCAAGCCG	180						
Db	121	TTCTCTGCGCGCTCTTTGTGTGGCAACATAGTGTGGCGCTAAGTGTGACGGCAAGCCG	180						
Qy	181	CAGCTGCTGACAGTGAACCAACCGTTTATCTTTAAACCTCTGTCACGACCTGTGTCAG	240						
Db	181	CAGCTGCTGACAGTGAACCAACCGTTTATCTTTAAACCTCTGTCACGACCTGTGTCAG	240						
Qy	241	ATTTCGCTGCTGAGCCCTCTGGGTGGTGACACTCTGTGCTCTTCTTGCCCTCAAC	300						
Db	241	ATTTCGCTGCTGAGCCCTCTGGGTGGTGACACTCTGTGCTCTTCTTGCCCTCAAC	300						
Qy	301	AGCCACTTCTGACAGGCGCTTGATTAGCTCAACCAACCTGTTCGCTTGCCAGCGTCAAC	360						
Db	301	AGCCACTTCTGACAGGCGCTTGATTAGCTCAACCAACCTGTTCGCTTGCCAGCGTCAAC	360						
Qy	361	ACCAATTGCTTGAGTGCAGTGGATGCGACTTGTATCATCATCAACCCCTCTCCTTACCGG	420						
Db	361	ACCAATTGCTTGAGTGCAGTGGATGCGACTTGTATCATCATCAACCCCTCTCCTTACCGG	420						
Qy	421	TCCAAGATGACCCAGCGCGCGGTTACCTGTCTCTTATGAGCACTGTGATTGAGCCATC	480						
Db	421	TCCAAGATGACCCAGCGCGCGGTTACCTGTCTCTTATGAGCACTGTGATTGAGCCATC	480						
Qy	481	CTGACAGCAATCTCTCACTTAAGCGCTGGGGCCAGCGCTGCTTTGATGAGCGCAATGCT	540						
Db	481	CTGACAGCAATCTCTCACTTAAGCGCTGGGGCCAGCGCTGCTTTGATGAGCGCAATGCT	540						
Qy	541	CTTGTCTTCATGATCTGGGGGGCCAGCCCCAGCTCACTATTTCTCAGCGTGTGTCCTTC	600						
Db	541	CTTGTCTTCATGATCTGGGGGGCCAGCCCCAGCTCACTATTTCTCAGCGTGTGTCCTTC	600						
Qy	601	ATCGTCATTCACATGATTTGATGATTTGCTCTACTCTCGTGTGTTCTGTGACGCGCGG	660						
Db	601	ATCGTCATTCACATGATTTGATGATTTGCTCTACTCTCGTGTGTTCTGTGACGCGCGG	660						
Qy	661	AGGACAGCATGCTCTGCTGTACAAATGTCAAGAGACACACCTTGGAAGTGTGAATCAAGAC	720						
Db	661	AGGACAGCATGCTCTGCTGTACAAATGTCAAGAGACACACCTTGGAAGTGTGAATCAAGAC	720						
Qy	721	TGTGTGAGATGAGATGAGAGGAGCAAGAAAGAGAGATTTCCAGATGAGAT	780						
Db	721	TGTGTGAGATGAGATGAGAGGAGCAAGAAAGAGAGATTTCCAGATGAGAT	780						
Qy	781	GAGTTTGGCGCCACGATGAAAGTGAAGTCAAGGCCAAGAGAGGCGACAGATGAAACCAAG	840						
Db	781	GAGTTTGGCGCCACGATGAAAGTGAAGTCAAGGCCAAGAGAGGCGACAGATGAAACCAAG	840						
Qy	841	GACGGACCTCGAAGGCCAAGAAAGAAAGCAACGGGACCAAGTGAAGTGTAGAGGC	900						
Db	841	GACGGACCTCGAAGGCCAAGAAAGAAAGCAACGGGACCAAGTGAAGTGTAGAGGC	900						

Qy	841	GACGGCAGCCTGAAAGGCCCAAGAAAGAAAGCA	CGGGGACCACTGAGAGTGTAGAGGCC	900	
Db	841	GACGGCAGCCTGAAAGGCCCAAGAAAGAAAGCA	CGGGGACCACTGAGAGTGTAGAGGCC	900	
Qy	901	AGGGGCAGCAGAGAGGTCAAGAGAGCAGCA	CGGTGGCCACGCA	CGGCAGCATGAGGGT	960
Db	901	AGGGGCAGCAGAGAGGTCAAGAGAGCAGCA	CGGTGGCCACGCA	CGGCAGCATGAGGGT	960
Qy	961	AAGGAAAGCAGACACCAAAAGTTGAGGAGAA	CAGCATGAAGGAGACAAGGGTTCGACAGAG	1020	
Db	961	AAGGAAAGCAGACACCAAAAGTTGAGGAGAA	CAGCATGAAGGAGACAAGGGTTCGACAGAG	1020	
Qy	1021	GTCAACCACTGACAGATTGACTTTGGGTGA	ATGATGAGTGTGGTGAAGAGCAGCATC	1080	
Db	1021	GTCAACCACTGACAGATTGACTTTGGGTGA	ATGATGAGTGTGGTGAAGAGCAGCATC	1080	
Qy	1081	AAATTTCAGTGGAGATGAGTGCAGAGGCA	ATGATCCCGGAGAGCTCCACCCAGTCTG	1140	
Db	1081	AAATTTCAGTGGAGATGAGTGCAGAGGCA	ATGATCCCGGAGAGCTCCACCCAGTCTG	1140	
Qy	1141	CGTAAACAGCAACAGCAACCTCTCTG	CGCCAGTGTCTACAGTGCAGAAAGCTCTAAAGTG	1200	
Db	1141	CGTAAACAGCAACAGCAACCTCTCTG	CGCCAGTGTCTACAGTGCAGAAAGCTCTAAAGTG	1200	
Qy	1201	ATCTTCATCATCATTTTCTCCTATATGTG	CTATCCTCGGGGCCCTTACCTGCTTTTATGACAGTC	1260	
Db	1201	ATCTTCATCATCATTTTCTCCTATATGTG	CTATCCTCGGGGCCCTTACCTGCTTTTATGACAGTC	1260	
Qy	1261	CTGGCCCGTGTGGGTGAGATGTGAAAA	CCCCAGGTACCCCCAGTGGGTGATACCATATATCATC	1320	
Db	1261	CTGGCCCGTGTGGGTGAGATGTGAAAA	CCCCAGGTACCCCCAGTGGGTGATACCATATATCATC	1320	
Qy	1321	TGGCTTTTCTTCTGACAGTGCATGATCC	ACCCCTATGTCTATATGGGTACATGACAAAGACC	1380	
Db	1321	TGGCTTTTCTTCTGACAGTGCATGATCC	ACCCCTATGTCTATATGGGTACATGACAAAGACC	1380	
Qy	1381	ATTAAAGAAAGAAATCCAGAGCATGTCTGA	AGAAAGTTCTTCTGCAAGGAAAGAAAGCCCCCGGAAA	1440	
Db	1381	ATTAAAGAAAGAAATCCAGAGCATGTCTGA	AGAAAGTTCTTCTGCAAGGAAAGAAAGCCCCCGGAAA	1440	
Qy	1441	GAAAGATAGCCACCCAGAGCTTGCCCGG	AAACAAGGGGTGGAGCTGAAGGCAAGATATGTCCCT	1500	
Db	1441	GAAAGATAGCCACCCAGAGCTTGCCCGG	AAACAAGGGGTGGAGCTGAAGGCAAGATATGTCCCT	1500	
Qy	1501	TCCTAAGCATTCGTGCTACTTTCTTTGA	1527		
Db	1501	TCCTAAGCATTCGTGCTACTTTCTTTGA	1527		

RESULT 13
US-10-276-243--2
Sequence 2, Application US/10276243
Publication No. US20030187219A1
GENERAL INFORMATION:
APPLICANT: Bayer AG
TITLE OF INVENTION: REGULATION OF HUMAN alpha ADRENERGIC RECEPTOR-LIKE G
TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR

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; FILE REFERENCE: L10063 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/276,243
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US 60/204,145
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/250,505
; PRIOR FILING DATE: 2000-12-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-243-2

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Query Match	99.9%	Score 1525.4	DB 6	Length 1527
Beet Local Similarity	99.9%	Pred. No. 0		
Matches 1526	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Oy	1	ATGACGTCACCTGSCACCAACAGCAGCCGCGAGAGTAACAGCACCACAACCTGCAATGCC	60	
Db	1	ATGACGTCACCTGSCACCAACAGCAGCCGCGAGAGTAACAGCACCACAACCTGCAATGCC	60	
Oy	61	CTCTCCAAAATGCCCATCAGCTTGCCCAACGAGCTCATCCGCTCAACCTGCTGGTTATC	120	
Db	61	CTCTCCAAAATGCCCATCAGCTTGCCCAACGAGCTCATCCGCTCAACCTGCTGGTTATC	120	
Oy	121	TTCTCTGCGCGCTCTTTTCGTGCGCAACATATGCTGGCGCTAGTGTGGACCGCAAGCG	180	
Db	121	TTCTCTGCGCGCTCTTTTCGTGCGCAACATATGCTGGCGCTAGTGTGGACCGCAAGCG	180	
Oy	181	CAGCTGCTGAGAGTGACCAACCGTTTATCTTTAACTCCCTCGACACGACTGCTGAG	240	
Db	181	CAGCTGCTGAGAGTGACCAACCGTTTATCTTTAACTCCCTCGACACGACTGCTGAG	240	
Oy	241	ATTTCGCTGTGAGCCCGCTGGTGGTGAGCACTGTGCTCTCTTCTGGCCCTCAAC	300	
Db	241	ATTTCGCTGTGAGCCCGCTGGTGGTGAGCACTGTGCTCTCTTCTGGCCCTCAAC	300	
Oy	301	AGCCACTTCTGCAACGCGCCCTGGTTAGCTTCACTCAACCTGTTCGCTTGCACAGGTCAAC	360	
Db	301	AGCCACTTCTGCAACGCGCCCTGGTTAGCTTCACTCAACCTGTTCGCTTGCACAGGTCAAC	360	
Oy	361	ACCATTGCTTGGTGTGAGTGATCGGTACTCTTGTCATCATCAACCCCTCTCCGTAACCG	420	
Db	361	ACCATTGCTTGGTGTGAGTGATCGGTACTCTTGTCATCATCAACCCCTCTCTTACCCG	420	
Oy	421	TCCAAGATGACCCACGCGCCGGTTCCTGCTCTATGAGCACCTGGATTGTGGCCATC	480	
Db	421	TCCAAGATGACCCACGCGCCGGTTCCTGCTCTATGAGCACCTGGATTGTGGCCATC	480	
Oy	481	CTGCAAGACACTCTCTCACTTACGCGTGGGGCCAGGCTGCTTTGATGAGCGCAATGCT	540	
Db	481	CTGCAAGACACTCTCTCACTTACGCGTGGGGCCAGGCTGCTTTGATGAGCGCAATGCT	540	
Oy	541	CTCGCTCCATGATCTGGGGGGCCAGGCCAGCTACACTATCTCAGCGTGGTGCCTTC	600	
Db	541	CTCGCTCCATGATCTGGGGGGCCAGGCCAGCTACACTATCTCAGCGTGGTGCCTTC	600	
Oy	601	ATCGTCATTCACATGATTTGTCATGATTTGCCGTACTCCGTTGATTCGTGACGCCGG	660	
Db	601	ATCGTCATTCACATGATTTGTCATGATTTGCCGTACTCCGTTGATTCGTGACGCCGG	660	
Oy	661	AGGCAAGATGCTCTGCTGTACATGTCACAGACACACAGCTTGGAAATGCCAGTCAAGAC	720	
Db	661	AGGCAAGATGCTCTGCTGTACATGTCACAGACACACAGCTTGGAAATGCCAGTCAAGAC	720	
Oy	721	TGTCGTGAGAAATGAGATGAAAGAGGAGCAGAAAGAAAGAGAGGATTCACAGATGAGAGT	780	
Db	721	TGTCGTGAGAAATGAGATGAAAGAGGAGCAGAAAGAAAGAGAGGATTCACAGATGAGAGT	780	
Oy	781	GAGTTTGGCGCCACAGATGAAAGGTGAGGTCAAGGCCAAGGAGGCGCAGATGGAAGCCAA	840	
Db	781	GAGTTTGGCGCCACAGATGAAAGGTGAGGTCAAGGCCAAGGAGGCGCAGATGGAAGCCAA	840	
Oy	841	GACGGCAGCTTGAAGGCCAAGAAAGAACACCGGGAACACTGATGAGATGATGAGAGCC	900	
Db	841	GACGGCAGCTTGAAGGCCAAGAAAGAACACCGGGAACACTGATGAGATGATGAGAGCC	900	
Oy	901	AGGGGCAAGCAGAGGTTCAGAGAGCAGCAGGTGGCAGCGACGGCAGATGGAAGGTT	960	
Db	901	AGGGGCAAGCAGAGGTTCAGAGAGCAGCAGGTGGCAGCGACGGCAGATGGAAGGTT	960	
Oy	961	AAGGAAGCAGACCAAAAGTTGAGAGAAACAGATGAAAGCAGACAAAGGTTCGACAGAG	1020	
Db	961	AAGGAAGCAGACCAAAAGTTGAGAGAAACAGATGAAAGCAGACAAAGGTTCGACAGAG	1020	
Oy	1021	GTCACCAAGTCAGCAATTGACTTGGGTGAGAGATGATGACGTTTGGTGAAGACGACATC	1080	

Db 1021 GTCAACGAGTGAATTGACTTGGGTAAAGTGCATGAGAGTTTGGTAAGACGACATC 1080
Qy 1081 AATTTCACTGAGATGAGTGCAGAGGAGTGAACATCCCGAGAGGCTCCACCCAGTGT 1140
Db 1081 AATTTCACTGAGATGAGTGCAGAGGAGTGAACATCCCGAGAGGCTCCACCCAGTGT 1140
Qy 1141 CGTAAACAGCAACAGCAACCTCTCTGCCCAGAGTGTCAACAGTGCMAAAGCTGTAAAGTG 1200
Db 1141 CGTAAACAGCAACAGCAACCTCTCTGCCCAGAGTGTCAACAGTGCMAAAGCTGTAAAGTG 1200
Qy 1201 ATCTTCATCATCATTTTCTCCATATGCTATGCCCTGAGGGCCCTACTGCTTTTACAGTTC 1260
Db 1201 ATCTTCATCATCATTTTCTCCATATGCTATGCCCTGAGGGCCCTACTGCTTTTACAGTTC 1260
Qy 1261 CTGGCCGTGTGGGTGATGTGCMAAACCAGTACCCCAAGTGGGTATGCATTAATCATC 1320
Db 1261 CTGGCCGTGTGGGTGATGTGCMAAACCAGTACCCCAAGTGGGTATGCATTAATCATC 1320
Qy 1321 TGGCTTTTCTTCTGCAAGTGTGCATCCACCCCTATGTCTATGCTTACATGCAAAAGCC 1380
Db 1321 TGGCTTTTCTTCTGCAAGTGTGCATCCACCCCTATGTCTATGCTTACATGCAAAAGCC 1380
Qy 1381 ATTAAAGAGAAATCCAGAGCATGTCTGAAGAGTTCTTCTGCAAGAAAGCCCGGAAA 1440
Db 1381 ATTAAAGAGAAATCCAGAGCATGTCTGAAGAGTTCTTCTGCAAGAAAGCCCGGAAA 1440
Qy 1441 GAAGATAGCAACCCAGACCTGCCCCGAAACAGAGGTGGGATGTAAGGCAAGTTGCTTC 1500
Db 1441 GAAGATAGCAACCCAGACCTGCCCCGAAACAGAGGTGGGATGTAAGGCAAGTTGCTTC 1500
Qy 1501 TCCTACGATTTCTGCTACTTTTCTTGA 1527
Db 1501 TCCTACGATTTCTGCTACTTTTCTTGA 1527

RESULT 14
US-10-436-715-13
; Sequence 13, Application US/10436715
; Publication No. US20040018976A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,
; FILE REFERENCE: D0262 NP
; CURRENT APPLICATION NUMBER: US/10/436,715
; CURRENT FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: U.S. 60/380,336
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1524)
US-10-436-715-13

Query Match 99.9%; Score 1525.4; DB 7; Length 1527;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAGTCCACCTGCACCAACGAGCGCGAGATGAAGACAGCAACGTCGATGCC 60
Db 1 ATGAGTCCACCTGCACCAACGAGCGCGAGATGAAGACAGCAACGTCGATGCC 60
Qy 61 CTCTCAAAATGCCATCAGCTGCGCCACGCGCATCATCGCTCAACCGTGTGTTATC 120
Db 61 CTCTCAAAATGCCATCAGCTGCGCCACGCGCATCATCGCTCAACCGTGTGTTATC 120
Qy 121 TTCCTGCGCGCTTTTCTGTCGCAACATAGTGTGGCGCTAGTGTTCGACGCGAAGCCG 180

Db 121 TTCCTGCGCGCTTTTCTGTCGCAACATAGTGTGGCGCTAGTGTTCGACGCGAAGCCG 180
Qy 181 CAGTGTCTGAGTGAACCAACGTTTATCTTTAACTCTCTGTACAGCACTGTGAG 240
Db 181 CAGTGTCTGAGTGAACCAACGTTTATCTTTAACTCTCTGTACAGCACTGTGAG 240
Qy 241 ATTTCGCTGTGGCCCCCTGGGTGTGGCCACTCTGTGTCTCTTCTGGCCCCCTCAAC 300
Db 241 ATTTCGCTGTGGCCCCCTGGGTGTGGCCACTCTGTGTCTCTTCTGTGCCCCCTCAAC 300
Qy 301 AGCACTTCTGACGGCCCTGTGTAGCTCAACCCAGCTGTGGCTTGTGCAAGGTCAAC 360
Db 301 AGCACTTCTGACGGCCCTGTGTAGCTCAACCCAGCTGTGGCTTGTGCAAGGTCAAC 360
Qy 361 ACCATTGTCTTGTGATGATGATGCTTATCTTGTCAATCATCAACCTCTCTCAACCG 420
Db 361 ACCATTGTCTTGTGATGATGATGCTTATCTTGTCAATCATCAACCTCTCTCAACCG 420
Qy 421 TCCAAGATGACCCAGCGCGGTTTACTGCTCTCTCTATGAGCACTGTGATGAGCCATC 480
Db 421 TCCAAGATGACCCAGCGCGGTTTACTGCTCTCTCTATGAGCACTGTGATGAGCCATC 480
Qy 481 CTGACAGCACTCTCTCACTTACGCGTGGGCAAGCTGCTTGTATGAGCGCAATGCT 540
Db 481 CTGACAGCACTCTCTCACTTACGCGTGGGCAAGCTGCTTGTATGAGCGCAATGCT 540
Qy 541 CTCTGCTCATGATCTGGGGGGCCAGCCCACTAATATCTCAGCGTGTCTTTC 600
Db 541 CTCTGCTCATGATCTGGGGGGCCAGCCCACTAATATCTCAGCGTGTCTTTC 600
Qy 601 ATGCTATTCCACTGATTTGTATGATATGCTGTCTACTCTCGTGTGTCTGTGACGCCGG 660
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Qy 661 AGGCAGCATGCTCTGCTGTATCAATGTCAAGAGACACAGCTTGAAGTGGGATCAAGAC 720
Db 661 AGGCAGCATGCTCTGCTGTATCAATGTCAAGAGACACAGCTTGAAGTGGGATCAAGAC 720
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Db 721 TGTGTGAGAAATGAGATGAGAGGAGCAGAGAAAGAGAGAGTTCCAGATGAGAGT 780
Qy 781 GAGTTTCCCGCCAGCATGAAGTGAAGGTCAAGGCCAAGAGGCGAGATGAAGCCAAAG 840
Db 781 GAGTTTCCCGCCAGCATGAAGTGAAGGTCAAGGCCAAGAGGCGAGATGAAGCCAAAG 840
Qy 841 GACGCGACCTGAAGGCCCAAGAGAGCAACGGGACCACTGAGATGATGAGGCC 900
Db 841 GACGCGACCTGAAGGCCCAAGAGAGCAACGGGACCACTGAGATGATGAGGCC 900
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Db 901 AGGGCAGCGAGAGGTGAGAGAGCAGCAGCGTGGCCAGCAGCGCAGCATGAGAGGT 960
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Db 961 AAGGAAGCAGCAACCAAGTTGAGAGAAACAGCATGAAGGACAGACAGAGGTGACAGAG 1020
Qy 1021 GTCAACGATGACGATTTGATTTGGGTGAAGATGATCATGAGTTTGGTGAAGACGACATC 1080
Db 1021 GTCAACGATGACGATTTGATTTGGGTGAAGATGATCATGAGTTTGGTGAAGACGACATC 1080
Qy 1081 AATTTCACTGAGATGAGTGCAGAGGAGTGAACATCCCGAGAGGCTCCACCCAGTGT 1140
Db 1081 AATTTCACTGAGATGAGTGCAGAGGAGTGAACATCCCGAGAGGCTCCACCCAGTGT 1140
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Db 1141 CGTAAACAGCAACAGCAACCTCTCTGCCCAGAGTGTCAACAGTGCMAAAGCTGTAAAGTG 1200
Qy 1201 ATCTTCATCATCATTTTCTCCATATGCTATGCCCTGAGGGCCCTACTGCTTTTACAGTTC 1260

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Oy	1261	CTGGCCGCTGTGGGTGGATGTGGAAACCCAGGTACCCAGTGGGTGATCACCATATATCATC	1320
Db	1261	CTGGCCGCTGTGGGTGGATGTGGAAACCCAGGTACCCAGTGGGTGATCACCATATATATC	1320
Oy	1321	TGGCTTTTCTTCTCTGCAGTGCATGCATCACCCCTATGTCTATGGCTCATCATGACAAAGCC	1380
Db	1321	TGGCTTTTCTTCTCTGCAGTGCATGCATCACCCCTATGTCTATGGCTCATCATGACAAAGCC	1380
Oy	1381	ATTAAAGAAAGAAATTCACAGACATGCTGAAGAAATTCTTCTGCAGAGAAAAGCCCCGAAA	1440
Db	1381	ATTAAAGAAAGAAATTCACAGACATGCTGAAGAAATTCTTCTGCAGAGAAAAGCCCCGAAA	1440
Oy	1441	GAAGTATGCCACCCAGACCTGCCCGCGAACAAGGGTGGGACTGAAGGCAMATTTGTCCCT	1500
Db	1441	GAAGTATGCCACCCAGACCTGCCCGCGAACAAGGGTGGGACTGAAGGCAMATTTGTCCCT	1500
Oy	1501	TCCTACGATTCCTGCTACTTTTCTCTTTGA	1527
Db	1501	TCCTACGATTCCTGCTACTTTTCTCTTTGA	1527

RESULT 15
US-10-343-650A-89
; Sequence 89, Application US/10343650A
; Publication No. US20040067499A1

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APPLICANT: HAGA, TATSUYA
TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
FILE REFERENCE: 31671-186347
CURRENT APPLICATION NUMBER: US/10/343,650A
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: JP 2000/237818
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: JP 2001/34434
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 694
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 89
LENGTH: 1527
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: (1)..(1527)
US-10/343-650A-89

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Query Match 99.98; Score 1525.4; DB 7; Length 1527;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY	1	TTGAGCTCAGCTGACCAACGACGGCGGAGATTAACAGACGCAACAGCTGATGCC	60
Db	1	ATGAGCTCAGCTGACCAACGACGGCGGAGATTAACAGACGCAACAGCTGATGCC	60
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Db	61	CTCTCCAAATATGCCATCAGCTGAGCCACGACATATCCGCTCAACCGTGTGGTATC	120
OY	121	TTCCCTCGCGCCTCTTTTGTGGGCAACATAGTCTGGGGCTTAGTATTGACGGCAAGCG	180
Db	121	TTCCCTCGCGCCTCTTTTGTGGGCAACATAGTCTGGGGCTTAGTATTGACGGCAAGCG	180
OY	181	CAGCTGTGACAGTGACCAACCGTTTATCTTTAACTCTCTGACACGACTGCTGCAG	240
Db	181	CAGCTGTGACAGTGACCAACCGTTTATCTTTAACTCTCTGACACGACTGCTGCAG	240
OY	241	ATTGGCTGTGAGCCCCCTGGGTGTGTGGCACTGTGTGCTCTTGTGAGCCCCCTCAAC	300
Db	241	ATTGGCTGTGAGCCCCCTGGGTGTGTGGCACTGTGTGCTCTTGTGAGCCCCCTCAAC	300
OY	301	AGCCACTTGTGACGAGCCCTGGTTAGCTCAACCCACTGTTGACTTGTGACGAGCTCAAC	360

Db	301	AGCACCCTTGCACGAGCCCTGCTTGAAGCTCACCCACCTGTTCCGCTTTCGACGCTCAAC	360
Qy	361	ACCAATGCTCTGATGATGAGATCGCTACTTGTCAATCAATCCACCTCTCTCTACCCG	420
Db	361	ACCAATGCTCGATGATGATGAGATCGCTACTTGTCAATCAATCCACCTCTCTCTACCCG	420
Qy	421	TCCAAGATGACCAAGCCGCGGTTTACTGCTCTCTATGGCAGCTGGAATTTGSGCATC	480
Db	421	TCCAAGATGACCAAGCCGCGGTTTACTGCTCTCTATGGCAGCTGGAATTTGSGCATC	480
Qy	481	CTGACAGGCACTCCCTCCACTAGGGGCGGGGCGGAGGCTGCTTTGATGAGCGCAATGCT	540
Db	481	CTGACAGGCACTCCCTCCACTAGGGGCGGGGCGGAGGCTGCTTTGATGAGCGCAATGCT	540
Qy	541	CTCTGCTCCATGATCTGGGGGGGCCAGGCCCCAGCTACACTATTCACGCTGTGTCTTC	600
Db	541	CTCTGCTCCATGATCTGGGGGGGCCAGGCCCCAGCTACACTATTCACGCTGTGTCTTC	600
Qy	601	ATTCGTCATTCACATGATTTGATATGATTTGCTGCTACTTCCTGCTGTCTGTGCACCCCG	660
Db	601	ATTCGTCATTCACATGATTTGATATGATTTGCTGCTACTTCCTGCTGTCTGTGCACCCCG	660
Qy	661	AGGCAAGCATGCTCTGCTGTCAATGTCAAGAGACACAGCTTGGAAAGTGGCAGTCAAGAC	720
Db	661	AGGCAAGCATGCTCTGCTGTCAATGTCAAGAGACACAGCTTGGAAAGTGGCAGTCAAGAC	720
Qy	721	TGTGTGAGATATGAGATGAAGAGAGGAGACAGAGAAGAAAGAGAGATTCCAGATGAGAT	780
Db	721	TGTGTGAGATATGAGATGAAGAGAGGAGACAGAGAAGAAAGAGAGATTCCAGATGAGAT	780
Qy	781	GAGTTTCGCGCCGACATGAAGGTGAGGTCAAGGCCAAGAGGGCAGATGGAATGGAAGCCAG	840
Db	781	GAGTTTCGCGCCGACATGAAGGTGAGGTCAAGGCCAAGAGGGCAGATGGAATGGAAGCCAG	840
Qy	841	GACGGCAGCCTGGAAGGCCAAGGAAGAAAGCAACGGGGACCACTGAGATGATGTAAGAGCC	900
Db	841	GACGGCAGCCTGGAAGGCCAAGGAAGAAAGCAACGGGGACCACTGAGATGATGTAAGAGCC	900
Qy	901	AGGGGACGAGAGAGTCAAGAGACGACGCTGGCCAGCGACGACGACGACGACGACGACGACG	960
Db	901	AGGGGACGAGAGAGTCAAGAGACGACGCTGGCCAGCGACGACGACGACGACGACGACGACG	960
Qy	961	AAGGAAGGACAGCACCAGGTTGAGGAGAACAGCATGAAGGAGACAGAAAGGTCGACAGAG	1020
Db	961	AAGGAAGGACAGCACCAGGTTGAGGAGAACAGCATGAAGGAGACAGAAAGGTCGACAGAG	1020
Qy	1021	GTCAACCACTGACAGTCTTGATCTTGGGTGAAGATGACATGAGTTTGGTGAAGACGACATC	1080
Db	1021	GTCAACCACTGACAGTCTTGATCTTGGGTGAAGATGACATGAGTTTGGTGAAGACGACATC	1080
Qy	1081	AATTTCACTGAGAGATGACGTGAAGGACGTGAACATCCCGGAGACCTCCCAACCCAGTCGT	1140
Db	1081	AATTTCACTGAGAGATGACGTGAAGGACGTGAACATCCCGGAGACCTCCCAACCCAGTCGT	1140
Qy	1141	CGTAACAGCAACAGCAACCTCTCTGCGCCAGTGTCTACCAAGTCGCAAAAGCTGTAAAGTG	1200
Db	1141	CGTAACAGCAACAGCAACCTCTCTGCGCCAGTGTCTACCAAGTCGCAAAAGCTGTAAAGTG	1200
Qy	1201	ATCTTCATCATATTTTCTCTATGTGTATCCCTGGGGCCCTATCTGCTTTTATGACATC	1260
Db	1201	ATCTTCATCATATTTTCTCTATGTGTATCCCTGGGGCCCTATCTGCTTTTATGACATC	1260
Qy	1261	CTGGCCGCTGGGTGAGATGAGAAACCAAGGTACCCAGTGGGGATGACATATATATC	1320
Db	1261	CTGGCCGCTGGGTGAGATGAGAAACCAAGGTACCCAGTGGGGATGACATATATATC	1320
Qy	1321	TGGCTTTTCTTCTGCACTGCTGATCCACCCCTATGTCTATGCTCATGCAACAAGCC	1380
Db	1321	TGGCTTTTCTTCTGCACTGCTGATCCACCCCTATGTCTATGCTCATGCAACAAGCC	1380
Qy	1381	ATTAAAGAGAAATTCAGAGCATGCTGAAGAGTTCTTCTGCAAGAAAGCCCCCGAA	1440
Db	1381	ATTAAAGAGAAATTCAGAGCATGCTGAAGAGTTCTTCTGCAAGAAAGCCCCCGAA	1440

Db	1381	ATTAAAGAAATCCAGACATGCTGAAGAAATTCTTCTGCAAGAAAAAGCCCCGAAA	1440
QY	1441	GAAGATAGCCACCCAGACCTGCCCGAA	CAGAGGTGGACTGAAGCAAGATTGCCCT 1500
Db	1441	GAAGATAGCCACCCAGACCTGCCCGAA	CAGAGGTGGACTGAAGCAAGATTGCCCT 1500
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Db	1501	TCCTACGATTCTGCTACTTTTCTTGA	1527

Search completed: December 10, 2005, 05:03:01
 Job time : 900 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2005, 03:03:28 ; Search time 161 Seconds
(without alignments)
3545.814 Million cell updates/sec

Title: US-10-712-615-1

Perfect score: 1527

Sequence: 1 atgacgtccactgcaccaccaa.....attctcactttctctga 1527

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	470.2	30.8	619	6	US-10-980-388-8
3	68.2	4.5	1685	6	US-10-750-185-36071
4	63	4.1	3372	6	US-10-750-185-44031
5	57.8	3.8	153376	7	US-11-121-086-5
6	57.6	3.8	246960	7	US-11-121-086-8
7	55.6	3.6	1207	6	US-10-750-185-26665
8	55.4	3.6	1984	6	US-10-502-893-1
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15	52.6	3.4	168516	7	US-11-121-086-3
16	51.6	3.4	153376	7	US-11-121-086-5
17	51	3.3	1225	6	US-10-955-054A-112
18	50.2	3.3	126552	7	US-11-121-086-1
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20	49.4	3.2	8747	6	US-10-955-054A-141
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23	48.2	3.2	175023	7	US-11-121-086-18

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	25	47.2	3.1	126552	7	US-11-121-086-1	Sequence 1, Appl1
	26	47.2	3.1	191684	7	US-11-121-086-2	Sequence 2, Appl1
	27	46.8	3.1	1089	7	US-11-110-274-2	Sequence 2, Appl1
	28	46.2	3.0	148920	7	US-11-121-086-90	Sequence 90, Appl1
	29	46.2	3.0	167116	7	US-11-121-086-44	Sequence 44, Appl1
	30	46.2	3.0	172543	7	US-11-121-086-6	Sequence 6, Appl1
	31	46	3.0	137671	7	US-11-121-086-47	Sequence 47, Appl1
	32	45.4	3.0	857	6	US-10-750-185-35457	Sequence 35457, A
	33	45.2	3.0	1380	6	US-10-875-716-1	Sequence 1, Appl1
	34	45.2	3.0	200628	7	US-11-121-086-62	Sequence 62, Appl1
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	37	44.2	2.9	176503	7	US-11-121-086-53	Sequence 53, Appl1
	38	43.4	2.8	193084	7	US-11-121-086-82	Sequence 82, Appl1
	39	43	2.8	1977	6	US-10-750-185-35938	Sequence 35938, A
	40	42.6	2.8	215308	7	US-11-121-086-77	Sequence 77, Appl1
	41	42.4	2.8	191684	7	US-11-121-086-2	Sequence 2, Appl1
	42	42.2	2.8	179666	7	US-11-121-086-67	Sequence 67, Appl1
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	44	41.8	2.7	138821	7	US-11-121-086-80	Sequence 80, Appl1
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ALIGNMENTS

RESULT 1
US-10-980-388-52
; Sequence 52, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiesch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325.US1
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 52
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-980-388-52

Query Match	99.9%	Score 1525.4	DB 6	Length 1527
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1526	Conservative	0	Mismatches 1	Indels 0
			Gaps	0
QY	1	ATGAGCTCACCTGCACCAACAGCAGCGGACAGAGTAACAGACAGCACCTGCATGCC	60	
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DB	61	CTTTCAAAATGCCCCATAGCCTGGCCACGGGCATATCCGCTCAACCGTGTGTTATC	120	
QY	121	TTTCCGCGCGCCTCTTTTGTGCGGCAACATAGTGTGCGGGCTAGTGTTCAGACGCAAGCG	180	
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QY	181	CAGCTGTGAGGTGATCAACCAACGGTTTATCTTTTAACTCTCGTACACGACCTGTGAG	240	
DB	181	CAGCTGTGAGGTGATCAACCAACGGTTTATCTTTTAACTCTCGTACACGACCTGTGAG	240	
QY	241	ATTTCGCTGTGGCCCCCTGGGTGTGSCACCTGTGTCTCTTCTGGCCCCCTCAAC	300	
DB	241	ATTTCGCTGTGGCCCCCTGGGTGTGSCACCTGTGTCTCTTCTGGCCCCCTCAAC	300	
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DB	361	ACCATTTGCTTGTGTCTAGGTGATGCTACTTGTGCATCATCAACCTCTCTCTTAACCG	420	
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QY	721	TGTGTGAGGAATGAGAGTAGAAGGAGGACAGAGAAAGAGAGATTCACAGATGAGAGT	780	
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QY	901	AGGGGACAGGAGAGGTGAGAGAGACACGTTGGCCAGGACGCGACATGAGAGGT	960	
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Db	1021	GTCAACCAAGTGCACATTTGCTTGGGTGAGATGACATGAGATTGGTGAAGCGACATC	1080
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Db	1081	AATTTCAGTGAAGATGACGTGAGGACAGTGAACATCCCGAGAGCCGCCACCCAGTCGT	1140
Qy	1141	CGTAAACGCAACAGCAACCCCTCTCTGCCCAAGTGTCTAACATGTCGTAAGTAAAGT	1200
Db	1141	CGTAAACGCAACAGCAACCCCTCTCTGCCCAAGTGTCTAACATGTCGTAAGTAAAGT	1200
Qy	1201	ATCTTCATCATATTTTCTCTCTATGTCATCCCTGGGGGCCCTACAGCTTTTAAAGAGTC	1260
Db	1201	ATCTTCATCATATTTTCTCTCTATGTCATCCCTGGGGGCCCTACAGCTTTTAAAGAGTC	1260
Qy	1261	CTGGCCGTGTGGGTGATGTCGAAACCCAGATACCCAGTGGGTGATCACCATATATCATC	1320
Db	1261	CTGGCCGTGTGGGTGATGTCGAAACCCAGATACCCAGTGGGTGATCACCATATATCATC	1320
Qy	1321	TGGCTTTTCTTCTCTGACAGTGTGATCACCCTCATGTCTATGTCATACGCAACAGACC	1380
Db	1321	TGGCTTTTCTTCTCTGACAGTGTGATCACCCTCATGTCTATGTCATACGCAACAGACC	1380
Qy	1381	ATTAAAGAGGAAATCCAGGACATGCTGAAGAAGTTCTTGCAGAGAAAGCCCGGAA	1440
Db	1381	ATTAAAGAGGAAATCCAGGACATGCTGAAGAAGTTCTTGCAGAGAAAGCCCGGAA	1440
Qy	1441	GAAATATGCAACCCAGACCTGCCGGAACAGAGGGTGGACTGAAGCAAGATTGTCCCT	1500
Db	1441	GAAATATGCAACCCAGACCTGCCGGAACAGAGGGTGGACTGAAGCAAGATTGTCCCT	1500
Qy	1501	TCTACGATTTCTGCTACTTTTCTTGA	1527
Db	1501	TCTACGATTTCTGCTACTTTTCTTGA	1527
RESULT 2			
US-10-980-388-8			
; Sequence 8, Application US/10980388			
; Publication No. US20050255490A1			
; GENERAL INFORMATION:			
APPLICANT: Vogeli, Gabriel			
APPLICANT: Parodi, Luis A.			
APPLICANT: Hiebsch, Ronald R.			
APPLICANT: Lind, Peter			
APPLICANT: Kaytee, Paul S.			
APPLICANT: Ruff, Valerie			
APPLICANT: Huff, Rita M.			
APPLICANT: Wood, Linda S.			
TITLE OF INVENTION: Novel G protein-Coupled Receptors Cross-Reference To Related Appl			
FILE REFERENCE: 00325-US1			
CURRENT APPLICATION NUMBER: US/10/980,388			
CURRENT FILING DATE: 2004-11-02			
PRIOR APPLICATION NUMBER: US/09/791,932			
PRIOR FILING DATE: 2001-02-23			
PRIOR APPLICATION NUMBER: 60/184,305			
PRIOR FILING DATE: 2000-02-23			
PRIOR APPLICATION NUMBER: 60/184,304			
PRIOR FILING DATE: 2000-02-23			
PRIOR APPLICATION NUMBER: 60/184,303			
PRIOR FILING DATE: 2000-02-23			
PRIOR APPLICATION NUMBER: 60/184,397			
PRIOR FILING DATE: 2000-02-23			
PRIOR APPLICATION NUMBER: 60/184,247			
PRIOR FILING DATE: 2000-02-23			
PRIOR APPLICATION NUMBER: 60/188,880			
PRIOR FILING DATE: 2000-03-13			
PRIOR APPLICATION NUMBER: 60/217,369			
PRIOR FILING DATE: 2000-07-11			
PRIOR APPLICATION NUMBER: 60/217,370			
PRIOR FILING DATE: 2000-07-11			
PRIOR APPLICATION NUMBER: 60/218,492			
PRIOR FILING DATE: 2000-07-20			

Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-980-388-8

Query Match 30.8%; Score 470.2; DB 6; Length 619;
Best Local Similarity 99.4%; Pred. No. 1,1e-111;
Matches 472; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAGCTCCACCTGCAACCAACAGCAGCGGAGAGTAACAGACCAACAGTCATGCCC 60
DB 145 ATGAGCTCCACCTGCAACCAACAGCAGCGGAGAGTAACAGACCAACAGTCATGCCC 204
QY 61 CTCTCCAAATGCGCATCAGCTGCGCCAGCGCATCATCGCTCAACCGTGTGTTATC 120
DB 205 CTCTCCAAATGCGCATCAGCTGCGCCAGCGCATCATCGCTCAACCGTGTGTTATC 264
QY 121 TTCTCGCGCGCTCTTTCGTGGGCAACATAGTGTGCGCTAGTGTGAGCGCAAGCCG 180
DB 265 TTCTCGCGCGCTCTTTCGTGGGCAACATAGTGTGCGCTAGTGTGAGCGCAAGCCG 324
QY 181 CAGCTGCTGAGGTGACCAACCGTTTATCTTTTAACTCTCTGTCACCGACTGTGCGAG 240
DB 325 CAGCTGCTGAGGTGACCAACCGTTTATCTTTTAACTCTCTGTCACCGACTGTGCGAG 384
QY 241 ATTTCGCTGTGGCCCCCTGGTGGTGGGCACTGTGCTCTCTTGTGGCCCCCTGAC 300
DB 385 ATTTCGCTGTGGCCCCCTGGTGGTGGGCACTGTGCTCTCTTGTGGCCCCCTGAC 444
QY 301 AGGCATCTTGACAGCGCGCGTGTAGCTTACCCACCTGTTGCGCTTGGCAGGCTCAAC 360
DB 445 AGGCATCTTGACAGCGCGCGTGTAGCTTACCCACCTGTTGCGCTTGGCAGGCTCAAC 504
QY 361 ACCATTGTCTTGTGTGATGATGCTGCTACTGTGCTCAATCCACCTCTCTCAACCG 420
DB 505 ACCATTGTGTGTGTGATGATGCTGCTACTGTGCTCAATCCACCTCTCTCAACCG 564
QY 421 TCCAAAGATGACCAAGCGCGCGTGTACTGCTCTCTATGAGCACTGGATTGGG 475
DB 565 TCCAAAGATGACCAAGCGCGCGGTACTGCTCTCTATGAGCACTGGATTGGG 619

RESULT 3

US-10-750-185-36071/c
; Sequence 36071, Application US/10750185
; Publication No. US200502603A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36071
; LENGTH: 1685
; TYPE: DNA
; ORGANISM: Bovine 19866880675545
US-10-750-185-36071

Query Match 4.5%; Score 68.2; DB 6; Length 1685;

Best Local Similarity 46.9%; Pred. No. 3.8e-08;
Matches 248; Conservative 0; Mismatches 278; Indels 3; Gaps 1;

QY 80 GCGTGCCAGGAGCATCCGCTCAACCGTGTGTTATCTTCCGCGGCTCTTTG 139
DB 1352 GCCAGGGCAGCGGTATCTCTATCTCTTTATCTACTCCGTGTGTGGGCTCT 1293
QY 140 TCGCAACATAGTGTGGGCTAGTGTGTCAGCGCAAGCGCAAGCTGTGAGTAGCA 199
DB 1292 GTGGAAATCTCAATGATCATCTAGTATCTCGCTACCCCAAGATGAAGAGGCCACCA 1233
QY 200 ACCGTTTATCTTTTAACTCTCTGTGTGTCACCGACTGTGAGATTGCTGTGGCCCT 259
DB 1232 ACATCTCAATCTCTCAACCTGCGCATGCGCAATGAGTGTCTAT--GCTTACGTCGCT 1176
QY 260 GGGTGTGACCACTGTGTGCTCTCTTGTGCGCCCTCAACAGCACTTGTGACGCGCC 319
DB 1175 TCGTGTACCTCTTCAATGATCTTTCGCACTGGCCCTTGGCGGCTACTCTGCGCTTG 1116
QY 320 TGGTTAGCTTCAACCACTGTGTGCGCTTGGCGAGCGTCAACCAATGTCTTGTGTGAG 379
DB 1115 TGGTCAAGCGTGAACGAGTCAACATGTTCACCAAGATCTAATGTGTGAGCTGTAGG 1056
QY 380 TGGATGCTACTTGTTCATCATCACTCTCTCTCTCAACCGCTTCAAGATGACCAAGCCG 439
DB 1055 TGGACCGCTAAGTGGCGCGTGTGACACCCCATGAAGGCCACAGCTACCCGCGCCACCG 996
QY 440 GCGGTACCTGCTCCCTATAGGACCTGATGTGGCCATCTCGAGAGACATCTCTCAAC 499
DB 995 TGGCAAGGTGTGTAATGTGGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 936
QY 500 TCTACGCGTGGGCGAGCGT 559
DB 935 TGGTCTTCTGCGGCAAGGGGCGCAACAGGAGCGGACCGGTGTGTGTGTGTGTGTGTGTGT 876
QY 560 GGGCAGCCCAAGCTAATCTTCAAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 608
DB 875 CCGAGCCCGCCAGCGCTGT 827

RESULT 4

US-10-750-185-44031/c
; Sequence 44031, Application US/10750185
; Publication No. US200502603A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44031
; LENGTH: 3372
; TYPE: DNA
; ORGANISM: Bovine 19866881908619
US-10-750-185-44031

Query Match 4.1%; Score 63; DB 6; Length 3372;
Best Local Similarity 45.6%; Pred. No. 1,1e-06;
Matches 222; Conservative 0; Mismatches 265; Indels 0; Gaps 0;

QY 131 CCTCTTTCGTGCAACATAGT 190
DB 2232 CCACCTGTGTGGCAACCTCTCATCATGTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2173

```
QY 191 AGGTGACCAACCGTTTATCTTTAACTTCCTCTGACCGACCTGTGACAGATTTGCTCG 250
DB 2172 CCCCCATGATCTCTGCTCCGCAACCTCTCCGTCTTGGAACATCTGCTCTCTCATCA 2113
QY 251 TGGCCCCGCTGGTGGGCGACCTGCGCCCTCTCTTGGGGCCGCAACAGCCATTCT 310
DB 2112 CCGCCCCAAGGTCCTGCTGGAGCTTCTTTTCAGAGAGAAAGACATCTCTTCCATGGCT 2053
QY 311 GCACGCGCCCTGGTTAGCTTACCTCACCTGTCGCTTCGCGCCGCTCAACACATGTTCT 370
DB 2052 GCGTCACGAGATGTTTTTCTTCCACCTCTCGGGGGGTGACAGATCTTCTCTCTGG 1993
QY 371 TGGTGTCACTGATGCTTACTTGTTCATATCAACCTCTCTCTCTTACCCGTCGAAGTGA 430
DB 1992 TCATGGCCCTTTGACAGCTACGTGGCCATCATAGCCCTCGACCTACGTGACCTGATGA 1933
QY 431 CCCAGCGCGGGTTAACCTGCTCTCTATAGGACCTGTGATTTGGCCATCTCGACAGACA 490
DB 1932 GTCAGGGGGGTGACCTGCTCTCATGTGGCTCTCGGGGGGGGCTTGTCTCACTCA 1873
QY 491 CTCCTTCACTTACGCGCTGGGGCCAGGCTGCTTGTGATGAGCGCAATGCTCTGCTCCA 550
DB 1872 TCGTCGAGATCTCCCTGTTACTCTCCCTCCCTCTCTGTGACCGAAGCTCTGGACACTT 1813
QY 551 TGATCTGGGGGGCCAGCCCAAGCTTACTATTTCTAGCGGTGTCTTCAATGTCATTC 610
DB 1812 TCTACTGGCAGCTCCCGCCAGTCTCTACACTTGTCCGTCAGGACACTGCTGTCTTGAAGC 1753
QY 611 CACTGAT 617
DB 1752 TCTTGAT 1746
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RESULT 5

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US-11-121-086-5
; Sequence 5, Application US/1121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 153376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-5
```

Query Match 3.8%; Score 57.8; DB 7; Length 153376;
Best Local Similarity 46.1%; Pred. No. 9.8e-05;
Matches 194; Conservative 0; Mismatches 227; Indels 0; Gaps 0;

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QY 702 GGAAGTGCAGTCAAGGACTGTGTGAGAAATGAGATTGAAGGAGGAGAGAGAAAGAA 761
DB 15679 GGAAGAGGAGAAACAGAGAGAGAGAGAAACAGAGGAGAGAGAGAAACAGAGAGGA 15738
QY 762 GGAGTTCCAGATGAGATGATTTTGCAGCCAGCATGAGAGTGAAGGTCAAGGCCAAGA 821
DB 15739 GGAAGAAACAGAGAGAGAGAGAAACAGAGAGAGAGAGAGAGAAACAGAGAGAGGA 15798
QY 822 GGGCAAGATGAAAGCCAGAGACGCGACCTGAAAGCCAAAGAAAGAAACGAGGACAG 881
DB 15739 GGAACAGAGAGAGAGAGAGAAACAGAGTCTAGGACACTGTGGGAGAGTCCAGATGCCAG 15858
QY 882 TGAAGTATGTAGAGGCCAGGGGCGACAGAGGTCAAGAGACAGACAGTGGCCAG 941
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DB 15859 GGGAGTGGAGACAGAGAGAGAGAGAAAGACAGAGAGAAAGAGAGAGAAACAGAG 15918
QY 942 CGACGCGAGCATGAGAGGTAAAGAAAGCAGACCAAAATTGAGAGAAACAGATGAAGGC 1001
DB 15919 GAGAGAGAGAGACAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 15978
QY 1002 AGACAAAGGTGGACAGAGGTTCACCACTGACGATTTGACTTGGGTAAAGTGAATGA 1061
DB 15979 ACAGAGAGAGAGAGAGAGAGAAACAGAGAGAGAGAGAAATGAGAGAGAGAGAGAG 16038
QY 1062 GTTTGGTAAGACGACATCAATTTTCAAGAGATGACGTGAGGACAGTGAACATCCCGA 1121
DB 16039 GGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 16098
QY 1122 G 1122
DB 16099 G 16099
```

RESULT 6

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US-11-121-086-8
; Sequence 8, Application US/1121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 246960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-8
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Query Match 3.8%; Score 57.6; DB 7; Length 246960;
Best Local Similarity 49.5%; Pred. No. 0.00013;
Matches 181; Conservative 0; Mismatches 179; Indels 6; Gaps 1;

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QY 119 TCTTCTCGCGCCCTCTTTCGTGGCAACATAGTCTGCGCTAGTGTGACGCGCAAGC 178
DB 120678 TCACTTCTCTCTGCGCGTGAATCGCAACGTCCTGTGATCTTGGAGCGGACCC 120737
QY 179 CGCAGCTCTGAGGTACCAACCTTTTATCTTTAACTCTCTCTCAACCGACTGCTGC 238
DB 120738 GGCAGACAGCAGATTCCACGAGACCTTCTGTTCCACTGAGCCGTGCGCACTCTGC 120797
QY 239 AGATTGCTGTGGGCGCCCTGCGGTGGGCGACCTGTGCTCTTCTTGGCCCTCA 298
DB 120798 TGTCTTATCTGCTCTTGTGCGCGTGGCGAGGGCTCTGTGG-----CTGGCTCTGG 120851
QY 239 ACAGCACTTTCTGACGCGCCCTGTTAGCTTACCTACCCACTGTGCTTTCGCAAGCTCA 358
DB 120852 GGAACCTTCTCTGCAAACTGTGATGCTCTGCAAAAGTCAACTTACTAGCAGACACC 120911
QY 359 ACACCATTTGTTGTGTGTCAGTGTGATGCTGCTACTTGTTCATATCAACCTCTCTTACC 418
DB 120912 TGCTCTGCGCTGACATCCCGGTGGACCGCTTACCTGGCCATTGTTCACCCCGTCCATGCGCT 120971
QY 419 GGTCAAGATAGCCAGGCGCGGTTACCGTCTCTATAGGCACTGGAATTGGGCA 478
DB 120972 ACCGCAAGCGCGCTCTCTTTCATCAATCACTGTTGGACATCTGGGCTGTGGCT 121031
QY 479 TCTTGC 484
DB 121032 TCTTCC 121037
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RESULT 7
US-10-750-185-26865/c
; Sequence 26865, Application US/10750185
; Publication No. US2005026603A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26865
; LENGTH: 1207
; TYPE: DNA
; ORGANISM: Bovine 1986881057836
US-10-750-185-26865

```

Query Match 3.6%; Score 55.6; DB 6; Length 1207;

Best Local Similarity 46.2%; Pred. No. 5.9e-05; Matches 184; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

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QY 93 CATCATCCGCTCAACCGCTGCTGTTATCTTCTGCGCGCTCTTTGTCGGCAACATAGT 152
DB 678 CATGTCCTCTTTGCTCTGCTGCTGCTATTTACCTGACCATATGATGGGATGAC 619
QY 153 GCTGGCGCTAGTGTGACGGCAAGCCGACGCTGCTGACGATCAACCGTTTATCTT 212
DB 618 TTATGAGCTGCTCATCTCCCGGACTCCAGCTCACTCATATGATCTGCTCG 559
QY 213 TAACCTCTGCTGACCGACTGCTGAGATTTGCTGCTGCGCCCTGGGTGGTGGCC 272
DB 558 TGCTCTCTCATATATGACATGGGGCTGCTTCCACAGTATTTGCCCCAGTTGCTGCCA 499
QY 273 CTCTGCTCTCTCTTCTGCGCCCTCAACAGCACTTTCGACCGCCCTGCTTACCTCAC 332
DB 498 TCTGCTCATGACGACCGACCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 439
QY 333 CAACCTGCTGCTCTGCGCCAGCTCAACCACTTGTCTGCTGCTGCTGCTGCTGCTGCT 392
DB 438 TTATGCTTGGGCTTACAGACACACTTGTATTTCTATCATGAGCTCTGGATGATACAT 379
QY 393 GTTCATCATCCACCCCTCTCTCCATCCCTGCAAGATGACCCGCGGCTTACCTGCT 452
DB 378 GGCATCTGTGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 319
QY 453 CCTCTATGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 490
DB 318 ACTGCGCTTCTGTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 281

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RESULT 8
US-10-502-893-1
; Sequence 1, Application US/10502893
; Publication No. US2005025529A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Healthcare AG
; APPLICANT: Goiz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Geerts, Andreas
; TITLE OF INVENTION: Human SH2 Receptor
; FILE REFERENCE: Lea 35 827
; CURRENT APPLICATION NUMBER: US/10/502,893
; PRIOR FILING DATE: 2004-07-27

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; PRIOR APPLICATION NUMBER: PCT/EP03/000479
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: EP 02001942.8
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1984
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-502-893-1

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Query Match 3.6%; Score 55.4; DB 6; Length 1984;

Best Local Similarity 44.6%; Pred. No. 7.9e-05; Matches 261; Conservative 0; Mismatches 321; Indels 3; Gaps 1;

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QY 107 CCGTCTGCTGTTATCTTCTGCGCGCTCTTTGTCGGCAACATAGTCTGCGCTAGTGT 166
DB 559 CCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 618
QY 167 TCGAGCGCAAGCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 226
DB 619 TCTGACTAGCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 678
QY 227 CCGACCTGCTGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 286
DB 679 CTGACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 738
QY 287 TCTGCGCTCTCAACAGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 346
DB 739 GCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 798
QY 347 TCGCCAGCTCAACCACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 406
DB 799 GCGCTCTCACTCTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 858
QY 407 CTCTCTCTTACCCCTGCTCAAGATGACCCAGCGCGCTTACCTGCTCTCTTATGAGCACTT 466
DB 859 CGTGGCTGCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 918
QY 467 GGA--TTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 523
DB 919 GAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 978
QY 524 TTGATGAGGCAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 583
DB 979 ACGCAGCGCACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1038
QY 584 TCAGCTGCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 643
DB 1039 TGGCGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1098
QY 644 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 688
DB 1099 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143

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RESULT 9
US-11-170-153-9
; Sequence 9, Application US/11170153
; Publication No. US2005026629A1
; GENERAL INFORMATION:
; APPLICANT: DELBESNUTTER, WILLY
; APPLICANT: WEBER, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: LOKEN, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; PRIOR FILING DATE: 2002-03-22

```

```

; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 9
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(942)
; OTHER INFORMATION: IGS4A truncated DNA long version
US-11-170-153-9
```

```

Query Match          3.5%; Score 53.8; DB 7; Length 1594;
Beet Local Similarity 46.5%; Pred. No. 0.00019;
Matches 209; Conservative 0; Mismatches 237; Indels 3; Gaps 1;
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```

QY 37 AACACGAGCCACGACGATGAGCCCTCTCCAAATGCCATCAGCTGAGCCACGAGCATC 96
   |||||
DB 133 AACACGACCGAGAGATATGAGCTTCTCTCGGACCTCGGCGCAGCCACTTCTTCTC 192
   |||||
QY 97 ATCCGCTCAACCGTGTGATATCTTCTCGCCGCTCTTTCGTGGCAACATAGTCTG 156
   |||||
DB 193 CCGGTGTGTGTGATATGCAATTTTGTGTGGGTGATTTGGCAATGCTCTGGTG 252
   |||||
QY 157 GGGCTAGTGTGACAGCGCAAGCCGACGCTGACAGTACCAACCGTTTATCTTTAAC 216
   |||||
DB 253 TGCCTGTGATTTCTGACAGCAGGCTATGAAGAGCCCAACTACTACTCTTTCAGC 312
   |||||
QY 217 CTCTCTGTACCGACCTGTGCAAGATTTGCTGTGGCCCTGGGTGTGGCAACCTCT 276
   |||||
DB 313 CTGGGGGTCTGTGACTCTCTGTCTCTCTTGAATCCCTGAGGTCTATGAGATG 372
   |||||
QY 277 GTGCTCTCTTGTGGCCCTCAACAGCACTT--CTGACGAGCCCTGTAGCTCACC 333
   |||||
DB 373 TGGCCCACTACCTTTCTTGTTCGGGCCCGTGGGCTGTACTTCAAGAGCCCTCTT 432
   |||||
QY 334 CACCTGTTCCTTGTGGCCGCTCAACACCATTTGTGTGATGATGCTACTTGG 393
   |||||
DB 433 GAGACCGTGTGCTTGGCTTCATCTTCAGCATCACCAACCGTACGCTGAGGCTG 492
   |||||
QY 394 TCCATCATCAACCTCTCTCTCAACCGGTCAAGATGACCGCGCGGTTACCTGCTC 453
   |||||
DB 493 GCCATCTCAACCCGTTCCGCGCCAAATGACAGAGACCCGCGGCCCTCAGAGATC 552
   |||||
QY 454 CTCTATGGCACTGTGATTTGGCCATCCT 482
   |||||
DB 553 CTCGGCATGCTGTGGGGCTTCTCCGCTG 581
   |||||
```

```

RESULT 10
US-11-170-153-11
; Sequence 11, Application US/11170153
; Publication No. US20050266529A1
; GENERAL INFORMATION:
; APPLICANT: DELERSNIJDER, WILLY
; APPLICANT: WEESP, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: LOKEN, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 11
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (64)..(942)
; OTHER INFORMATION: IGS4A truncated DNA short version
US-11-170-153-11
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```

Query Match          3.5%; Score 53.8; DB 7; Length 1594;
Beet Local Similarity 46.5%; Pred. No. 0.00019;
Matches 209; Conservative 0; Mismatches 237; Indels 3; Gaps 1;
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QY 37 AACACGAGCCACGACGATGAGCCCTCTCCAAATGCCATCAGCTGAGCCACGAGCATC 96
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DB 133 AACACGACCGAGAGATATGAGCTTCTCTCGGACCTCGGCGCAGCCACTTCTTCTC 192
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QY 97 ATCCGCTCAACCGTGTGATATCTTCTCGCCGCTCTTTCGTGGCAACATAGTCTG 156
   |||||
DB 193 CCGGTGTGTGTGATATGCAATTTTGTGTGGGTGATTTGGCAATGCTCTGGTG 252
   |||||
QY 157 GGGCTAGTGTGACAGCGCAAGCCGACGCTGACAGTACCAACCGTTTATCTTTAAC 216
   |||||
DB 253 TGCCTGTGATTTCTGACAGCAGGCTATGAAGAGCCCAACTACTACTCTTTCAGC 312
   |||||
QY 217 CTCTCTGTACCGACCTGTGCAAGATTTGCTGTGGCCCTCTTGTGGGTGTGGCAACCTCT 276
   |||||
DB 313 CTGGGGGTCTGTGACTCTCTGTCTCTCTTGAATGCCCTGAGAGTCTATGAGATG 372
   |||||
QY 277 GTGCTCTCTTGTGGCCCTCAACAGCACTT--CTGACGAGCCCTGTAGCTCACC 333
   |||||
DB 373 TGGCCCACTACCTTTCTTGTTCGGGCCCGTGGGCTGTACTTCAAGAGCCCTCTT 432
   |||||
QY 334 CACCTGTTCCTTGTGGCCGCTCAACACCATTTGTGTGATGATGCTACTTGG 393
   |||||
DB 433 GAGACCGTGTGCTTGGCTTCATCTTCAGCATCACCAACCGTACGCTGAGGCTG 492
   |||||
QY 394 TCCATCATCAACCTCTCTCTCAACCGGTCAAGATGACCGCGCGGTTACCTGCTC 453
   |||||
DB 493 GCCATCTCAACCCGTTCCGCGCCAAATGACAGAGACCCGCGGCCCTCAGAGATC 552
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QY 454 CTCTATGGCACTGTGATTTGGCCATCCT 482
   |||||
DB 553 CTCGGCATGCTGTGGGGCTTCTCCGCTG 581
   |||||
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RESULT 11
US-11-170-153-1
; Sequence 1, Application US/11170153
; Publication No. US20050266529A1
; GENERAL INFORMATION:
; APPLICANT: DELERSNIJDER, WILLY
; APPLICANT: WEESP, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: LOKEN, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 1
; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(1299)
; OTHER INFORMATION: IGS4A long version
US-11-170-153-1
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Query Match          3.5%; Score 53.8; DB 7; Length 1658;
Beet Local Similarity 46.5%; Pred. No. 0.00019;
Matches 209; Conservative 0; Mismatches 237; Indels 3; Gaps 1;
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QY 37 AACAGACGACACGTCGATGCCCCCTCTCCAAATGCCCACAGCTCGGCCCAAGGAGATC 96
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DB 133 AACAGACGACGAGAGATATCGGCTTCTCTGCGGACCTCGGCGCAGCCACTTCTTCTC 192
QY 97 ATCCGCTCAACCGTGTGGTATCTTCTCGGCCCTCTTGTGGCAACATAGTGTG 156
    |||||
DB 193 CCGGTGTCTGTGTATGTGCAATTTTGTGTGGGGGTCAATGGCAATGTCTGTG 252
QY 157 GCGCTAGTGTGACGCGCAAGCCGACGCTGTCAGGTGACCAACGGTTTATCTTTAAC 216
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DB 253 TGCCTGTATTTGTGACGACCAAGGCTATGAAAGCCGCCCACTACTACTCTTACG 312
QY 217 CTCCTGTACACGACCTGCTGCAAGATTTGCTGTGCCCCCTGTGGTGTGGCACTCT 276
    |||||
DB 313 CTGGCGGTCTGTACCTCTGCTGTCTGTCTTGGAAATGCCCTGAGAGGCTATGAGATG 372
QY 277 GTGGCTCTCTTGTGGCCCCCTCAACAGCCACTT---CTGACAGGCCCTGTAGCTTAC 333
    |||||
DB 373 TGGCGCACTACCTCTTCTTGTGTGGGCCCGGTGGGCTACTTCAAGACGGCCCTCTT 432
QY 334 CACCTGTGCGCTTTCGCGACGCTCAACACCATTTGTGTGATGATGCTACTTGG 393
    |||||
DB 433 GAGACCGTGTGCTTGGCTTCCATCTCAGCATCACACCGTCAAGCTGTGAGCGCTACGTG 492
QY 394 TCCATATCCACCCCTCTCTCTTCCACCGTCCAGATGACCCGAGCGCGGTACTCTCTC 453
    |||||
DB 493 GCCATCTTACACCGTTCCGCGCAACCTGACAGACGCCGGCGCGGCTCAGAGATC 552
QY 454 CTCATATGACCTGTGATTTGGCCATCTT 482
    |||||
DB 553 CTCGGCATGTCTGGGGCTTCTCCGTGCT 581
    |||||
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RESULT 12

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US-11-170-153-3
; Sequence 3, Application US/11/170153
; Publication No. US2005026529A1
; GENERAL INFORMATION:
; APPLICANT: DELEERSNIJDER, WILLY
; APPLICANT: WEESP, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: LOKEN, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(1299)
; OTHER INFORMATION: IGS4A short version
US-11-170-153-3
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Query Match 3.5%; Score 53.8; DB 7; Length 1658;

Best Local Similarity 46.5%; Pred. No. 0.00019;

Matches 209; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

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QY 37 AACAGACGACACGTCGATGCCCCCTCTCCAAATGCCCACAGCTCGGCCCAAGGAGATC 96
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DB 133 AACAGACGACGAGAGATATCGGCTTCTCTGCGGACCTCGGCGCAGCCACTTCTTCTC 192
QY 97 ATCCGCTCAACCGTGTGGTATCTTCTCGGCCCTCTTGTGGCAACATAGTGTG 156
    |||||
DB 193 CCGGTGTCTGTGTATGTGCAATTTTGTGTGGGGGTCAATGGCAATGTCTGTG 252
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QY 157 GCGCTAGTGTGACGCGCAAGCCGACGCTGTGACAGTGAACCAACCGTTTATCTTTAAC 216
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DB 253 TGCCTGTATTTGTGACGACCAAGGCTATGAAAGCCGCCCACTACTACTCTTACG 312
QY 217 CTCCTGTACACGACCTGCTGCAAGATTTGCTGTGCCCCCTGTGGTGTGGCACTCT 276
    |||||
DB 313 CTGGCGGTCTGTACCTCTGCTGTCTGTCTTGGAAATGCCCTGAGAGGCTATGAGATG 372
QY 277 GTGGCTCTCTTGTGGCCCCCTCAACAGCCACTT---CTGACAGGCCCTGTAGCTTAC 333
    |||||
DB 373 TGGCGCACTACCTCTTCTTGTGTGGGCCCGGTGGGCTACTTCAAGACGGCCCTT 432
QY 334 CACCTGTGCGCTTTCGCGACGCTCAACACCATTTGTGTGATGATGCTACTTGG 393
    |||||
DB 433 GAGACCGTGTGCTTGGCTTCCATCTCAGCATCACACCGTCAAGCGTGTGAGCGCTACGTG 492
QY 394 TCCATATCCACCCCTCTCTCTTCCACCGTCCAGATGACCCGAGCGCGGTACTCTCTC 453
    |||||
DB 493 GCCATCTTACACCGTTCCGCGCAACCTGACAGACGCCGGCGCGGCTCAGAGATC 552
QY 454 CTCATATGACCTGTGATTTGGCCATCTT 482
    |||||
DB 553 CTCGGCATGTCTGGGGCTTCTCCGTGCT 581
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RESULT 13

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US-11-170-153-5
; Sequence 5, Application US/11/170153
; Publication No. US2005026529A1
; GENERAL INFORMATION:
; APPLICANT: DELEERSNIJDER, WILLY
; APPLICANT: WEESP, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: LOKEN, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(1299)
; OTHER INFORMATION: IGS4B long version
US-11-170-153-5
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Query Match 3.5%; Score 53.8; DB 7; Length 1658;

Best Local Similarity 46.5%; Pred. No. 0.00019;

Matches 209; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

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QY 37 AACAGACGACACGTCGATGCCCCCTCTCCAAATGCCCACAGCTCGGCCCAAGGAGATC 96
    |||||
DB 133 AACAGACGACGAGAGATATCGGCTTCTCTGCGGACCTCGGCGCAGCCACTTCTTCTC 192
QY 97 ATCCGCTCAACCGTGTGGTATCTTCTCGGCCCTCTTGTGGCAACATAGTGTG 156
    |||||
DB 193 CCGGTGTCTGTGTATGTGCAATTTTGTGTGGGGGTCAATGGCAATGTCTGTG 252
QY 157 GCGCTAGTGTGACGCGCAAGCCGACGCTGTCAGGTGACCAACGGTTTATCTTTAAC 216
    |||||
DB 253 TGCCTGTATTTGTGACGACCAAGGCTATGAAAGCCGCCCACTACTACTCTTACG 312
QY 217 CTCCTGTACACGACCTGCTGCAAGATTTGCTGTGCCCCCTGTGGTGTGGCACTCT 276
    |||||
DB 313 CTGGCGGTCTGTACCTCTGCTGTCTGTCTTGGAAATGCCCTGAGAGGCTATGAGATG 372
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QY 277 GTCCTCTCTTGTGGCCCTCAACAGCCACT---CTGACAGGCTGTGTTAGCTTACCC 333
DB 373 TGGCCCAATACCTCTTCTTGTGTGGCCCGCGGGCTGTACTTCAAGAGCCGCTCTTT 432
QY 334 CACCTGTTGCGCTTGGCCGACGCTCAACACCATTTGTTGTGTCAGTGTGATGCTACTTG 393
DB 433 GAGACCGTGTGTTTCCCTCCATCTCCAGATCACCACCGTCAGCGTGAAGGCTACGTG 492
QY 394 TCCATCATCCACCTCTCTCTCTCAACCCGTCGAAGATGACCAGCCGCGGTTACCTGCTC 453
DB 493 GCCATCTCAACACCGTTCCGCGCAAACTGACAGAGACCCGGCGCGGCTCCTGAGATC 552
QY 454 CTCTATGACCTGATTTGTGGCCATCTT 482
DB 553 CTCGGCATGTCTGGGCTTCTCCGTGCT 581
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RESULT 14

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US-11-170-153-7
; Sequence 7, Application US/11170153
; Publication No. US20050266529A1
; GENERAL INFORMATION:
; APPLICANT: DELEBSNIDER, WILLY
; APPLICANT: WEESP, GUY NYS
; APPLICANT: VENERA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: BERGER, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(1299)
; OTHER INFORMATION: IGS4B short version
US-11-170-153-7
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Query Match 3.5%; Score 53.8; DB 7; Length 1658;

Best Local Similarity 46.5%; Pred. No. 0.00019;

Matches 209; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

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QY 37 AACAGACGACACGTCATGCCCTCTCCAAATGCCATCAGCTGGCCCAAGGCATC 96
DB 133 AACAGACGACGAGATATCTGGCTTCTCTGGGACCTCGGCGACGACCATTTCTTCTTC 192
QY 97 ATCCGCTCAACGCTGTGTTATCTTCTCGCCGCTCTTTGTCGGCAACATAGCTG 156
DB 193 CCGGTCTGTGTGTATGTGCAATTTTGTGGTGGGATCATTTGGCAATGTCTGTG 252
QY 157 GCGTAGTGTGAGGAGGACGCGAGCTGTGTCAGTGTGACCAACGTTTATCTTAAAC 216
DB 253 TGCCTGTATTTCTGAGACCAAGGCTATGAAAGCGCCACCACTACTACTCTTTCAAG 312
QY 217 CTCCTGTACGAGCTGTGATGATTTGCTGTGAGCCCTCGGTGTGTGGCACCTCT 276
DB 313 CTGGCGGTCTGACCTCTGCTGTGCTTGTGAATGCCCTGAGAGCTATGAGATG 372
QY 277 GTCCTCTTTCTGGGCCCTCAACAGCCACT---CTGACAGGCTGTGTTAGCTTACCC 333
DB 373 TGGCCCAATACCTCTTCTTGTGTGGCCCGCGGGCTGTACTTCAAGAGCCGCTCTTT 432
QY 334 CACCTGTTGCGCTTGGCCGACGCTCAACACCATTTGTTGTGTCAGTGTGATGCTACTTG 393
DB 433 GAGACCGTGTGTTTCCCTCCATCTCCAGATCACCACCGTCAGCGTGAAGGCTACGTG 492
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QY 394 TCCATCATCCACCTCTCTCTTACCCCTCAAGATGACCCAGCGCGGTTACTGCTC 453
DB 493 GCCATCTCAACACCGTTCCGCGCAAACTGACAGACCCGGCGCGGCTCCTGAGATC 552
QY 454 CTCTATGACCTGATTTGTGGCCATCTT 482
DB 553 CTCGGCATGTCTGGGCTTCTCCGTGCT 581
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RESULT 15

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US-11-121-086-3
; Sequence 3, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 168516
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-3
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Query Match 3.4%; Score 52.6; DB 7; Length 168516;

Best Local Similarity 46.0%; Pred. No. 0.0022;

Matches 178; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

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QY 785 TTGCGCGCCAGCATGATGATGATCAAGCCCAAGAGGCGAGAAATGGAAGCCAGAGC 844
DB 68503 TTGAGAGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 68562
QY 845 GCAAGCTTAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 904
DB 68563 AGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 68622
QY 905 GCAGGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 964
DB 68623 GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 68682
QY 965 AAGCAGACCAAAAGTTGAGAGAAACAGCATGAAAGGAGAGAGAGAGAGAGAGAGTCA 1024
DB 68683 CAGAAAGGAGAGAAATAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 68742
QY 1025 ACCAGTGCAGCATTTGATTTGGTGAATGACATGAGATTTGGTGAACGATCAATT 1084
DB 68743 ACAAATGAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 68802
QY 1085 TCAGTGAGATGAGCTGAGAGAGATGA 1111
DB 68803 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 68829
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Search completed: December 10, 2005, 05:05:52

Job time : 165 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-10-712-615-1
Perfect score: 1527
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	296.4	19.4	655	BB179791	BB179791 BB179791
2	268.4	17.6	644	BY723772	BY723772 BY723772
3	227.4	14.9	646	CNS0490M	AL280651 Tetradon
4	184.6	12.1	641	CK254611	CK254611 1307373 N
5	176.6	11.6	620	BY724046	BY724046 BY724046
6	156.6	10.3	772	DR860076	DR860076 JGI CABG4
7	141.6	9.3	645	CO934586	CO934586 AGENCOURT
8	122.8	8.0	1064	CNS03511	AL282450 Tetradon
9	107	7.0	1587	AY421262	AY421262 Mus muscu
10	98.6	6.5	1590	AY421261	AY421261 Pan trogl
11	97	6.4	1590	AY421260	AY421260 Homo sapi
12	94.4	6.2	793	DO032256	DO032256 Homo sapi
13	92.2	6.0	721	CP147813	CP147813 AGENCOURT
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17	85.6	5.6	722	CP147810	CP147810 AGENCOURT
18	85	5.6	802	CK843215	CK843215 JGI CAK1
19	84.8	5.6	979	AL279030	AL279030 Tetradon
20	84	5.5	1397	AY399427	AY399427 Pan trogl
21	84	5.5	1401	AY399426	AY399426 Homo sapi
22	83.4	5.5	853	AY409236	AY409236 Homo sapi

C	23	81.4	5.3	440	1	AM63056	h164405.x
C	24	81.2	5.3	731	5	BY731738	BY731738
C	25	80.4	5.3	803	7	CK146110	CK146110 AGENCOURT
C	26	78.6	5.1	729	8	DR003001	DR003001 TC108456
C	27	78.4	5.1	677	2	BB626313	BB626313 BB626313
C	28	78.4	5.1	1818	4	AK034239	AK034239 Mus muscu
C	29	78	5.1	637	6	CD618076	CD618076 Mus muscu
C	30	77.8	5.1	705	7	CO959341	CO959341 AGENCOURT
C	31	77.4	5.1	640	6	CD618070	CD618070 56030361H
C	32	77.4	5.1	640	6	CD618071	CD618071 56030361H
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C	34	76.2	5.0	682	7	CO959039	CO959039 AGENCOURT
C	35	75.8	5.0	1046	10	AY407666	AY407666 Mus muscu
C	36	75.6	5.0	997	10	CNS005TE	AL060767 Drosophila
C	37	74.8	4.9	1072	10	AY398881	AY398881 Pan trogl
C	38	74.8	4.9	1708	4	AY325170	AY325170 Rattus no
C	39	74.6	4.9	498	3	BM090260	BM090260 505437 MA
C	40	74.2	4.9	608	5	BY724644	BY724644 BY724644
C	41	74.2	4.9	4435	4	AK049671	AK049671 Mus muscu
C	42	73.8	4.8	662	7	CN721896	CN721896 E0831F01
C	43	73.6	4.8	969	10	AY407665	AY407665 Pan trogl
C	44	73.4	4.8	987	10	CNS00418	AL066537 Drosophila
C	45	73.2	4.8	1072	10	AY398880	AY398880 Homo sapi

ALIGNMENTS

RESULT 1
BB179791
LOCUS
DEFINITION
BB179791 RIKEN full-length enriched, adult male hypothalamus Mus musculus cDNA clone A230080N06 3', mRNA sequence.
VERSION
BB179791.2 GI:16269966
SOURCE
EST.
MUS musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 655)
Hara, A., Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Konda, Y., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M., and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
On Jun 29, 2000 this sequence version replaced gi:8838874.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,

TITLE
JOURNAL
PUBMED
COMMENT

Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashitume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shigawara,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenhiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Kono,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,W. and Hayashizaki,Y.
Direct Submision
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES

source

Location/Qualifiers
1..620
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A230080N06"
/sex="male"
/tissue_type="hypothalamus"
/dev_stage="adult"
/lab_host="DRI0B"
/clone_lib="RIKEN full-length enriched, adult male
hypothalamus"
/note="Site 1: Salt; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAAAGCTCTTTTCTTTTCTTTTCTTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCGACGTATTAATTAATTAATCCCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
Phi I."

Query Match 11.6%; Score 176.6; DB 5; Length 620;
Best Local Similarity 75.0%; Pred. No. 2.2e-31;
Matches 246; Conservative 0; Mismatches 80; Indels 2; Gaps 2;

QY 1 ATGAGCTCCACTGCACCAACGACGCGGAGAGTACAGCAGCCACGTCGATGCC 60
DB 292 ATGCCACCCAGCTGACATTAACAGTACTCAAGAGAACATGACGATGAGTGGCTCCCC 351
QY 61 CTCCTCAAAATGCCATGACCTGCGCCAGGCATCATCCGTCACAGCTGCTATC 120
DB 352 CTCCTCAAGATCCATTAATGATGATGACGACGATCATCCGCTCATGTTGCTGCTC 411
QY 121 TTCCTGCGCGCTCTTTCGTCGCGCAACATAGTGTGCGCTAGTGTGCGCGCAAGCCG 180
DB 412 ATCCCTGGTGTAGCTCTTCTGTGATACGATGAGTGTGATGATGACGCTAGCA 471
QY 181 CAGCTGTGACAGGTACCAACCGTTTATCTTTAACTCTCTGTCACGACCTGTGACG 240
DB 472 AACTGTGCTGACAGTACCAACCGCTTCAATTAACCTGCTGTACGACCTGTGACG 531
QY 241 ATTTGGCTGTGCGCCCGGTGGTGGGCACTGTCGCTCTTGTGCGCCCTCAAC 300
DB 532 GTTGCTGTGCGGCGCCCGCTGGGT-GTGTCACCTGCATTCCTTCTTGAGCTCTC-AC 589
QY 301 AGCCACTTCTGCACGCGCCCTGTTAGCC 328
DB 590 ATCCACTTNTGCATCGCTGTGTTAGCC 617

RESULT 6
DR860076
LOCUS
DEFINITION
JGI CABG4788.fwd NIH_XGC_tropBcl xenopus tropicalis cDNA clone
IMAGE:7836743 5', mRNA sequence.
ACCESSION
DR860076 GI:71516634
VERSION
DR860076.1 GI:71516634
KEYWORDS
SOURCE
ORGANISM
Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 772)
Richardson,P., Lucas,S., Rokhaar,D., Dettler,J.C., Ng,D.C.,
Brokstein,P. and Lindquist,E.A.
DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
Other ESTs: JGI CABG4788.rev
Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Robert M. Grainger
cDNA library Preparation: Bruce Blumberg Laboratory, University of
California, Irvine
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LNLN:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Plate: CABG 0049 row: h column: 21
High quality sequence stop: 772.

FEATURES

source

Location/Qualifiers
1..772
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/strain="N6 (Nigerian 6th generation inbred)"
/db_xref="taxon:8364"

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/clone="IMAGE:7836743"  
/tissue_type="Stomach"  
/dev_stage="Adult"  
/lab_host="ElectronMAX DH10B T1 Phage Resistant cells"  
/clone_lib="NIH XGC tropstol"  
/note="Vector: pCS107, Site 1: EcoRI, Site 2: XhoI, The  
library was prepared from 5 ug of poly A+ RNA by oligo-dT  
priming  
(5'-ACTATGCGCGCCGCTAGAGCCCTCGAGTTTCTTTTCTTTT-3') and  
Stratascript reverse transcriptase. After ligation of  
EcoRI adapters (5'-AATTCGACGAGG-3') followed by kinasing  
adapters and by XhoI digestion, the cDNA was size selected  
by chromatography on Sepharose CL-2B columns and fractions  
containing cDNAs larger than 1000 bp were ligated into  
EcoRI/XhoI-digested pCS107. Reference for library  
construction: Current Genomics 4, 635-644. Library  
constructed by Michelle Tabb and Bruce Blumberg (Dept of  
Developmental and Cell Biology, University of California,  
Irvine)."
```

ORIGIN

Query Match 10.3%; Score 156.6; DB 8; Length 772;

Best Local Similarity 60.3%; Pred. No. 1.5e-26;
Matches 258; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

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Oy 83 TGGCCACGCGATCATCCGCTCAACCGTGTGTTATCTTCTCGCCGCTTTGCTG 142  
Db 345 TGCCGACACCATCTCTCAGAGATTGTCATCATTTCCCTCTTGTCTTTATTG 404  
Oy 143 GCACATATGTGTGGCGCTAGTGTGACGCGACGCGAGCTGCTGACGATGACCAAC 202  
Db 405 GAAACATATATGCTCTGTGTGTTTCATCGAAAGCTCAGCTGCTCCAGTAGAACC 464  
Oy 203 GTTTATCTTTTAACTCTCTGTGACGACCTGCTGAGATTTCGCTGCGCCCTGGG 262  
Db 465 GATTATTTTCACTGCTGTGAGTGTGATCTTCTGACAGCACTTTGGTTAGCTTGG 524  
Oy 263 TGTGCGCACTCTGTGCTCTCTTCTGTGCGCCCTCAACGACCTTCTGACGCGCTG 322  
Db 525 TCATGTATACCTCCCTCCCTGATATCTGCGCCCTTGGATATAGTCTTTGTGAGAGTGG 584  
Oy 323 TTAGCTTACACCACTGTTCGCTTGGCGAGCGTCAACCACTGTCTTGTGTCAATGG 382  
Db 585 TGTGCTATATGATTTATTTGATTTGACAGAGTAAACATCAAGTTGTTGTGG 644  
Oy 383 ATGCTACTTGTGATCATCCACCTCTCTCTCAACCGGTCAAGATGACCGACGCGG 442  
Db 645 ACAATATCTGGCCATATCATCTTTGTCTATATCCCAAGATGACCCCAAGAGAG 704  
Oy 443 GTTACCTGCTCTCTATAGGACCTGATTTGGCACTCTGAGAGCACTCTGCACTCT 502  
Db 705 GAAGCTTCTGATATTTGCACTTGATTTTCAAGTGTCTCCANAGCAACCCACTCTCT 764  
Oy 503 ACGGCTGG 510  
Db 765 ATGCTGG 772
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RESULT 7

LOCUS CO934586 645 bp mRNA linear EST 16-AUG-2004
DEFINITION AGENCOURT_3048563 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:7262003 5', mRNA sequence.

ACCESSION CO934586
VERSION CO934586.1 GI:51289263

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo
1 (bases 1 to 645)

REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapdb-remail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
Plate: IRB16 row: a column: 09
High quality sequence stop: 170.

FEATURES

source

location/Qualifiers
1..645

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/organism="Homo sapiens"  
/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clone="IMAGE:7262003"  
/tissue_type="mixed"  
/lab_host="DH10B"  
/clone_lib="NIH_MGC_145"  
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:  
varies by clone; ORFs were PCR-amplified and cloned into  
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XmiI/XhoI-3',  
5'-EcoRV-XmiI/NotI-3', EcoRI (7A cloned, non-directional).  
For information about which gene each clone represents,  
please visit our anonymous ftp site at  
ftp://image.lnl.gov/image/rearrayed\_plates/IRB16.presv.dat  
A Note: this is a NIH_MGC Library."
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ORIGIN

Query Match 9.3%; Score 141.6; DB 7; Length 645;

Best Local Similarity 87.0%; Pred. No. 6.1e-23;
Matches 167; Conservative 0; Mismatches 24; Indels 1; Gaps 1;

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Oy 1 ATGAGCTCACCCTGACCAAGACGCGCGAGATACAGACGACACGTCATGCTCC 60  
Db 39 ATGAGCTCACCCTGACCAAGACGCGCGAGATACAGACGACACGTCATGCTCC 98  
Oy 61 CTCTCAAAATGCCCATGAGCTGTGCGCCAGCATCATCCGCTCAACCGTGTGTTATC 120  
Db 99 CTCTCAAAATGCCCATGAGCTGTGCGCCAGCATCATCCGCTCAACCGTGTGTTATC 158  
Oy 121 TTCTGCGCGCC-TTTTTGTGCGGACATATGCTGTGCGCTAGTGTTCAGCGCAACC 179  
Db 159 TTCTGCGCGCCCTTTTCATCAAAATATATGATAGATGATGAGAGTACTATCC 218  
Oy 180 GCAGCTGTGCA 191  
Db 219 ACATCTCAAGCA 230
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RESULT 8

LOCUS CNS03V11 1064 bp DNA linear GSS 01-SEP-2000
DEFINITION Tetradon nigroviridis genome survey sequence PUC-Orl end of clone
062121 of library G from Tetradon nigroviridis, genomic survey
sequence.

ACCESSION AL262450
VERSION AL262450.1 GI:7984076

KEYWORDS GSS; genome survey sequence.
SOURCE Tetradon nigroviridis

ORGANISM

Tetradon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neocleostei;
Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE 1

AUTHORS Roest Croillius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F., Saurin, W., and Weissenbach, J.

TITLE Estimate of human gene number provided by genome-wide analysis using Tetradon nigroviridis DNA sequence

JOURNAL Nat. Genet. 25 (2), 235-238 (2000)

REFERENCE PUBLISHED 10835645

AUTHORS 2

TITLE Roest Croillius, H., Jaillon, O., Dasilva, C., Ozouf-Coetaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A., and Weissenbach, J.

JOURNAL Characterization and repeat analysis of the compact genome of the freshwater pulmonate Tetradon nigroviridis

REFERENCE PUBLISHED 10899143

AUTHORS 3 (bases 1 to 1064)

TITLE Genome Res. 10 (7), 939-949 (2000)

JOURNAL Direct Submission

REFERENCE PUBLISHED 112-APR-2000

AUTHORS Genoscope.

TITLE Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetradon>.

FEATURES source 1. 1064 /organism="Tetradon nigroviridis" /mol_type="genomic DNA" /db_xref="taxon:99883" /clone_lib="cg" /note="Genoscope sequence ID : COBG062A11SP1 end : PUC-Orig"

ORIGIN

Query Match 8.0%; Score 122.8; DB 11; Length 1064; Best Local Similarity 60.9%; Pred. No. 2.3e-18; Matches 196; Conservative 2; Mismatches 124; Indels 0; Gaps 0;

QY 379 GTGGATCGCTACTTGTTCATCATCCCTCTCTCTCAACCGGTCAAGATGACCCAGCCG 438

DB 8 KTGATCGCTACTGTGCTATCATACACCCGCTGTCTATCCACCGGTATGACCCCTCAC 67

QY 439 CGGGTTACCTGCTCCATGAGCCTGATTTGGCCATCTCCGACAGACATCCCTCA 498

DB 68 CTGGACCAATATGATCATCTGCACTGGGTCTCACTGCTACGACAGACAGCCGCC 127

QY 499 CTCTACGGCTGGGCGACAGGCTGCTTGTATGAGCGCAATGCTCTGCTCATGATCTGG 558

DB 128 CTCTAMGGCTGGGCGACCGTTGACTTTGACCGCGGTACAAAGTGTCTCGGTGG 187

QY 559 GGGGCGACGCCAGCTACATATTCTCAGCGGTGTCTTCAATCGTCAATCGATGATT 618

DB 188 TCGTCCAGCCTGTCTATCTCATCATGTGTCCACGCTGTCTTCTGCTGCTGGTGG 247

QY 619 GTCATATTGCGCTACTACCGTGTCTTGTGAGAGCCCGAGAGGACAGATGCTGCTGG 678

DB 248 ATATGTTGGGGGTATCTGATGATGTTTTCGAGACAGCCGAGAGGAAAGCGCTGATG 307

QY 679 TACATGTCTAAGACAGACACT 700

DB 308 CACCCCATACAGACGCAATCTT 329

RESULT 9

LOCUS AY421262 1587 bp DNA linear GSS 12-DEC-2003

DEFINITION Mus musculus HCM7498 gene, VIRTUAL TRANSCRIPT, partial sequence,

ACCESSION AY421262

VERSION AY421262.1 GI:397777219

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE PUBLISHED 14671302

AUTHORS 2 (bases 1 to 1587)

TITLE Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B., Ferriere, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D., and Cargill, M.

JOURNAL Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

REFERENCE PUBLISHED 14671302

AUTHORS 2 (bases 1 to 1587)

TITLE Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B., Ferriere, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D., and Cargill, M.

JOURNAL Direct Submission

REFERENCE PUBLISHED 16-NOV-2003

AUTHORS Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.

FEATURES source 1. 1587 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" <1. >1587 /locus_tag="HCM7498"

ORIGIN

Query Match 7.0%; Score 107; DB 10; Length 1587; Best Local Similarity 48.6%; Pred. No. 1.6e-14; Matches 293; Conservative 0; Mismatches 310; Indels 0; Gaps 0;

QY 106 ACCGTCTGTGTTATCTTCTCGCGGCTTTTGTGCGCAATAGTGTGGCTAGTG 165

DB 91 ATGGCATATCATATCACTACTGTCTTGTCTGTGCGCACTGTGATGATGATCACC 150

QY 166 TTGACGCGAAGCGGAGCTGTGACAGGTGACCAACGGTTTATCTTTAACTCTCTGTC 225

DB 151 TTGTACAAAGATGCTACCTCTCAACCTTCAGCAAGATGTTGTTTCAAGCTGACCTTG 210

QY 226 ACCGACTGTGCAATTTGCTGTGCGGCTTGGTGTGTGCGCACTCTGTGCTCTC 285

DB 211 TCCAACTTCTGTGTGCGGTGTGCGGCTTGTGTGTGCTGCTGCTCAATCCGAGG 270

QY 286 TTCTGCGCCCTCAAGCAGCACTTTCAGCGGCTGTTAGCCTCAACCACTGTCGCG 345

DB 271 GAATGATTTTGGCGGTGTGTGTGCAACTTCTGCGCTCTCTCACTGCTGATCAG 330

QY 346 TTGCGCAGGTCAACCAATTTGTTGTGTGTGATGTGATGTGCTATGTTCATCATCAC 405

DB 331 TGACGACATGTGTACCTTGGGATCATTTGCATGATGTGATACGCGGTGTAT 390

QY 406 CCTCTCTCTACCGCTGCAAGATGACAGCGCGGTTTACTGTCTCTATAGGACAC 465

DB 391 CCAATGTGTACCCCAATGAATCAAGAGAACCGAGTGTGATGCTCTGCTCATATC 450

QY 466 TGGATTGTGGCACTCTGACAGCACTCTCCACATCTACGGGCGGAGCGAGGCTGCTT 525

DB 451 TGGCTCACTCTCTCATTTGGGTGTGTGCGGCTCTTATTTGGTTGATCATCGGTGATTT 510

QY 526 GATGACGCAATGCTCTGTCTTCATGATGTGGGGGCGAGCCCGACGTAATATTCTC 585

DB 511 GATGATTTCAAGATGATGTGTGCGGCTGACCAAGAACCGGCTACACATTTTC 570

QY 586 AGGTGTGTCTCTATCTGCTATTCATGATTTGTATGATGCTCTGCTACCTCGGTG 645

DB 571 TGGCATGTGTGTGCGGCTGTGCTTCTTTCATCATCATGTAGTGTGACGGTTTCATC 630

Qy	646	TTCTGTGCAGCCCGGAGGACGACGATCTCTCTGTCATCAATGTCTACAGACACAGCTTGGA	705
Db	631	TTCCGGGTGGCCAGGCTCAAGCCCGAAAGGTGCATGTGGCAGCGTGGTCACTGTGAG	690
Qy	706	GTG 708	
Db	691	GAG 693	
RESULT 10			
LOCUS	AY421261	1590 bp	DNA linear
DEFINITION	Pan troglodytes HCM7498 gene, VIRTUAL TRANSCRIPT, partial sequence.		
ACCESSION	AY421261		
VERSION	AY421261.1	GI:39777218	
KEYWORDS	SS.		
SOURCE	Pan troglodytes (chimpanzee)		
ORGANISM	Pan troglodytes		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Pan.		
AUTHORS	Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanendbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Slnsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2 (bases 1 to 1590)		
AUTHORS	Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanendbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Slnsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence as made by sequencing genomic exons and ordering them based on alignment.		
FEATURES	Location/Qualifiers		
source	1..1590		
gene	/organism="Pan troglodytes"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9598"		
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ORIGIN	/locus_tag="HCM7498"		
Query Match	6.5%;	Score 98.6;	DB 10;
Best Local Similarity	47.4%;	Pred. No.1,7e-12;	
Matches	296;	Conservative	0;
		Mismatches	322;
		Indels	0;
		Gaps	0;
Qy	84	GGCCAGGCGATCATCGGCTCAACCGCTGGTTATCTTCCTCGCGGCTTTCTGCG	143
Db	72	GGGCGTCATCATCACCCAGTTCATCGCATCTGTCACTACCAATTTTGTCTGCTGG	131
Qy	144	CAACATAGTCGTGGGCGCTAGTGTTCAGACGGCAAGCCGAGCTGTCTGACAGTCAACCG	203
Db	132	AAACCTGGTCATCGGTGATCACTTGTATCAAGAAAGTCTTACCTCTCACCCCTCAGCAMA	191
Qy	204	TTTATCTTTAACTCTCTCTGTCAACGACCTGCTGCAGATTTTCGCTGCGGCCCCCTGGGT	263
Db	192	GTTGCTCTTTCAGCTGACCTCTGTCAACTTCTCTGCTGTCCGTGGTGGTCTGCTTTGT	251
Qy	264	GGTGGCACCTCTGTGCTCTCTTCTTGCGCCCTCAACAGCACTTTCAGACGGCCCTGGT	323
Db	252	GGTACGAGCTCATTCGAGGAGATGTGATTTTGTGTAGTGTGTGCAACTTCTCTGC	311
Qy	324	TAGCTTCAACCCACTGTTCCTGCTTGGCCAGGCTCAACACCATTTCTTGGTGTCACTGGA	383
Db	312	CCTCTCTTACCTCGTATGATGCTCGGCGAGCATGTCTAACCTCTGGGGTTCATTTGCATGA	371

QY	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	JOURNAL	PUBLISHED	REFERENCES	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	ORIGIN	
QY	AY421260	Homo sapiens HCM7498 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.	AY421260	1	GI:39777217	GSS.	Homo sapiens (human)	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Eucleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.	Science 302 (5652), 1960-1963 (2003)	14671302	2 (bases 1 to 1590)	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.	Direct Submission	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	This sequence as made by sequencing genomic exons and ordering them based on alignment.	Location/Qualifiers	gene	
QY	672	TGCGACATCGTATCGTGAGAG 696	684	TGTCAAGACACAGCTTGAAGT 708	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671
QY	672	TGCGACATCGTATCGTGAGAG 696	684	TGTCAAGACACAGCTTGAAGT 708	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671
QY	672	TGCGACATCGTATCGTGAGAG 696	684	TGTCAAGACACAGCTTGAAGT 708	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671
QY	672	TGCGACATCGTATCGTGAGAG 696	684	TGTCAAGACACAGCTTGAAGT 708	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671
QY	672	TGCGACATCGTATCGTGAGAG 696	684	TGTCAAGACACAGCTTGAAGT 708	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671
QY	672	TGCGACATCGTATCGTGAGAG 696	684	TGTCAAGACACAGCTTGAAGT 708	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671	624	GATTCCTGTACTCCGTGGTCTGTGACGCCGAGGACAGCATGCTGTGTACAA 683	612	GCTGTGTGCTATGGCTTATCTTCCCGTGGCGAGGTCAGGACGCAAGTGCATG 671
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Db 72 GGGCGTCATCATCACCAGTTCATCGCCATATGTCATCACCATTGTCGCTGGG 131
QY 144 CAACATAGTGTGGCGCTAGTGTGTCAGCGCAAGCGGACGTGTCAGAGTGCACACCG 203
Db 132 AAACCTGTGTCATGTGTGTACCTTTGTAACAAGAGTCTTACCTTCAACCTCAGCAACA 191
QY 204 TTTTATCTTTAACTTCCTGTCACCGACCTGTGCAAGATTTGCTGTGGCCCCCTGGGT 263
Db 192 GTTCGCTTCAGCTGACCTGTGTCACAACTTCCTGCTGCTGGTGTGTGCTTCTTGT 251
QY 264 GGTGGCCACCTCTGTGCTCTCTTCTGCCCCCTCAACAGCACTTTCGACGGCCCTGGT 323
Db 252 GGTGACAGAGCTTCATCCGACGGAATGATCTTTGTGTGTGTGTGCAACTTCTCTCG 311
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QY 384 TCGCTACTTGTCCATATCCACCCCTCTCTCTTACCCGTCAGATGACCCAGCGCGG 443
Db 372 CCGCTACTATGCTGCTCTGTACCCCATGGTGTACCCCATGAAATCAGAGGGAACCGGGG 431
QY 444 TTAACCTGCTCTTATAGGACCTGTGATTTGGCCATCTGACAGACATCTTCACTCTA 503
Db 432 TGTGATGGACCTTGTCTACATCTGCTCTCACTGCTCATCGCTGCTGACCCCTGTT 491
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Db 552 GGAAGCTGTGCTACACGGCTTCTGAGAGATCTGTGTGCTTCCCTTTTGTGTGAT 611
QY 624 GATGCTCTGCTACTCCGTGTGTCTGTGTGACGCCGAGGACAGCATGCTCTGTGTA 683
Db 612 GCTGTGTGTCTATGAGCTTCACTTCCGCGTGGCCAGGGTCAAGGACGCAAGGTGAC 671
QY 684 TGTCAAGAGACACAGCTTGGAAGTG 708
Db 672 TGGCACAGTGTCTATCTGTGAGAG 696

RESULT 12
D0032256 793 bp DNA linear GSS 02-JUN-2005
LOCUS Homo sapiens ADRAID gene, VIRUTAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION D0032256
VERSION D0032256.1 GI:66883465
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 793)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(ex) Plos Biol. 3 (6), E170 (2005)
JOURNAL PUBLISHED 15869325
2 (bases 1 to 793)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of

FEATURES alignment.
source location/Qualifiers
1..793
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ORIGIN
Query Match 6.2%; Score 94.4; DB 11; Length 793;
Best Local Similarity 51.5%; Pred. No. 1.5e-11;
Matches 271; Conservative 0; Mismatches 246; Indels 9; Gaps 2;

QY 137 TGTGCGCAATAGTGTGCGGCTAGTGTGTCAGGCGCAAGCGGACGTGTGTCAGTGA 196
Db 14 TGGCAGGTAACTGTCTGTATCTCTCACTGAGCCCTGCAACCGCCACCTGCAAGACGTGA 73
QY 197 CCAACCGTTTATCTTAACTCTGTCACCGACCTGTGAGATTGCTGTGGCC 256
Db 74 CCACTATTTCATCTGTAACCTGCGCGTGGACCTGCTGTGAGCGCACCTTACTGC 133
QY 257 CCTGGGTGGGCACTCTGTGCTCTCTTGTGCCCCCTCAACAGCACTTGTGACGG 316
Db 134 CTTTCTGGGCAACATGAGAGTTCTGGGCTTCTGGGCTTGTGGCGGCTTCTGTGAGG 193
QY 317 CCTGTGTAGCTCACCCACCTGTGCTTGTGCGCCAGCGTCAACACCATTTCTGTGT 376
Db 194 TATGGGCGCCGCTGAGCGTGTGCTGTGTCAGCGCCCTCACTCTCAAGCTTGTGACCAT 253
QY 377 CAGTGTATGCTACTTGTGTCATATCCACCTCTCTCTCAACCGTCAGATGACCGAG 436
Db 254 CGTGTACCGGTACGTGGGCGTGGCGCACTCAAGTAAGACGATCATATGACGAGC 313
QY 437 GCGCGGTATCTGCTCTCTATGAGCACTGATTTGTGSCCATCTGTGAGAGCATCTTC 496
Db 314 GCAAGCGGCGCCGATCTGTGCGCTGTGAGTGTGAGTGTGAGTGTGAGG 373
QY 497 CACTTACGCGTGGGGCGAGGCTGCTTGTATGAGCGCAATGCTCTGTCTCATATCT 556
Db 374 CCTGTGGGCTGGAAGAGAGCCGTCGCCCTGA---CGAGCGCTTCTGCGATATACCG 430
QY 557 GGGGGCCAGCCCGCACTACATCTCAGGTGTGTCTTCACTGATTCATTCACCTGA 616
Db 431 AGGAGG-----CGGCTACGCTGTCTTCTCTCCGTGTGCTTCTTACTGCGCATG 484
QY 617 TTGTCAATGATTCCTCTACTCTCGTGTGTGTGTGTGTCAGCCCGAG 662
Db 485 CGGTATCTGTGTATGTACTGCGCGTGTACTGTGTGCGGCGAG 530

RESULT 13
CF147813 721 bp mRNA linear EST 25-JUL-2003
LOCUS CF147813
DEFINITION AGENCOURT 14740180 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:6971910 5', mRNA sequence.
ACCESSION CF147813
VERSION CF147813.1 GI:33244081
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 721)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB102 row: c column: 05
High quality sequence stop: 684.

FEATURES

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/clone="IMAGE:6971910"
/issue_type="mixed"
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/clone_1fb="NIH_MGC_145"
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XbaI/XhoI-3',
5'-BcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clone represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/reatarrayed_plates/IRB1.presv.dat
a Note: this is a NIH_MGC library."

ORIGIN

Query Match 6.0%; Score 92.2; DB 6; Length 721;
Best Local Similarity 49.5%; Pred. No. 5.1e-11;
Matches 266; Conservative 0; Mismatches 268; Indels 3; Gaps 1;
QY 75 CATGAGCCGCGCCACGAGATATCGCTCAACCGCTGTTATTTCTCGCGCCCTC 134
DB 90 CATGCGCGTGAGAGACTTGTCACGCTGTGTGTGCGCTGATCTTGGCGCTGGCGCT 149
QY 135 TTTCGTGGGCAATAGTGTGCGCTAGTGTGTCAGCGCAAGCCG--CAGCTGTGCA 191
DB 150 GGTGGGCAACAGCTGATATACCGTGTGCGCGGCAAGCCGCGGAGGCGGAG 209
QY 192 GGTGACCAACCGTTTATCTTAACCTCTGTCACGACCTGTGACAGATTGCTCTG 251
DB 210 CACCAACCACTGTTCATCTCACTGACATCGCGACCTGGGCTTACCTGCTTCTG 269
QY 252 GGGCCCTGTGTGTGTGCGCACTGTGTCTCTTCTGCGCCCTTAAGCAGCTTCTG 311
DB 270 CATCCCTTTCAGGCGCACGCTGTACCGCTGCCACCTGGGTGTGGGCGCTTCACTG 329
QY 312 CAGGCGCTGTAGGCTCACCCACCTGTGCGCTTGGCGGAGGTCAACCACTTCTT 371
DB 330 CAAATTCATCACTACTTCTTCAACGCTGTCACTGTGTGAGCATTTCACTGCGCC 389
QY 372 GGTGTAGTGTATGCTACTTGTTCATCAACCCCTCTCTCTCAACCGTCAAGATGAC 431
DB 390 GATGTCCGTGAGACCGCTACGTGCGCATGTGACACTGCGCGCTCTCTCTCTCAAGGT 449
QY 432 CCAAGGCGCGGTACTCTCTCTATAGGACCTGTGATTTGTGCGCATCTTGAAGGAC 491
DB 450 GTCCGCGCAACGCGCTGTGTGGGTGTGCACTGTGGGCGCTGTCCATTTGCAATGCGCTC 509
QY 492 TCCCTCACTCTACGGGTGGGCGAGGCTGCTTTGATGAGCGCAATGCTCTGTGTCAT 551
DB 510 GCCCGGTGCTTACACACAGGCGCTTTCACACCGCGCGGCAAGCAACCTTTGCTG 569
QY 552 GATCTGGGGGCGAGCCCAAGTACATATTCTCAAGCTGTGTCTCTTATCTGCTCAT 608
DB 570 GGAGGAGTGTGGCGGACCTTGGCACAAGAGGCTTACGTGTGTGTGACCTTGTGCTT 626

RESULT 14

DD032257 768 bp DNA linear GSS 02-JUN-2005
LOCUS
DEFINITION Pan troglodytes ADRA1D gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DD032257
VERSION DD032257.1 GI:66863466
KEYWORDS
SOURCE
ORGANISM Pan troglodytes (chimpanzee)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
REFERENCE 1 (bases 1 to 768)
Nijelsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civejlo,D.,
White,T.J., Snieky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
AUTHORS
REFERENCE 2 (bases 1 to 768)
Nijelsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civejlo,D.,
White,T.J., Snieky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES

source
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/mol_type="genomic DNA"
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ORIGIN

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Best Local Similarity 53.4%; Pred. No. 3.4e-10;
Matches 186; Conservative 0; Mismatches 162; Indels 0; Gaps 0;
QY 173 GCAGCCGCGAGCTGTGAGGTGACCAACCGTTTATCTTAACCTCTCTGTACGAGC 232
DB 25 GCAACCGCACCTGAGACCGCTCAACCACTATTATGTGACCTGCGCGCGAGC 84
QY 233 TGTCTGAGATTTGCTGTGCGCCCTGTGAGGTGCGCACTGTGCTCTCTTGTGGC 292
DB 85 TGTCTGTGAGCGCACCGTACTGCTTCTGCGCACCATGAGGTGCTGTGGCTTCTGGG 144
QY 293 CCTCAAGACGACCTTGTGACGCGCGGTGTTAGCTCACCAACCTGTGTGCGTGGCA 352
DB 145 CTTTGGCGGCGCTTGTGACGATGAGCGCGCTGTGACGTGTGTGCTGACCGCT 204
QY 353 GCGTCAACCACTTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 412
DB 205 CCATCTGAGCTCTGACACATCTCGTGTGAGCGGTGAGCGGTGAGCGGTGAGCGGTGAG 264
QY 413 CCTACCGGTCAAGATGACCAAGCGCGCGGTGATCTCTCTCTATAGGACCTGTGATG 472
DB 265 AGTACCCAGCCATCATGTGACCGGCAAGCGCGCGGTGATCTCTCTCTGTGTGTG 324
QY 473 TGGCATCTGTGAGGACACTCTCTCACTTACGCTGTGGGCGGAGGCTG 520
DB 325 TAGCCCTGTGTGTGTCGTGAGGCGCTGTGCGGTGAGGAGGCGCG 372

RESULT 15

AI457674 386 bp mRNA linear EST 13-APR-1999
LOCUS AI457674/c
DEFINITION tJ48f06.xl Soares NSF_P8_9W_OT_PA_P_S1 Homo sapiens cDNA clone

IMAGE:2144771.3' similar to gb:M76446 ALPHA-1A ADRENERGIC RECEPTOR (HUMAN); mRNA sequence.

ACCESSION A1457674
VERSION A1457674.1 GI:4310543

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 386)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Insert Length: 672 Std Error: 0.00
Seq primer: -40UP from Gibco

High quality sequence stop: 353.

FEATURES
Location/Qualifiers

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/mol_type="mRNA"
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/clone="IMAGE:2144771"
/lab_host="DH10B"

/clone_1lb="Soares_NSP_F8_9W_OT_PA_P_S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI;

Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro.

Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was

PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following

libraries and clones: Soares NBHP pool 1:
309384-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -

150407, 151176-152327 Soares NB2HF8-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NBHP

pool 1: 723720-726407, 739080-740999 Subtraction by Bento

Soares and M. Patricia Bonaldo."

ORIGIN

Query Match 5.8%; Score 88.4; DB 1; Length 386;

Best Local Similarity 53.1%; Pred. No. 3.7e-10;
Matches 188; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

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DB 365 GCGCAGGGGGTGGGCGCTGGGCGCTTCTTCGCGAGCCTTCATCTTATGGCCGTCAGGT 306

QY 145 AACATAGTGTGGCGCTAGTGTGACGCGAAGCGCAGTGTGACAGGTGACCAACCGT 204

DB 305 AACCTGCTGTATCTCTCAAGTGGCTGCAACCGCACTGACAGCGTCAACCAATAT 246

QY 205 TTATCTTAACCTCTCTGTCACCGACTGTGTCAGATTTCGCTGTGGCCCTGGGTG 264

DB 245 TTCATGTGAACCTGGCGCGGACCTGCTGTAGGCGCACGTTACTGCGCCCTCTCG 186

QY 265 GTGGCCACTCTGTGCTCTCTTGTGGCCCTCAACAGCACTTCTGCAAGCGCCCTGTT 324

DB 185 GCCACCATGAGGTTTGGGCTTGTGGGCTTGGCGCGGCTTCTGCAACGATAGGCC 126

QY 325 AGCCTACCCACCTGTTGGCTTGGCAGGTCACACCACTTGTGTTGATGATGAT 384

DB 125 GCCGTGAGCTGTGTGCTGCAAGCGCTTCATCTCAAGCTTCTGCAACATCTTCGTGAC 66

QY 385 CGCTACTGTTCATCATCAACCTCTCTCTACCGCTCCAGATGACCCAGCGC 438

DB 65 CGGTAGTGGGCGTGGCGCACTCACTCAAGTACCCAGCATCATGACCGAGCGC 12

Search completed: December 10, 2005, 03:03:23
Job time : 4328 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 23:55:31 ; Search time 5234 Seconds
(without alignments)

16583.865 Million cell updates/sec

Title: US-10-712-615-1

Perfect score: 1527

Sequence: 1 atgcagctccaccctgcaccaa.....attctgctactttctctga 1527

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_scs:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1527	100.0	1527	6	BD095705 Novel gua
2	1527	100.0	1527	6	AX497863 Sequence
3	1527	100.0	1580	6	AX497909 Sequence
4	1527	100.0	175465	14	AL356783 Sequence
5	1525.4	99.9	1527	6	BD144320 Novel G-P
6	1525.4	99.9	1527	6	CQ736967 Sequence
7	1525.4	99.9	1527	6	AR679058 Sequence
8	1525.4	99.9	1527	6	AX148174 Sequence
9	1525.4	99.9	1527	6	AX230165 Sequence
10	1525.4	99.9	1527	6	AX355868 Sequence
11	1525.4	99.9	1527	6	AX497907 Sequence
12	1525.4	99.9	1527	6	AX543321 Sequence
13	1525.4	99.9	1527	6	AX549297 Sequence
14	1525.4	99.9	1527	8	AB083588 Homo sapi
15	1525.4	99.9	1527	8	AF411115 Homo sapi
16	1525.4	99.9	1527	8	BC069439 Homo sapi
17	1525.4	99.9	1659	6	AX080495 Sequence
18	1525.4	99.9	1659	6	AX497906 Sequence

19	1525.4	99.9	1658	6	AX646733 Sequence
20	1525.4	99.9	1658	8	AB065937 Homo sapi
21	1525.4	99.9	1920	6	AX355867 Sequence
22	1525.4	99.9	7524	6	AX543323 Sequence
23	1525.4	99.9	140628	14	AC016468 Sequence
24	1525.4	99.9	172280	8	AL390879 Human DNA
25	1524	99.8	1524	6	BD173594 Novel G P
26	1522.4	99.7	1524	6	BD173595 Novel G P
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32	1520.6	99.6	1527	6	AX497908 Sequence
33	1515.8	99.3	1527	6	AX459697 Sequence
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35	1456.4	95.4	1458	6	AX342674 Sequence
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37	912.2	61.0	179648	9	AL672122 Mouse DNA
38	912.2	59.7	135462	14	AC123499 Rattus no
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40	855.4	56.0	1197	6	AX543324 Sequence
41	855.4	56.0	1530	6	AX286523 Sequence
42	722.2	47.3	835	10	BV208535 GPR101_20
43	649.6	42.5	1697	6	AX647119 Sequence
44	649.6	42.5	70254	14	AC024415 Homo sapi
45	600.2	39.3	951	6	AX657432 Sequence

ALIGNMENTS

RESULT 1	BD095705	1527 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD095705	Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use.			
DEFINITION	BD095705	Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use.			
ACCESSION	BD095705	Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use.			
VERSION	BD095705.1	GI:22641293			
KEYWORDS	WO 0148188-A/17.				
SOURCE	WO 0148188-A/17.				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (baes 1 to 1527)	Saito, Y., Noriyuki, Morikawa, Yoshida, K., Watanabe, S., Oda, T., Suwa, M., Sugiyama, T., Kishimoto, T., Kanzaki, K., Yaeuda, S. and Inoue, Y.			
AUTHORS	Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use				
TITLE	Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use				
JOURNAL	Patent: WO 0148188-A 17 05-JUL-2001; HELIX RESEARCH INSTITUTE, SHINICHIRO MATSUMOTO, TANAKI ODA, YOKO SAITO, NORIYUKI MORIKAWA, KENJI YOSHIDA, MAKIKO SUWA, TOMOYASU SUGIYAMA, TOSHIMITSU KISHIMOTO, KOJI KANZAKI, SHINICHIRO YASUDA, YOSHITSUGU INOUE				
COMMENT	OS Homo sapiens (human) PN WO 0148188-A/17 PD 05-JUL-2001 PF 28-DEC-2000 WO 2000JP009408 PR 28-DEC-1999 JP 99P 375152, 31-MAR-2000 JP 00P 101339 PI SHUNICHIRO MATSUMOTO, TANAKI ODA, YOKO SAITO, NORIYUKI PI MORIKAWA, KENJI YOSHIDA, PI MAKIKO SUWA, TOMOYASU SUGIYAMA, TOSHIMITSU KISHIMOTO, KOJI KANZAKI, PI SHINICHIRO YASUDA, YOSHITSUGU INOUE PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C07K14/705, PC C07K16/28, PC C12P21/02, C12Q1/02, C12Q1/68, A61K31/711, A61K48/00, A61P43/00, PC G01N33/15, PC G01N33/50 CC Novel guanosine triphosphate-bound protein-coupled receptors and genes				

CC encoding them, and their production and use
FH Key Location/Qualifiers
FT source 1..1527
FT /organism='Homo sapiens (human)'.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 9,5e-236;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCTCCACCTGGACCAACAGCAGCGCGAGAGTAACAGACGCCACACGTCATGCCCC 60
DB 1 ATGAGCTCCACCTGGACCAACAGCAGCGCGAGAGTAACAGACGCCACACGTCATGCCCC 60
QY 61 CTCTCCAAATATGCCATCAGCTGGGCCAGGCATCATCCGCTCAACCGTGTGTATC 120
DB 61 CTCTCCAAATATGCCATCAGCTGGGCCAGGCATCATCCGCTCAACCGTGTGTATC 120
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DB 121 TTCCTGCGCGCTCTTGTGTGGCAACATAGTGTGGGCTAGTGTGGAGGCGCAAGCG 180
QY 181 CAGCTGTGAGAGTACCAACCGTTTATCTTTAACTCTCTGTGACGACCTGCTGAG 240
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QY 241 ATTGCTGTGTGGCCCCCTGGGTGTGGCACTCTGTGCTCTCTTGTGGCCCCCTCAAC 300
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DB 481 CTGACAGACATCCCTCCACTCTAAGCTGGGGGCGGCTGCTTTGATGAGGCAATGCT 540
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DB 601 ATGCTCATTCACATGATTTGTCAATGATGCTGTCTCTACTCCGTGTGTCTGTGACGCCG 660
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DB 781 GAGTTTCCGCGCGACATGAG 840
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DB 841 GACGCGAGCTGAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCC 900

DB 841 GACGCGAGCTGAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCC 900
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DB 901 AGGGCAGCGAGAGAGTTCAG 960
QY 961 AAGGAGGACACCAAGAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 AAGGAGGACACCAAGAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
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DB 1021 GTCAACGAGTGCAGATTTGATCTTGGGTGAAGATGATCATGTGAGTTTGGTAAGACGATC 1080
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DB 1141 CGTAAACAGCAACAGCAACCTCTCTGCGCAGAGTCTTCCAGTGCATGCTTAAAGT 1200
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QY 1501 TCCTACGATTTGCTACTTTTCTTTGA 1527
DB 1501 TCCTACGATTTGCTACTTTTCTTTGA 1527
RESULT 2
AX497863 1527 bp DNA linear PAT 26-SEP-2002
LOCUS Sequence 1 from Patent WO0240670.
DEFINITION AX497863
ACCESSION AX497863
VERSION AX497863.1 GI:23342970
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 Battaglini, P., Feder, J., Mintier, G., Nelson, T., Ramanathan, C.,
Westphal, R., Cacece, A., Barber, L., Hawken, D. and Kornacker, M.
A novel human g-protein coupled receptor, hgrbm78, expressed
highly in brain
Patent: WO 0240670-A 1 23-MAY-2002;
Bristol-Myers Squibb Company (US)
JOURNAL
TITLE
AUTHORS
FEATURES
SOURCE Location/Qualifiers
1..1527
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 1527; DB 6; Length 1527;
Best Local Similarity 100.0%; Pred. No. 9.5e-296;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 CTCTCCAAATGCGCATCAGCTGCGCCAGCGATATCCGCTCAACCGGTGTTATC 120
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RESULT 3
AX497909 1580 bp DNA linear PAT 26-SEP-2002
LOCUS AX497909
DEFINITION Sequence 47 from Patent WO0240670.
ACCESSION AX497909
VERSION AX497909.1 GI:23342984
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 Baccaglino, P., Feder, J., Mintier, G., Nelson, T., Ramanathan, C.,
Westphal, R., Cacace, A., Barber, L., Hawken, D., and Kornacker, M.
A novel human G-protein coupled receptor, hgrprhny8, expressed
highly in brain
Patent: WO 0240670-A 47 23-MAY-2002;
JOURNAL Bristol-Myers Squibb Company (US)
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/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 9.5e-296;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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 LOCUS Homo sapiens chromosome X clone RP13-13121, 7 unordered pieces.
 DEFINITION
 AL356783 AL356783 GI:14456213
 ACCESSION
 VERSION HTG; HTGS_PHASE1; HTGS_CANCELLED.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
 1 Heath, P.
 Direct Submission
 Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 Requesters: Clonerequest@sanger.ac.uk
 On Jun 14, 2001 this sequence version replaced gi:14329943.
 COMMENT
 ----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: b13121
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: plasmid; L08752; 100% of reads
 Chemistry: Dye-terminator BT-amerham; 3% of reads Chemistry:
 Dye-terminator Big Dye; 64% of reads
 Consensus quality: 173062 bases at least Q40
 Consensus quality: 174012 bases at least Q30
 Consensus quality: 174525 bases at least Q20
 Insert size: 174665; sum-of-coverage
 Quality coverage: 5.89x in Q20 bases; sum-of-coverage

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 7 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 102859: contig of 102859 bp in length
 * 102860 102859: gap of 100 bp
 * 102960 126878: contig of 23919 bp in length

DB	106663	TCCTACGATTCTGCTACTTTTCCTTGA	106689
RESULT 5			
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LOCUS	BD144320	1527 bp	DNA
DEFINITION	Novel G-protein coupled receptors.		linear
ACCESSION	BD144320		
VERSION	BD144320.1	GI:27850078	
KEYWORDS	JP 2002112793-A/45.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.		
REFERENCE	1 (bases 1 to 1527)		
AUTHORS	Haga, T., Takada, S. and Miyake, N.		
TITLE	Novel G-protein coupled receptors		
JOURNAL	Patent: JP 2002112793-A 45 16-APR-2002;		
	JAPAN SCIENCE AND TECHNOLOGY CORP		
COMMENT	OS Homo sapiens (human)		
	PN JP 2002112793-A/45		
	PD 16-APR-2002		
	PF 09-FEB-2001 JP 2001034434		
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	PC C12N15/09, A01K67/027, A61K38/00, A61K39/395, A61K39/395, A61K45/00, PC A61K48/00.		
	PC A61P3/00, C07K14/705, C07K16/28, C07K19/00, C12N1/15, C12N1/19, PC C12N1/21.		
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Query Match	99.9%;	Score 1525.4;	DB 6; Length 1527;
Best Local Similarity	99.9%;	Pred. No. 2e-295;	
Matches 1526; Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
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QY	121	TTCCTGCGCGCTCTTTCGTGCGCAACATAGTGTGCGGTAGTGTGCGCAAGCGG	180
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DB	241	ATTGGCTGCTGCGCCCTCTGGTGTGGCGCACTCTGTGCGCTCTTCTTGCGCCCTCAAC	300
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VERSION
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homnidae; Homo.

REFERENCE
1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
AUTHORS Kites, such as nucleic acid arrays, comprising a majority of
TITLE humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 22901 06-SEP-2002;
PE Corporation
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ORIGIN
Query Match 99.9%; Score 1525.4; DB 6; Length 1527;
Best Local Similarity 99.9%; Pred. No. 2e-295; 1; Indels 0; Gaps 0;
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DEFINITION AR679058
ACCESSION AR679058

VERSION AR679058.1 GI:67620281
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1527)
AUTHORS Unetc,D.J., Chen,R., Richman,J.G., Connolly,D.T., Hakak,Y.,
Behan,D.P. and Chalmers,D.T.
TITLE Human G protein-coupled receptors and modulators thereof for the
treatment of metabolic-related disorders
JOURNAL Patent: US 6902902-A 15 07-JUN-2005;
Arena Pharmaceuticals, Inc.; San Diego, CA
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LOCUS AX148174
DEFINITION Sequence 15 from Patent WO0136471.
ACCESSION AX148174
VERSION AX148174.1 GI:14347080
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
AUTHORS Homo sapiens
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Chen,R., Dang,H.T. and Lowitz,K.P.
TITLE Endogenous and non-endogenous versions of human g protein-coupled
receptors
JOURNAL Patent: WO 0136471-A 15 25-MAY-2001;
Arena Pharmaceuticals, Inc. (US)
FEATURES
Location/Qualifiers

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LOCUS AX230165
DEFINITION Sequence 52 from Patent WO0162797.
ACCESSION AX230165
VERSION AX230165.1 GI:15592183
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 Vogeli, G., Wood, L.S., Parodi, L.A. and Lind, P.
Novel g protein-coupled receptors
Patent: WO 0162797-A 52 30-AUG-2001;
PHARMACIA & UPJOHN COMPANY (US)
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Best Local Similarity 99.9%; Pred. No. 2e-295;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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LOCUS AX355868 1527 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 2 from Patent WO0188126.
ACCESSION AX355868
VERSION AX355868.1 GI:18620521
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homnidae; Homo.

REFERENCE 1 Ramakrishnan, S.
TITLE Regulation of human _g(a)1a7adrenergic receptor-like G
protein-coupled receptor
JOURNAL Patent: WO 0188126-A 2 22-NOV-2001;
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Best Local Similarity 99.9%; Pred. No. 2e-295;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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ACCESSION	AX497907		
VERSION	AX497907.1	GI:23342982	
KEYWORDS			
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ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Bukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 Bataglino, P., Feder, J., Mintier, G., Nelson, T., Ramathan, C., Westphal, R., Cacace, A., Barber, L., Hawken, D. and Kornacker, M. A novel human G-protein coupled receptor, hGPR108, expressed highly in brain		
JOURNAL	Patent: WO 0240670-A 45 23-MAY-2002;		
FEATURES	Bristol-Myers Squibb Company (US)		
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ACCESSION	AX543321	GI:25276744	
VERSION	AX543321.1		
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ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Li, Z., Cravchik, A., Milehina, N., Wei, M.H., Ketchum, K.A., di Francesco, V. and Beasley, E.M.		
JOURNAL	Isolated human G-protein coupled receptors, nucleic acid molecules encoding human GPCR proteins, and uses thereof		
FEATURES	Patent: WO 0205191.1 A 1 01-Aug-2002; PE Corporation (NY) (US)		
source	Location/Qualifiers		
ORIGIN	1..1527		
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Db      ||||| 841 GACGGCAGCCTGAAAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Qy      ||||| 901 AGGGGAGAGAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
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Db      ||||| 1141 CGTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
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LOCUS DEFINITION Sequence 582 from Patent WO02061087.
ACCESSION AX549297
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VERSION AX549297.1 GI:25813959
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 Burner, G.C., Roush, C.L. and Brown, J.P.
Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
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Patent: WO 02061087-A 582 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
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Matches 1526; Conservative 0; Mismatches 1;
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QY	1021	GTCAACCAAGTGCATTAAGCTTTGGGTGAAGTACATGGAATTTGGTGAAGACATC	1080
Db	1021	GTCAACCAAGTGCATTAAGCTTTGGGTGAAGTACATGGAATTTGGTGAAGACATC	1080
QY	1081	AATTTCAGTGAAGATGACGTCCAGGACAGGAACATCCCGAAGGCTCCACCCAGTGGT	1140
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DEFINITION	Homo sapiens GPCR gene for putative G-protein coupled receptor, complete CDS, clone:hGPCR6.
ACCESSION	AB083588
VERSION	AB083588.1 GI:20152239
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE	1
AUTHORS	Takeda,S., Kadowaki,S., Haga,T., Takeesu,H. and Mitaku,S.
TITLE	Identification of G protein-coupled receptor genes from the human

JOURNAL REFERENCE AUTHORS TITLE JOURNAL	genome sequence Unpublished 2 (bases 1 to 1527) Takeda,S., Kadowaki,S., Haga,T., Takeaeu,H. and Mitaku,S. Direct Submission Submitted (10-APR-2002) Shigeaki Takeda, Gunma University, Department of Biological and Chemical Engineering, Faculty of Engineering, 1-5-1, Kiryu, Gunma 376-8515, Japan (E-mail:etakeda@ce.gunma-u.ac.jp), Tel:+81-277-30-1434, Fax:+81-277-30-1434)
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Oy	1261	CTGGCCGTGTGGGTGATGTCGAAACCAGGATACCCACGTGGGTGATCACCATATCATC	1320
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ACCESSION	AF411115				
VERSION	AF411115.1				
KEYWORDS	GI:16566340				
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SOURCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.				
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TITLE	11574155 2 (bases 1 to 1527) Lee, D. K., Nguyen, T., Lynch, K. R., Cheng, R., Vanti, W. B., Arkhitko, O., Lewis, T., Evans, J. F., George, S. R., and O'Dowd, B. F. Direct Submission Submitted (17-AUG-2001) Department of Pharmacology, University of Toronto, 8 Taddle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada				
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Searched: 4996997 seqs, 3332346308 residues

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Post-Processing: Minimum Match 0%
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Listing first 45 summaries

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4	1527	100.0	1527	14	Aea33069 Human G-P
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7	1527	100.0	1584	8	ACF03567 Human NOV
8	1527	100.0	4718	9	ACCS8886 Human G-P
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41	1520.6	99.6	1527	5	Aa508265 Human GPC
42	1520.6	99.6	1527	11	AD196537 Human mut
43	1520.6	99.6	1527	14	ADw44710 Human RUP
44	1520.6	99.6	1527	14	Aea33114 Human GPC
45	1520.6	99.6	1527	14	Aeb20894 Human RUP

ALIGNMENTS

RESULT 1	AAH73517	strand; DNA; 1527 BP.
ID	AAH73517	
AC	AAH73517	
DT	25-SBP-2001 (first entry)	
XX	Human G protein-coupled receptor GPRV72 coding sequence.	
XX	Human; guanosine triphosphate binding protein-coupled receptor;	
XX	KM G protein-coupled receptor; GPRV8; GPRV12; GPRV16; GPRV21; GPRV40;	
XX	KW GPRV47; GPRV51; GPRV71; GPRV72; cancer; liver cirrhosis;	
XX	KW Alzheimer's disease; cytosolic; hepatotropic; nootropic;	
XX	KW neuroprotective; gene therapy; peptide therapy; ds.	
OS	Homo sapiens.	
XX		
XX	WO200148188-A1.	
PN		
PD	05-UTL-2001.	
XX		
PF	28-DEC-2000; 2000WO-JP009408.	
XX		
PR	28-DEC-1999; 99JP-00375152.	
PR	31-MAR-2000; 2000JP-00101339.	
XX	(HELI-) HELIX RES INST.	
PA		
XX	Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;	
PI	Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;	
PI	WPI; 2001-425662/45.	
DR	P-PDB; Aa64126.	
DR		
XX		
PT	New DNA encoding guanosine triphosphate binding protein coupled receptors	
PT	and their expression products for screening potential anticancer and	
PT	nootropic drugs and in diagnosis of these diseases.	
XX	Claim 1, Page 143-144; 170pp; Japanese.	
PS		
XX	The invention relates to nine human guanosine triphosphate binding	
CC		

CC protein (G protein)-coupled receptors designated GPRv6, GPRv12, GPRv16,
CC GPRv21, GPRv40, GPRv47, GPRv51, GPRv71 and GPRv72, and to the genes
CC encoding them. These genes and proteins and antibodies against the
CC protein are useful in the treatment, prevention, diagnosis and
CC investigation of diseases associated with G protein-coupled receptors,
CC including cancer, cirrhosis of the liver and Alzheimer's disease. The
CC present sequence is a G protein-coupled receptor coding sequence of the
CC invention
XX

Sequence 1527 BP; 347 A; 439 C; 419 G; 322 T; 0 U; 0 Other;

Query Match 100.0%; Score 1527; DB 4; Length 1527;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGTCACCTGGACCAACAGCAGCGGAGAGTAACAGAGCCACAGTCGATGCC 60
DB 1 ATGAGTCACCTGGACCAACAGCAGCGGAGAGTAACAGAGCCACAGTCGATGCC 60
QY 61 CTCTCAAAATGCCATCAGCTGGCCCAAGGATCATCCGCTCAACCGTGTGTTATC 120
DB 61 CTCTCAAAATGCCATCAGCTGGCCCAAGGATCATCCGCTCAACCGTGTGTTATC 120
QY 121 TTCTCCGCGGCTCTTTGCTGGGCAACATAGTGTGGGCTAGTGTGTCAGGCAAGCCG 180
DB 121 TTCTCCGCGGCTCTTTGCTGGGCAACATAGTGTGGGCTAGTGTGTCAGGCAAGCCG 180
QY 181 CAGTGTGTCAGAGTACCAACCGTTTATCTTTAACCTCTGTCACGAGCTGTGACG 240
DB 181 CAGTGTGTCAGAGTACCAACCGTTTATCTTTAACCTCTGTCACGAGCTGTGACG 240
QY 241 ATTTGCGTGTGGCCCTGGGTGGTGGCCACCTGTGCTCTCTTCTGGCCCTCAAC 300
DB 241 ATTTGCGTGTGGCCCTGGGTGGTGGCCACCTGTGCTCTCTTCTGGCCCTCAAC 300
QY 301 AGGCACTTCTGACAGCCCTGGTTAGCCCTCAACCCCTGTGGCTTGGCCAGCGTCAAC 360
DB 301 AGGCACTTCTGACAGCCCTGGTTAGCCCTCAACCCCTGTGGCTTGGCCAGCGTCAAC 360
QY 361 ACCATTGCTTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 361 ACCATTGCTTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 TCCAAAGTATCCAGCGCGCGGTTAAGCTGCTCTCTATGAGCACTGATGAGGATC 480
DB 421 TCCAAAGTATCCAGCGCGCGGTTAAGCTGCTCTCTATGAGCACTGATGAGGATC 480
QY 481 CTGCAAGATCTCTCCACTCTTACCGCTGGGCGAGGCTGCTTGTATGAGGCAATGCT 540
DB 481 CTGCAAGATCTCTCCACTCTTACCGCTGGGCGAGGCTGCTTGTATGAGGCAATGCT 540
QY 541 CTCTGCTCATGATCTGGGGGGGCGAGCCAGCTACATATTCTAGCGTGTGCTTCT 600
DB 541 CTCTGCTCATGATCTGGGGGGGCGAGCCAGCTACATATTCTAGCGTGTGCTTCT 600
QY 601 ATGCTCATTCACGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
DB 601 ATGCTCATTCACGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 661 AGGCGCATGCTCTGCTGTAACAATGTCAGAGACACAGTTGGAAAGTGAAGTCAAGAC 720
DB 661 AGGCGCATGCTCTGCTGTAACAATGTCAGAGACACAGTTGGAAAGTGAAGTCAAGAC 720
QY 721 TGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
DB 721 TGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 781 GAGTTTCGCGCGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATG 840
DB 781 GAGTTTCGCGCGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 841 GACGCGAGCTGTAAGGCCAAGAGAGACAGCGGGAACAGTGAAGTGTGTAGAGGCC 900
DB 841 GACGCGAGCTGTAAGGCCAAGAGAGACAGCGGGAACAGTGAAGTGTGTAGAGGCC 900

DB 841 GACGCGAGCTGTAAGGCCAAGAGAGACAGCGGGAACAGTGAAGTGTGTAGAGGCC 900
QY 901 AGGCGCAGCGAGAGTGCAGAGAGAGCAGCAGCGTGGCCAGCAGCAGCAGTGAAGGT 960
DB 901 AGGCGCAGCGAGAGTGCAGAGAGAGCAGCAGCGTGGCCAGCAGCAGCAGTGAAGGT 960
QY 961 AAGGAGGCGAGCAGCAAGGTTGAGAGAAACAGCATGAAGGCGAGACAGGCTGCGACAAG 1020
DB 961 AAGGAGGCGAGCAGCAAGGTTGAGAGAAACAGCATGAAGGCGAGACAGGCTGCGACAAG 1020
QY 1021 GTCAACAGTGCAGATTCAGTGGGTGAAGTGCATGATGATGATGATGATGATGATG 1080
DB 1021 GTCAACAGTGCAGATTCAGTGGGTGAAGTGCATGATGATGATGATGATGATGATG 1080
QY 1081 AATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
DB 1081 AATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1141 CGTAAACAGCAACAGCAACCTCTCTGCTCCAGTGTCTACAGTGCAGAACTGTAAAGT 1200
DB 1141 CGTAAACAGCAACAGCAACCTCTCTGCTCCAGTGTCTACAGTGCAGAACTGTAAAGT 1200
QY 1201 ATCTTCATCATCTTTTCTCTATGATGATGATGATGATGATGATGATGATGATGATG 1260
DB 1201 ATCTTCATCATCTTTTCTCTATGATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1261 CTGGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
DB 1261 CTGGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 TGGCTTTTCTCTGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1380
DB 1321 TGGCTTTTCTCTGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1380
QY 1381 ATTAAGAGGAATCCAGAGCATGCTGAAGAGTCTTCTGCAAGGAAGGCCCGGAAA 1440
DB 1381 ATTAAGAGGAATCCAGAGCATGCTGAAGAGTCTTCTGCAAGGAAGGCCCGGAAA 1440
QY 1441 GAAAGTACGACCCAGACCTGCGCGGAAACAGAGGCTGGAGCTGAAGGCAAGTTTCCCT 1500
DB 1441 GAAAGTACGACCCAGACCTGCGCGGAAACAGAGGCTGGAGCTGAAGGCAAGTTTCCCT 1500
QY 1501 TCTTACGATTCGCTACTTTTCTTTGA 1527
DB 1501 TCTTACGATTCGCTACTTTTCTTTGA 1527

RESULT 2
ABLS3719
ID ABL53719 standard; cDNA; 1527 BP.
XX
XX
AC ABL53719;
XX
DT 24-JUN-2002 (first entry)
XX
DE G-protein coupled receptor AXOR69 cDNA.
XX
XX G-protein coupled receptor; receptor; AXOR69; human; anti-HIV; virucide;
KW antimicrobial; analgesic; cytostatic; antidiabetic; anorectic; anabolic;
KW antiaesthetic; antiparkinsonian; cardiant; cerebroprotective;
KW hypotensive; hypertensive; antileptic; antiaesthetic; antiallergic;
KW antileptic; tranquilizer; neuroleptic; nootropic; anticonvulsant;
KW vaccine; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
XX
FH Key
FT CDS Location/Qualifiers
FT 1..1527
FT /tag= a
FT /product= "AXOR69"
XX
XX
XX GB2367295-A.

03-APR-2002.
12-JUN-2001; 2001GB-00014287.
16-JUN-2000; 2000US-00596400.
(SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM PLC.
(SMIK) SMITHKLINE BEECHAM PLC.
Elshourbagy N, Gattu M, Shabon U;
WPI; 2002-294789/34.
P-PSDB; ABB75712.
An isolated human G-protein coupled (77M) receptor AXOR 69 polypeptide, for treating diseases such as obesity, stroke and anxiety.
Claim 2; Page 27; 34pp; English.

The present sequence is that of cDNA encoding a human G-protein coupled receptor, termed AXOR69 (see ABB75712). AXOR69 shows homology to other members of the G-protein coupled receptor family, such as the human adrenergic alpha-1a receptor. The invention provides AXOR69 polypeptides and polynucleotides, and methods for producing such polypeptides by recombinant techniques. Also provided are methods for using the AXOR69 polypeptides and polynucleotides to screen for compounds that stimulate or inhibit AXOR69 levels or activity. The polypeptides, polynucleotides, agonists and antagonists are used to treat conditions associated with AXOR69 imbalance, including bacterial, fungal, protozoan and viral infections, particularly HIV-1 and HIV-2 infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, depression, delirium, dementia and severe mental retardation, and dyskinesias such as Huntington's disease and Gilles de la Tourette syndrome. The polynucleotides can also be used for diagnosing mutations, in chromosome localisation studies, in pharmacogenomics, and to construct transgenic animals. The polypeptides and polynucleotides are also useful as vaccines

Sequence 1527 BP; 347 A; 439 C; 419 G; 322 T; 0 U; 0 Other;

Query Match 100.0%; Score 1527; DB 6; Length 1527;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGACGTCACCTGCACCAACAGCAGCGAGATGACAGCAGCAGTCATGCC 60
1 ATGACGTCACCTGCACCAACAGCAGCGAGATGACAGCAGCAGTCATGCC 60
61 CTCTCCAAATGCGCATCAGCGCCAGCGCATCATCCGCTCAACCGTGTGTTATC 120
61 CTCTCCAAATGCGCATCAGCGCCAGCGCATCATCCGCTCAACCGTGTGTTATC 120
61 CTCTCCAAATGCGCATCAGCGCCAGCGCATCATCCGCTCAACCGTGTGTTATC 120
121 TTCCTGCGCGCTTTTGTGCGCAATAGTCTGCGCTAGTGTGCGCGCAAGCCG 180
121 TTCCTGCGCGCTTTTGTGCGCAATAGTCTGCGCTAGTGTGCGCGCAAGCCG 180
121 TTCCTGCGCGCTTTTGTGCGCAATAGTCTGCGCTAGTGTGCGCGCAAGCCG 180
181 CAGCTCTCAGGTGACCAACGCTTTATCTTAACTCTGTCACCGACCTGTCGAG 240
181 CAGCTCTCAGGTGACCAACGCTTTATCTTAACTCTGTCACCGACCTGTCGAG 240
181 CAGCTCTCAGGTGACCAACGCTTTATCTTAACTCTGTCACCGACCTGTCGAG 240
241 ATTTCGCTGCTGCGCGCTGCGGTGAGTGCACCTCTGCTCTTCTTGGCCCTCAAC 300
241 ATTTCGCTGCTGCGCGCTGCGGTGAGTGCACCTCTGCTCTTCTTGGCCCTCAAC 300
241 ATTTCGCTGCTGCGCGCTGCGGTGAGTGCACCTCTGCTCTTCTTGGCCCTCAAC 300
301 AGCATTCTGCAACGCGCGCTGCTGAGCTTCAACCCACCTGTTGCGCTTGGCAAC 360
301 AGCATTCTGCAACGCGCGCTGCTGAGCTTCAACCCACCTGTTGCGCTTGGCAAC 360

361 ACCATTGCTTGTGTGTCAGTGTGATGCTGCTAATTGCTCATCATCACCCTCTCTCAACCG 420
361 ACCATTGCTTGTGTGTCAGTGTGATGCTGCTAATTGCTCATCATCACCCTCTCTCAACCG 420
421 TCCAAATGACCCAGCGCGCGTTAACTGCTCTCTTAAGGACCTGTGATGCGGCATC 480
421 TCCAAATGACCCAGCGCGCGTTAACTGCTCTCTTAAGGACCTGTGATGCGGCATC 480
421 TCCAAATGACCCAGCGCGCGTTAACTGCTCTCTTAAGGACCTGTGATGCGGCATC 480
481 CTGCAAGACCTCTCTCACTTACGCGTGGGCGCAGGCTGCTTGTGATGCGGCATGCT 540
481 CTGCAAGACCTCTCTCACTTACGCGTGGGCGCAGGCTGCTTGTGATGCGGCATGCT 540
541 CTGCTCTCATGATCTGCGGCGCGCAAGCCAGCTACACTAATTCAGCGTGTGCTTC 600
541 CTGCTCTCATGATCTGCGGCGCGCAAGCCAGCTACACTAATTCAGCGTGTGCTTC 600
541 CTGCTCTCATGATCTGCGGCGCGCAAGCCAGCTACACTAATTCAGCGTGTGCTTC 600
601 ATGCTATTCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
601 ATGCTATTCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
661 AGCAGCATGCTCTGCTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 720
661 AGCAGCATGCTCTGCTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 720
721 TGTGTGAAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 780
721 TGTGTGAAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 780
781 GAGTTTCCGCGCGCAGCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
781 GAGTTTCCGCGCGCAGCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
841 GAGGAGCTGTAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 900
841 GAGGAGCTGTAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 900
901 AGGCGAGCGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 960
901 AGGCGAGCGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 960
961 AAGGAAGGCAAGCAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGG 1020
961 AAGGAAGGCAAGCAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGG 1020
961 AAGGAAGGCAAGCAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGG 1020
1021 GTCAACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080
1021 GTCAACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080
1081 AATTTCAATGAGATGACCTGAGGAGTGAACATCCCGAGAGCTCCACCAAGTCTGT 1140
1081 AATTTCAATGAGATGACCTGAGGAGTGAACATCCCGAGAGCTCCACCAAGTCTGT 1140
1141 CGTAACAGCAAGCAAGCTCTCTGCGCGAGGTGCTTACAGTGAAGTGTAAAGT 1200
1141 CGTAACAGCAAGCAAGCTCTCTGCGCGAGGTGCTTACAGTGAAGTGTAAAGT 1200
1201 ATCTTCATGATATTTTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
1201 ATCTTCATGATATTTTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
1261 CTGCGCGTGTGAGTGAATGCAAAACAGTATCCCAAGTGGTATGACATTAATCATC 1320
1261 CTGCGCGTGTGAGTGAATGCAAAACAGTATCCCAAGTGGTATGACATTAATCATC 1320
1261 CTGCGCGTGTGAGTGAATGCAAAACAGTATCCCAAGTGGTATGACATTAATCATC 1320
1321 TGGCTTTTCTTCTGAGTGTGATCAACCCCTATGCTATGAGCTATGACAAAGAC 1380
1321 TGGCTTTTCTTCTGAGTGTGATCAACCCCTATGCTATGAGCTATGACAAAGAC 1380
1381 ATTAAGAAGGAATCCAGGACATGCTGAAGAGTCTTCTGAAGGAAGGAAGGCGCGGAA 1440
1381 ATTAAGAAGGAATCCAGGACATGCTGAAGAGTCTTCTGAAGGAAGGAAGGCGCGGAA 1440
1381 ATTAAGAAGGAATCCAGGACATGCTGAAGAGTCTTCTGAAGGAAGGAAGGCGCGGAA 1440
1441 GAAGATAGCCACCAAGCTGCGCGGAAACAGAGGTGGAGTGAAGGCAAGATTGTCTCT 1500

Dn		1441	GAAAGTAGCACCACGACTCGCCGGACAGAGGTGGAGCTGAAGCAATTTCTCCTT	1500
Oy		1501	TCTTAAGATTCTGCTACTCTTTTCCTTGA	1527
Dn		1501	TCTTAAGATTCTGCTACTCTTTTCCTTGA	1527
			RESULT 3	
ID	AAD41159		standard; cDNA; 1527 BP.	
AC	AAD41159;			
DT	30-OCT-2002	(first entry)		
DE	Human HGPBMY8 cDNA.			
KW	Human; G-protein coupled receptor; GPCR; HGPBMY8; drug screening; neurological disorder; brain; immunological; cell growth; cyostatic; neoplastic disease; CAMP; signalling pathway; immune disorder; cancer; gene therapy; tumour; gene; ss.			
OS	Homo sapiens.			
FH	Key	Location/Qualifiers		
CDS	1..1527			
FT	/tag= a	/product= "Human HGPBMY8 protein"		
FT	/replace(370, G)			
FT	/tag= b			
FT	/standard_name= "single nucleotide polymorphism"			
FT	/replace(1055, G)			
FT	/tag= C	/standard_name= "single nucleotide polymorphism"		
FT	/replace(1192, A)			
FT	/tag= d	/standard_name= "single nucleotide polymorphism"		
FT	/replace(1193, A)			
FT	/tag= e	/standard_name= "single nucleotide polymorphism"		
FT	/replace(1194, G)			
FT	/tag= f	/standard_name= "single nucleotide polymorphism"		
PD	WO200240670-A2.			
PX	23-MAY-2002.			
PF	14-NOV-2001; 2001WO-US043909.			
PX	14-NOV-2000; 2000US-0248285P.			
PR	14-FEB-2001; 2001US-0266581P.			
PR	27-JUL-2001; 2001US-0308285P.			
PR	04-SEP-2001; 2001US-0317166P.			
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.			
PI	Battaglinio P, Feder J, Mantler G, Ramanathan C;			
PI	Weepthal R, Cacace A, Barber L, Hawken D, Kornacker M;			
DR	WPI; 2002-519383/55.			
DR	P-PSDB; AA25236.			
PT	A substantially purified human G-protein coupled receptor polypeptide, termed HGPBMY8, useful for treating a neurological disorder or brain disorder in a mammal.			
PS	Claim 1; Page 160-161; 223pp; English.			
CC	The invention relates to human G-protein coupled receptor (GPCR), termed HGPBMY8 and its corresponding nucleic acid. HGPBMY8 DNA is useful for screening for candidate compounds which are small molecules, biological			
CC				

CC agents, therapeutics or drugs. HGPBMY8 or its homologue is useful for
CC treating a neurological disorder or a disease, a disorder or condition
CC related to the brain in a mammal. It is used for treating or preventing
CC neurological disorders, conditions or diseases and for inducing an
CC immunological response in a mammal. HGPBMY8 DNA, protein and its
CC antibody are useful in the diagnosis, treatment or prevention of
CC disorders associated with aberrant or uncontrolled cellular growth and/
CC or function, such as neoplastic diseases e.g., cancers and tumours and
CC diseases or disorders related to the brain, e.g., neurological disorders.
CC HGPBMY8 DNA and protein are useful for modulating intracellular cAMP
CC associated signalling pathways. An expression vector containing HGPBMY8
CC DNA is useful to treat or prevent neoplastic disorders such as cancer or
CC tumour, immune disorders or neurological disorders. HGPBMY8 DNA is used
CC in gene therapy. The present sequence is human HGPBMY8 cDNA
XX
SQ Sequence 1527 BP, 347 A, 439 C, 419 G, 322 T, 0 U, 0 Other;

Query Match	100.0%	Score 1527/	DB 6/	Length 1527/	
Best Local Similarity	100.0%	Pred. No. 0/			
Matches 1527/	Conservative	0/	Mismatches	0/	Indels
					Gaps
QY	1	ATGAGCTCACCCTGCAACCAAGCAGCAGCGGCGAGAGTAACAGCAGCAGCAGCTGCATGCC	60		
Db	1	ATGAGCTCACCCTGCAACCAAGCAGCAGCGGCGAGAGTAACAGCAGCAGCAGCTGCATGCC	60		
QY	61	CTTCCAAAATGCCCATCAGCCTGGCCCAAGGCAATCATCCGCTCAACCGTGTGTTATC	120		
Db	61	CTTCCAAAATGCCCATCAGCCTGGCCCAAGGCAATCATCCGCTCAACCGTGTGTTATC	120		
QY	121	TTTCCGCGCGGCTCTTTTGTGGGCAAAATAGTGCTGGGCGTAGTGTTCAGAGCGAAAGCG	180		
Db	121	TTTCTCGCGGCTCTTTGTGGGCAAAATAGTGCTGGGCGTAGTGTTCAGAGCGAAAGCG	180		
QY	181	CAGCTGTGAGGTGACCAACCGTTTATCTTTTAACTCTCTGTACCGACCTGTGTGAG	240		
Db	181	CAGCTGTGAGGTGACCAACCGTTTATCTTTTAACTCTCTGTACCGACCTGTGTGAG	240		
QY	241	ATTTCGCTGTGGCCCCCTGGGTGTGGCCACCTTGTGCTCTCTTCTGGGCCCTCAAC	300		
Db	241	ATTTCGCTGTGGCCCCCTGGGTGTGGCCACCTTGTGCTCTCTTCTGGGCCCTCAAC	300		
QY	301	AGCCACTCTGCAAGGCGCCCTGATTAGCTCAACCCACCTGTTGCGCTTGCAGCGCTCAAC	360		
Db	301	AGCCACTCTGCAAGGCGCCCTGATTAGCTCAACCCACCTGTTGCGCTTGCAGCGCTCAAC	360		
QY	361	ACCATTGCTTGTGTCTAGTGGATGCTACTTGTTCATCATCCACTCTCTCTCTCAACCG	420		
Db	361	ACCATTGCTTGTGTCTAGTGGATGCTACTTGTTCATCATCCACTCTCTCTCTCAACCG	420		
QY	421	TCCAAAGTAGCCAGCGCGCGGTTAAGCTGCTCCCTATAGGCAAGCTGGATGTGGCCATC	480		
Db	421	TCCAAAGTAGCCAGCGCGCGGTTAAGCTGCTCCCTATAGGCAAGCTGGATGTGGCCATC	480		
QY	481	CTGCAGAGCACTCTCTCACTTACCGGTGGGGCCAGGCTGCTTGTGATGAGCGCAATGCT	540		
Db	481	CTGCAGAGCACTCTCTCACTTACCGGTGGGGCCAGGCTGCTTGTGATGAGCGCAATGCT	540		
QY	541	CTGTGCTCAATGATTTGGGGGGCCAGGCCCAAGCTACTATTTCTAGGGTGTGTCTTTC	600		
Db	541	CTGTGCTCAATGATTTGGGGGGCCAGGCCCAAGCTACTATTTCTAGGGTGTGTCTTTC	600		
QY	601	ATGTCATTTCACTGATATGTATGATTTGCTGTACTCTCGTGGTGTTCGTGTCAGGCGG	660		
Db	601	ATGTCATTTCACTGATATGTATGATTTGCTGTACTCTCGTGGTGTTCGTGTCAGGCGG	660		
QY	661	AGGAGCATGCTCTGCTGTACATGTCAAGAGACACAGCTTGGAGTGGAGTCAAGAGAC	720		
Db	661	AGGAGCATGCTCTGCTGTACATGTCAAGAGACACAGCTTGGAGTGGAGTCAAGAGAC	720		
QY	721	TGTGTGAGGATGAGAGTAGAAGAGGAGACAGAGAAAGAGAGATTTCCAGATGAGAT	780		
Db	721	TGTGTGAGGATGAGAGTAGAAGAGGAGACAGAGAAAGAGAGATTTCCAGATGAGAT	780		


```
QY 781 GAGTTTCCGCCGCGCATGTAAGGTGAGTCAAGGCCAAGAGGCGCAAGATGGAAGCCAAAG 840
DB 781 GAGTTTCCGCCGCGCATGTAAGGTGAGTCAAGGCCAAGAGGCGCAAGATGGAAGCCAAAG 840
QY 841 GACGGAGGCTGAAGGCGCAAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
DB 841 GACGGAGGCTGAAGGCGCAAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 901 AGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
DB 901 AGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY 961 AAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
DB 961 AAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
QY 1021 GTCAACCATGTCGACGATTGACTTGGGTGAAAGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 GTCAACCATGTCGACGATTGACTTGGGTGAAAGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 AATTTCAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1081 AATTTCAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1141 CGTACAGAGCAAGCAAGCCCTCTGCGCCAGGTGCTACAGTGAAGGCTGCTAAAGTG 1200
DB 1141 CGTACAGAGCAAGCAAGCCCTCTGCGCCAGGTGCTACAGTGAAGGCTGCTAAAGTG 1200
QY 1201 ATCTTATCATCTTTTCTCTATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 1260
DB 1201 ATCTTATCATCTTTTCTCTATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 1260
QY 1261 CTGGCCGTGAGGTGATGTCGAAACCCAGGTACCCAGTGGGTGATGATGATGATGATGATGATG 1320
DB 1261 CTGGCCGTGAGGTGATGTCGAAACCCAGGTACCCAGTGGGTGATGATGATGATGATGATGATG 1320
QY 1321 TGGCTTTTCTCTGTCGATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 1380
DB 1321 TGGCTTTTCTCTGTCGATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 1380
QY 1381 ATTAGAAGGAATCCAGGATGTCGAAAGATTTCTTTCGCAAGAAAAGCCCCGGAAG 1440
DB 1381 ATTAGAAGGAATCCAGGATGTCGAAAGATTTCTTTCGCAAGAAAAGCCCCGGAAG 1440
QY 1441 GAAGATAGGCAACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
DB 1441 GAAGATAGGCAACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
QY 1501 TCTACGATTCGCTACTTTTCTTGA 1527
DB 1501 TCTACGATTCGCTACTTTTCTTGA 1527

RESULT 4
AEA33069
ID AEA33069 standard; DNA; 1527 BP.
XX
AC AEA33069;
XX
DT 11-AUG-2005 (first entry)
XX
DB Human G-protein coupled receptor HGRPMY8 gene Seg1.
XX
KM protein purification; cytosolic; neuroprotective; antiparkinsonian;
KM tranquilizer; hypotension; anti-HIV; virucide; osteopathic cancer;
KM asthma; allergy; HIV infection; osteoporosis; Parkinson's disease;
KM anxiety disorder; hypertension; neurological disease; gene; ds; HGRPMY8;
KM G protein coupled receptor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1527
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FT /*tag= a
FT /product= "Human G-protein coupled receptor HGRPMY8
FT protein"
XX
PN MO2005048951-A2.
XX
PD 02-JUN-2005.
XX
PF 12-NOV-2004; 2004MO-US038387.
XX
PR 13-NOV-2003; 2003US-00712615.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI Battaglini P, Feder JN, Mintier G, Nelson TC, Ramathanan CS;
PI Westphal R, Cacace AM, Barber LE, Hawken DR, Kornacker MG;
XX WPI; 2005-395945/40.
XX DR P-PSDB; AEA33070.
XX
PT New isolated human G-protein coupled receptor, HGRPMY8, and encoding
PT polynucleotide, useful for diagnosing or treating cancer, asthma,
PT allergies, HIV, osteoporosis, anxiety, hypertension and neurological
PT diseases.
XX
PS Claim 1; SEQ ID NO 1; 261bp; English.
XX
CC This invention relates to a novel isolated human G-protein and the DNA
CC sequence which encodes it. The invention may be useful for the
CC development of compounds with a cytosolic, neuroprotective,
CC antiparkinsonian, tranquilizer, hypotension, anti-HIV, virucide or
CC osteopathic activity acting as G-protein antagonists. The methods and
CC compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of the human G-protein coupled receptor,
CC HGRPMY8, such as cancer, asthma, allergies, HIV infections,
CC osteoporosis, Parkinson's disease, anxiety, hypertension and neurological
CC diseases. The present sequence is that of the human HGRPMY8 gene of the
CC invention.
XX
SQ Sequence 1527 BP; 347 A; 439 C; 419 G; 322 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 1527; DB 14; Length 1527;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCTCCAGCTGCAACCAAGCAGCAGCGGAGAGTACAGAGCCACAGTGCATGCC 60
DB 1 ATGAGCTCCAGCTGCAACCAAGCAGCAGCGGAGAGTACAGAGCCACAGTGCATGCC 60
QY 61 CTCTCCAAATGCCATCACTGAGGCTGCGCCAGGAGATATCGCTCAACCGTGTGATTATC 120
DB 61 CTCTCCAAATGCCATCACTGAGGCTGCGCCAGGAGATATCGCTCAACCGTGTGATTATC 120
QY 121 TTCCTGCGCGCTCTTTCGTCGCAACATAGTGTGCGCTAGTGTGAGCGCAAGCGG 180
DB 121 TTCCTGCGCGCTCTTTCGTCGCAACATAGTGTGCGCTAGTGTGAGCGCAAGCGG 180
QY 181 CAGCTGCTGAGAGTGAACCAACCGTTTATCTTAACTCTCTGTCACGACCTGTGAG 240
DB 181 CAGCTGCTGAGAGTGAACCAACCGTTTATCTTAACTCTCTGTCACGACCTGTGAG 240
QY 241 ATTTCGCTGAGGCGGCTGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB 241 ATTTCGCTGAGGCGGCTGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
QY 301 AGCAGCTTTCGACGCGGCTGAGTGAAGTCAACCACTGTTGCGCTTCCGACAGGTCAAC 360
DB 301 AGCAGCTTTCGACGCGGCTGAGTGAAGTCAACCACTGTTGCGCTTCCGACAGGTCAAC 360
QY 361 ACCATTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 ACCATTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
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QY 421 TCCAAGATGACCCAGCGCGCGGTTACCTGCTCCTCTATGAGCAGCTGATGTGSCATC 480
DB 421 TCCAAGATGACCCAGCGCGCGGTTACCTGCTCCTCTATGAGCAGCTGATGTGSCATC 480
QY 481 CTGCGAGACACTCTCCCACTCTAAGCGCTGGGGCCAGGCGCTTTGATGAGCGCAATGCT 540
DB 481 CTGCGAGACACTCTCCCACTCTAAGCGCTGGGGCCAGGCGCTTTGATGAGCGCAATGCT 540
QY 541 CTCTGCTCCATGATCTGGGGGGCCAGCCCACTACATAATCTCAGCGTGTCTCTTC 600
DB 541 CTCTGCTCCATGATCTGGGGGGCCAGCCCACTACATAATCTCAGCGTGTCTCTTC 600
QY 601 ATCTGCTATTCAGTATGTCTCATGATTTGCTGCTACTCCGCTGCTTCTGTGACAGCCCG 660
DB 601 ATCTGCTATTCAGTATGTCTCATGATTTGCTGCTACTCCGCTGCTTCTGTGACAGCCCG 660
QY 661 AGGCGACATGCTCTCTCTGTCACAAATGTCAAGAGACACAGCTTGGAAAGTGCAGTCAAGAC 720
DB 661 AGGCGACATGCTCTCTCTGTCACAAATGTCAAGAGACACAGCTTGGAAAGTGCAGTCAAGAC 720
QY 721 TGTGTGAGAAATGAGATGATGAAGGAGAGAGAGAAAGAGAGAGTTCAGAGATGAGAGT 780
DB 721 TGTGTGAGAAATGAGATGATGAAGGAGAGAGAGAGAAAGAGAGAGTTCAGAGATGAGAGT 780
QY 781 GAGTTTCGCGCGCAGCATGAGTGAAGTGAAGTCAAGGCCAAGAGAGGCGCAATGGAAGCCAG 840
DB 781 GAGTTTCGCGCGCAGCATGAGTGAAGTGAAGTCAAGGCCAAGAGAGGCGCAATGGAAGCCAG 840
QY 841 GACGCGCAGCTTGAAGGCGCAAGAGAGACACGCGGACCAAGTGAAGTGTGAAGGCGC 900
DB 841 GACGCGCAGCTTGAAGGCGCAAGAGAGACACGCGGACCAAGTGAAGTGTGAAGGCGC 900
QY 901 AGGGGAGAGAGAGAGTCAAGAGAGACAGTGGTGGCCAGGCGCAGTGAAGGAGT 960
DB 901 AGGGGAGAGAGAGAGTCAAGAGAGACAGTGGTGGCCAGGCGCAGTGAAGGAGT 960
QY 961 AAGGAAGGAGAGACCAAAAGTTGAGAGAA CAGCATGAGAGAGACAAAGGCTGCAGAG 1020
DB 961 AAGGAAGGAGAGACCAAAAGTTGAGAGAA CAGCATGAGAGAGACAAAGGCTGCAGAG 1020
QY 1021 GTCAACCAATGAGCATTTGACTTGGTGAAGATGATGATGATGATGATGATGATGATGATG 1080
DB 1021 GTCAACCAATGAGCATTTGACTTGGTGAAGATGATGATGATGATGATGATGATGATGATG 1080
QY 1081 AATTTCAAGTGAAGATGAGTCAAGAGAGTGAACATCCCGAGAGCCTCCACCACTGCTCT 1140
DB 1081 AATTTCAAGTGAAGATGAGTCAAGAGAGTGAACATCCCGAGAGCCTCCACCACTGCTCT 1140
QY 1141 CGTAAACAGACAGCAACCCCTCTCTGCGCAGGTGCTAC CAGTGCAGAACTGCTAAAGT 1200
DB 1141 CGTAAACAGACAGCAACCCCTCTCTGCGCAGGTGCTAC CAGTGCAGAACTGCTAAAGT 1200
QY 1201 ATCTTCATCATCTATTTTCTCTATGTCATCTCTGAGGCGCTCACTGCTTTTGAAGATC 1260
DB 1201 ATCTTCATCATCTATTTTCTCTATGTCATCTCTGAGGCGCTCACTGCTTTTGAAGATC 1260
QY 1261 CTGGCCGCTGAGGTGATGTCGAAACCCAGGTACCCCAAGTGGTATCA CATAATCATC 1320
DB 1261 CTGGCCGCTGAGGTGATGTCGAAACCCAGGTACCCCAAGTGGTATCA CATAATCATC 1320
QY 1321 TGGCTTTTCTCTGAGTGTGATCAACCCCTATGTCTATGCTATGCTATGCA CAGAAC 1380
DB 1321 TGGCTTTTCTCTGAGTGTGATCAACCCCTATGTCTATGCTATGCTATGCA CAGAAC 1380
QY 1381 ATTAAAGAGAAATCCAGGACATGCTGAAGAAAGTTTCTTCTGCAAGAAAAAGCCCCGAAA 1440
DB 1381 ATTAAAGAGAAATCCAGGACATGCTGAAGAAAGTTTCTTCTGCAAGAAAAAGCCCCGAAA 1440
QY 1441 GAAGATAGGCAACCCAGACCTGCGCCGGAACAGAGGGTGGAGCTGAAGGCAAGATTGCTCT 1500
DB 1441 GAAGATAGGCAACCCAGACCTGCGCCGGAACAGAGGGTGGAGCTGAAGGCAAGATTGCTCT 1500
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QY 1501 TCCTACGATCTGCTACTTTCTTTGA 1527
DB 1501 TCCTACGATCTGCTACTTTCTTTGA 1527

RESULT 5
ADD41170
ID ADD41170 standard; DNA; 1580 BP.
XX
XX AAD41170;
XX 30-OCT-2002 (first entry)
XX
DE Human HGPBMY8 DNA #1.
XX
XX Human; G-protein coupled receptor; GPCR; HGPBMY8; drug screening;
XX neurological disorder; brain; immunological; cell growth; cytostatic;
XX neoplastic disease; cAMP; signalling pathway; immune disorder; cancer;
XX gene therapy; tumour; gene; de.
XX
XX Homo sapiens.
XX
XX WO20240670-A2.
XX
XX 23-MAY-2002.
XX
XX 14-NOV-2001; 2001WO-US043909.
XX
XX 14-NOV-2000; 2000US-0248285P.
XX 14-FEB-2001; 2001US-026581P.
XX 27-JUL-2001; 2001US-0308285P.
XX 04-SEP-2001; 2001US-0317166P.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Batagljino P, Feder J, Mintler G, Nelson T, Ramanathan C,
XX Westphal R, Cacace A, Barber L, Hawken D, Kornacker M,
XX WPI; 2002-519383/55.
XX
XX A substantially purified human G-protein coupled receptor polypeptide,
XX termed HGPBMY8, useful for treating a neurological disorder or brain
XX disorder in a mammal.
XX
XX Disclosure; Page 207; 223p; English.
XX
XX The invention relates to human G-protein coupled receptor (GPCR), termed
XX HGPBMY8 and its corresponding nucleic acid. HGPBMY8 DNA is useful for
XX screening for candidate compounds which are small molecules, biological
XX agents, therapeutic or drugs. HGPBMY8 or its homologue is useful for
XX treating a neurological disorder or a disease, a disorder or condition
XX related to the brain in a mammal. It is used for treating or preventing
XX neurological disorders, conditions or diseases and for inducing an
XX immunological response in a mammal. HGPBMY8 DNA, protein and its
XX antibody are useful in the diagnosis, treatment or prevention of
XX disorders associated with aberrant or uncontrolled cellular growth and/
XX or function, such as neoplastic diseases e.g., cancers and tumours and
XX diseases or disorders related to the brain, e.g., neurological disorders.
XX HGPBMY8 DNA and protein are useful for modulating intracellular cAMP
XX associated signalling pathways. An expression vector containing HGPBMY8
XX DNA is useful to treat or prevent neoplastic disorders such as cancer or
XX tumours, immune disorders or neurological disorders. HGPBMY8 DNA is used
XX in gene therapy. The present sequence is human HGPBMY8 DNA
XX
XX Sequence 1580 BP; 357 A; 456 C; 430 G; 337 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 1527; DB 6; Length 1580;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCTCACTGACCAACGACGCGCGGAGTAAACAGAGCCACAGCTGATGCCCC 60
DB 32 ATGAGCTCACTGACCAACGACGCGCGGAGTAAACAGAGCCACAGCTGATGCCCC 91
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QY 61 CTCCTCAAAATGECATCAAGCTGCGCCAGGCGATCATCCGCTCAACCGTGTGTTATC 120
Db 92 CTCCTCAAAATGECATCAAGCTGCGCCAGGCGATCATCCGCTCAACCGTGTGTTATC 151
QY 121 TTCCTGCGCGCCCTTTTCGTGCGCAACATATGCTGGCGCTATGTTGACGCCAAGCCG 180
Db 152 TTCCTGCGCGCCCTTTTCGTGCGCAACATATGCTGGCGCTATGTTGACGCCAAGCCG 211
QY 181 CAGCTCTGAGGTGACCAACCGTTTATCTTAACTCTGTCACCGACCTGTGCGAG 240
Db 212 CAGCTCTGAGGTGACCAACCGTTTATCTTAACTCTGTCACCGACCTGTGCGAG 271
QY 241 ATTTCGCTGTGCGCCCTGTGGTGTGCGCCACCTGTGCTCTCTTGTGCGCCCTCAAC 300
Db 272 ATTTCGCTGTGCGCCCTGTGGTGTGCGCCACCTGTGCTCTCTTGTGCGCCCTCAAC 331
QY 301 AGCAGCTTGTGACAGCGCCCTGTGGTGTGAGCTTACCCACTGTGCGCTTGTGCGAGCTAAC 360
Db 332 AGCAGCTTGTGACAGCGCCCTGTGGTGTGAGCTTACCCACTGTGCGCTTGTGCGAGCTAAC 391
QY 361 ACCATTGTCTGTGTTGTCAGTGTGTCGTAATTGTGCTATGTCACCCCTCTCTCAACCG 420
Db 392 ACCATTGTCTGTGTTGTCAGTGTGTCGTAATTGTGCTATGTCACCCCTCTCTCAACCG 451
QY 421 TCCAGATGACCCAGCGCGCGGTTACCTGCTCTCTATGSCACTGGAATTGTGCGCATC 480
Db 452 TCCAGATGACCCAGCGCGCGGTTACCTGCTCTCTATGSCACTGGAATTGTGCGCATC 511
QY 481 CTGACAGAGACTCTTCCACTCTACCGGCTGTGGGCGCAGGCTGCTTTGATGAGCGCAATGCT 540
Db 512 CTGACAGAGACTCTTCCACTCTACCGGCTGTGGGCGCAGGCTGCTTTGATGAGCGCAATGCT 571
QY 541 CTCTGTCCATGATCTGTGGGGGGGCGACCCCAAGTAACATATTTCAAGCGTGTGCTCTTC 600
Db 572 CTCTGTCCATGATCTGTGGGGGGGCGACCCCAAGTAACATATTTCAAGCGTGTGCTCTTC 631
QY 601 ATCGTATTCACTGATGTTGTCATGATTTGCTGCTACCTCGTGTGTTCTGTGACGCCG 660
Db 632 ATCGTATTCACTGATGTTGTCATGATTTGCTGCTACCTCGTGTGTTCTGTGACGCCG 691
QY 661 AGGACGACATGCTCTGCTGTACATATGTCAGAGACACACAGCTTGGAAAGTGCAGTCAAGAC 720
Db 692 AGGACGACATGCTCTGCTGTACATATGTCAGAGACACACAGCTTGGAAAGTGCAGTCAAGAC 751
QY 721 TGTGTGAGATGAGATGAGAGGAGGACGAGAAAGAGAGAGTTCAGAGATGAGAGT 780
Db 752 TGTGTGAGATGAGATGAGAGGAGGAGGACGAGAAAGAGAGAGTTCAGAGATGAGAGT 811
QY 781 GAGTTTCGCGCGCCAGCATGAGGTGAGTCAAGGCCAAGAGGCGCAAGATGAAAGCCAAAG 840
Db 812 GAGTTTCGCGCGCCAGCATGAGGTGAGTCAAGGCCAAGAGGCGCAAGATGAAAGCCAAAG 871
QY 841 GACGCGAGCCTGAAGGCCCAAGGAAGAGACCGGGGACAGTGAAGTATGTGAAGGCC 900
Db 872 GACGCGAGCCTGAAGGCCCAAGGAAGAGACCGGGGACAGTGAAGTATGTGAAGGCC 931
QY 901 AGGGGACAGGAGAGGTGAGAGAGAGACGCTGTGCGCCAGCGACATGAGAGGCT 960
Db 932 AGGGGACAGGAGAGGTGAGAGAGAGACGCTGTGCGCCAGCGACATGAGAGGCT 991
QY 961 AAGGAAGGACGACCAAGTTGAGAGAGACAGCATGAGGACAGCAAGGGTGCACAGAG 1020
Db 992 AAGGAAGGACGACCAAGTTGAGAGAGAGACAGCATGAGGACAGCAAGGGTGCACAGAG 1051
QY 1021 GTCAACCAAGTGCAGATTTGACTTGTGGTGAAGATGACATGAGAGTTTGTGAAGAGCATC 1080
Db 1052 GTCAACCAAGTGCAGATTTGACTTGTGGTGAAGATGACATGAGAGTTTGTGAAGAGCATC 1111
QY 1081 AATTTAGTGAAGATGACGTCGAGGAGAGTAAATATCCCGAGAGCTTCCACCCAGTCTGT 1140
Db 1112 AATTTAGTGAAGATGACGTCGAGGAGAGTAAATATCCCGAGAGCTTCCACCCAGTCTGT 1171
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QY 1141 CGTAACAGACAGCAACCTCTCTGCGCCAGGTGCTACCAAGTGTCTAAAGT 1200
Db 1172 CGTAACAGACAGCAACCTCTCTGCGCCAGGTGCTACCAAGTGTCTAAAGT 1231
QY 1201 ATCTTATCATATTTTCTCTATGTCATATCCCTGAGGCGCTACTGCTTTTAAAGATC 1260
Db 1232 ATCTTATCATATTTTCTCTATGTCATATCCCTGAGGCGCTACTGCTTTTAAAGATC 1291
QY 1261 CTGGCCGTGTGGGTGATGTCGAAACCCAGGTACCCAGTGGGTATCAACATATCATC 1320
Db 1292 CTGGCCGTGTGGGTGATGTCGAAACCCAGGTACCCAGTGGGTATCAACATATCATC 1351
QY 1321 TGGCTTTTCTCTGTCAGTGTGTCATCAACCCCTATGTCTATGTGCTACATGCAAGACC 1380
Db 1352 TGGCTTTTCTCTGTCAGTGTGTCATCAACCCCTATGTCTATGTGCTACATGCAAGACC 1411
QY 1381 ATTAAAGAAAGAAATCCAGACATGCTGAAGAAAGTTTCTGCAAGAAAGAGCCCGGAA 1440
Db 1412 ATTAAAGAAAGAAATCCAGACATGCTGAAGAAAGTTTCTGCAAGAAAGAGCCCGGAA 1471
QY 1441 GAAAGATGACACCCAGACCTGCGCGGAGACAGAGGGGTGAAGGCAAGATTGTCCT 1500
Db 1472 GAAAGATGACACCCAGACCTGCGCGGAGACAGAGGGGTGAAGGCAAGATTGTCCT 1531
QY 1501 TCCTACGATTCGTCTACTTTTCTTGA 1527
Db 1532 TCCTACGATTCGTCTACTTTTCTTGA 1558
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RESULT 6
AEA33115
ID AEA33115 standard; DNA; 1580 BP.
XX
XX AEA33115;
XX
XX 11-AUG-2005 (first entry)
XX
XX Human GPCR HGRPMY8 gene region SegId47.
XX
XX protein purification; cytosolic; neuroprotective; antiparkinsonian;
XX tranquillizer; hypotension; anti-HIV; virucide; osteopathic; cancer;
XX asthma; allergy; HIV infection; osteoporosis; Parkinsons disease;
XX anxiety disorder; hypertension; neurological disease; gene; de; HGRPMY8;
XX G protein coupled receptor.
XX
XX Homo sapiens.
XX
XX WO2005048951-A2.
XX
XX 02-JUN-2005.
XX
XX 12-NOV-2004; 2004WO-US038387.
XX
XX 13-NOV-2003; 2003US-00712615.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Battaglini P, Feder JN, Mintier G, Nelson TC, Ramanathan CS;
XX Westphal R, Cacace AM, Barber LE, Hawken DR, Kornacker MG;
XX WPI; 2005-395945/40.
XX
XX New isolated human G-protein coupled receptor, HGRPMY8, and encoding
XX polynucleotide, useful for diagnosing or treating cancer, asthma,
XX allergies, HIV, osteoporosis, anxiety, hypertension and neurological
XX diseases.
XX
XX disclosure; SEQ ID NO 47; 261bp; English.
XX
XX This invention relates to a novel isolated human G-protein and the DNA
XX sequence which encodes it. The invention may be useful for the
XX development of compounds with a cytosolic, neuroprotective,
XX antiparkinsonian, tranquillizer, hypotension, anti-HIV, virucide or
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CC osteopathic activity acting as G-protein antagonists. The methods and
 CC compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of diseases or conditions associated with
 CC aberrant expression or activity of the human G-protein coupled receptor,
 CC HGPBMW8, such as cancer, asthma, allergies, HIV infections,
 CC osteoporosis, Parkinson's disease, anxiety, hypertension and neurological
 CC diseases. The present sequence is that of a region of the human HGPBMW8
 CC gene of the invention.
 CC XX

Sequence 1580 BP; 357 A; 456 C; 430 G; 337 T; 0 U; 0 Other;

Query Match 100.0%; Score 1527; DB 14; Length 1580;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGTCACCTGACCAACAGCAGCGGAGAGTAAACAGAGCCACAGTCATGCC 60
 DB 32 ATGAGTCACCTGACCAACAGCAGCGGAGAGTAAACAGAGCCACAGTCATGCC 91
 QY 61 CTCTCAAAATGCCATCAGCCTGGCCAGCGCATCATCCGCTCAACCGCTGTATC 120
 DB 92 CTCTCAAAATGCCATCAGCCTGGCCAGCGCATCATCCGCTCAACCGCTGTATC 151
 QY 121 TTCCTGCGCGCTTTTGTGTGGCAACATAGTGGCGCTAGTGTGGAGGCAAGCCG 180
 DB 152 TTCCTGCGCGCTTTTGTGTGGCAACATAGTGGCGCTAGTGTGGAGGCAAGCCG 211
 QY 181 CAGCTGTCAGAGTGAACCAACCGTTTAACTTTAACTCTGTCACCGACCTGTGAG 240
 DB 212 CAGCTGTCAGAGTGAACCAACCGTTTAACTTTAACTCTGTCACCGACCTGTGAG 271
 QY 241 ATTTGGCTGTGGCCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300
 DB 272 ATTTGGCTGTGGCCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 331
 QY 301 ACCCACTTGTGACGGCCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
 DB 332 ACCCACTTGTGACGGCCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 391
 QY 361 ACCATTTGTTGGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 392 ACCATTTGTTGGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 451
 QY 421 TCCAAAGTGAACCGAGCGCGGTTAAGTCTCTCTATGGAAGTGTGGCATC 480
 DB 452 TCCAAAGTGAACCGAGCGCGGTTAAGTCTCTCTATGGAAGTGTGGCATC 511
 QY 481 CTGCAAGACATCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 540
 DB 512 CTGCAAGACATCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 571
 QY 541 CTCTGTCATGATCTGGGGGCGAGCCAGCTACATATTCTAGCGTGTCTTC 600
 DB 572 CTCTGTCATGATCTGGGGGCGAGCCAGCTACATATTCTAGCGTGTCTTC 631
 QY 601 ATGTCATTCACCTGATTTGATGATGATGATGATGATGATGATGATGATGAT 660
 DB 632 ATGTCATTCACCTGATTTGATGATGATGATGATGATGATGATGATGATGAT 691
 QY 661 AAGGAGCATGCTGTGTGAACAATGCAAGAGACAGAGTGAAGTGAAGTGAAG 720
 DB 692 AAGGAGCATGCTGTGTGAACAATGCAAGAGACAGAGTGAAGTGAAGTGAAG 751
 QY 721 TGTGTGAATAGAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 DB 752 TGTGTGAATAGAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 811
 QY 781 GAGTTTCCGCGCCAGCATGAAGGTGATGAGGCAAGAGGCAAGTGAAGCCAG 840
 DB 812 GAGTTTCCGCGCCAGCATGAAGGTGATGAGGCAAGAGGCAAGTGAAGCCAG 871
 QY 841 GACGCGAGCTGAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCC 900

DB 872 GACGCGAGCTGMAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCC 931
 QY 901 AAGGCGACGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGT 960
 DB 922 AAGGCGACGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGT 991
 QY 961 AAGGAGCGACGACCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 DB 992 AAGGAGCGACGACCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1051
 QY 1021 GTCAACGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080
 DB 1052 GTCAACGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1111
 QY 1081 AATTTCACTGAGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1140
 DB 1112 AATTTCACTGAGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1171
 QY 1141 CGTAAACAGCAACAGACCTCTCTGCGCAGAGTCTACAGTGAAGTGTCTTAAATG 1200
 DB 1172 CGTAAACAGCAACAGACCTCTCTGCGCAGAGTCTACAGTGAAGTGTCTTAAATG 1231
 QY 1201 ATCTTCATCATATTTTCTCCATAGTGTATCCCTGGGCGCTACTGCTTTTATGACATC 1260
 DB 1232 ATCTTCATCATATTTTCTCCATAGTGTATCCCTGGGCGCTACTGCTTTTATGACATC 1291
 QY 1261 CTGGCGGTGTGGTGAATGTGAAACCGAGTATCCCAAGTGGTATCATCAATATATC 1320
 DB 1292 CTGGCGGTGTGGTGAATGTGAAACCGAGTATCCCAAGTGGTATCATCAATATATC 1351
 QY 1321 TGGCTTTTCTTCCGCAATGTCATCCACCCCTATGTCTATGGTATATCAACAGACC 1380
 DB 1352 TGGCTTTTCTTCCGCAATGTCATCCACCCCTATGTCTATGGTATATCAACAGACC 1411
 QY 1381 ATTAAGAAGAAATCCAGATGCTGAAGAGTCTCTGCAAGAAAGCCCGGAAA 1440
 DB 1412 ATTAAGAAGAAATCCAGATGCTGAAGAGTCTCTGCAAGAAAGCCCGGAAA 1471
 QY 1441 GAAGATAGCCACCCAGACCTGCGCGGAAACAGAGGTGGAGCTGAAGGAGATTGCTCT 1500
 DB 1472 GAAGATAGCCACCCAGACCTGCGCGGAAACAGAGGTGGAGCTGAAGGAGATTGCTCT 1531
 QY 1501 TCCTAAGATTCGCTACTTTTCTTTGA 1527
 DB 1532 TCCTAAGATTCGCTACTTTTCTTTGA 1558

RESULT 7
 ACF03567
 ID ACF03567 standard; cDNA, 1584 BP.
 XX
 AC ACF03567;
 XX
 DT 15-SEP-2003 (first entry)
 XX
 DE Human NOV14a protein encoding cDNA SEQ ID NO:41.
 XX
 XX Human; NOV1; cytosolic; cardiac; antiinflammatory; immunosuppressive;
 KW antiallergic; haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic;
 KW anorectic; antiaesthetic; nephrotropic; antifibrilic; hepatotropic;
 KW neuroprotective; nootropic; antibacterial; vinicide; antiparasitic;
 KW relaxant; anticonvulsant; hypotensive; vasotropic; antiparkinsonian;
 KW vulnery; angiogenic; antiangiogenic; gene therapy; vaccine; cancer;
 KW cardiomyopathy; atherosclerosis; hypertension; diabetes; inflammation;
 KW autoimmune disorder; allergy; blood disorder; AIDS; obesity; asthma;
 KW acquired immunodeficiency syndrome; nephropathy; cirrhosis; arthritis;
 KW Alzheimer's disease; Parkinson's disease; gout; infection; stroke;
 KW muscular dystrophy; epilepsy; wasting disorder; chromosome X; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200294870-A2.
 XX

PD 28-NOV-2002.
XX
PF 02-NOV-2001; 2001WO-US051580.
XX
PR 02-NOV-2000; 2000US-0245291P.
PR 02-NOV-2000; 2000US-0245317P.
PR 07-NOV-2000; 2000US-0246562P.
PR 08-NOV-2000; 2000US-0246871P.
PR 26-JAN-2001; 2001US-0264389P.
PR 26-JAN-2001; 2001US-0264423P.
PR 29-JAN-2001; 2001US-0264799P.
XX
PA (CURA-) CUBAGEN CORP.
XX
PI Groese WM, MacDougall JR, Smithson G, Millet I, Stone DJ,
PI Gunther E, Ellerman K, Alsebrook JP, Lepley DM, Bugues CE,
PI Spytek KA, Edinger SR, Gangoli EA, Gorman L, Taupier RJ, Li L,
PI Guo X, Fernandes ER, Varney CM, Tchernev VT, Casman SO, Shenoy S,
PI Mishra V, Furtak K, Baumgartner JC, Colman SD,
XX
DR MPI; 2003-140359/13.
DR P-PSDB; ABR57432.
XX
PT New NOVX polypeptide useful for preventing or treating NOVX-associated
PT disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and
PT in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Claim 8; Page 129; 346pp; English.
XX
CC ACF03547 to ACF03570 encode the human NOVX proteins (I) given in ABR57412
CC to ABR57435. (I) have cytostatic, cardiant, antiinflammatory, nootropic,
CC immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiabetic,
CC antiatherosclerotic, anorectic, antiasthmatic, nephroprotective, virucide,
CC antiautistic, hepatotropic, neuroprotective, antibacterial, relaxant,
CC antiparasitic, anticonvulsant, hypotensive, vasotropic, antiparkinsonian,
CC vulnerary, angiogenic, and angiogenic activities, and can be used in
CC gene therapy and vaccines. The NOVX polypeptides and their antibodies can
CC be used to determine the presence or absence of (I) in a sample. The NOVX
CC polypeptides, polynucleotides encoding them, and antibodies against them,
CC are useful in manufacturing a medicament for treating or preventing a
CC syndrome associated with a NOVX-associated disorder such as hypertension,
CC cardiomyopathy, atherosclerosis, cancer, diabetes, asthma, inflammation,
CC autoimmune disorders, allergies, blood disorders, obesity, acquired
CC immunodeficiency syndrome (AIDS), immunoglobulin (Ig) A nephropathy,
CC cirrhosis, arthritis, Alzheimer's disease, Parkinson's disease, goitre,
CC infections (e.g. bacterial, viral, parasitic), stroke, muscular
CC dystrophy, epilepsy, and other wasting disorders associated with chronic
CC diseases. ACF03571 to ACF03644 represent PCR primers and probes for NOVX
CC sequence, which are used in an example from the present invention
XX
SQ Sequence 1584 BP; 359 A; 457 C; 430 G; 338 T; 0 U; 0 Other:
Query Match 100.0%; Score 1527; DB 8; Length 1584;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCTGCACCTGACCAACAGACGCGGAGAGTAACAGACCAACAGTCATGCC 60
DB 31 ATGAGCTGCACCTGACCAACAGACGCGGAGAGTAACAGACCAACAGTCATGCC 90
QY 61 CTCTCCAAATGCGCATCAGCCTGGCCACGCGCATCATCGCTCAACCGTGTGTTATC 120
DB 91 CTCTCCAAATGCGCATCAGCCTGGCCACGCGCATCATCGCTCAACCGTGTGTTATC 150
QY 121 TTCTCTGGCGGCTTTTGTGCGCAATAGTGTCTGCGCTATGTTTGAGCGCAAGCCG 180
DB 151 TTCTCTGGCGGCTTTTGTGCGCAATAGTGTCTGCGCTATGTTTGAGCGCAAGCCG 210
QY 181 CAGCTGCTGAGGTCACCAACCGTTTATCTTTAACTCTGTCACCGACCTGTGCGAG 240
DB 211 CAGCTGCTGAGGTCACCAACCGTTTATCTTTAACTCTGTCACCGACCTGTGCGAG 270
QY 241 ATTTCGCTGTGGCCCCCTGGGTGTGGCCACCTCTGTGCTCTCTTGTGGCCCCCTAAC 300

DB 271 ATTTCGCTGTGGCCCCCTGGGTGTGGCCACCTCTGTGCTCTCTTGTGGCCCCCTAAC 330
QY 301 AGCATTCTGACAGGCGCCGTGTTAGCTACACCACTGTCGCTTCGCGACGTCACAC 360
DB 331 AGCATTCTGACAGGCGCCGTGTTAGCTACACCACTGTCGCTTCGCGACGTCACAC 390
QY 361 ACCATTGTCTTGAGTGTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 391 ACCATTGTCTTGAGTGTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 450
QY 421 TCCAAATGACCCAGGCGCGGTTTCTGCTCTCTTATGAGCACTGATTTGTGGCATC 480
DB 451 TCCAAATGACCCAGGCGCGGTTTCTGCTCTCTTATGAGCACTGATTTGTGGCATC 510
QY 481 CTGCAAGACCTCTCACTGATACGCGTCGCGGCGAGCGTCGCTTATGAGGCAATGCT 540
DB 511 CTGCAAGACCTCTCACTGATACGCGTCGCGGCGAGCGTCGCTTATGAGGCAATGCT 570
QY 541 CTCTGCTCATGATCTGGGCGGCGCAGCCCGACGCTACATATTCTCAGCGTGTCTTC 600
DB 571 CTCTGCTCATGATCTGGGCGGCGCAGCCCGACGCTACATATTCTCAGCGTGTCTTC 630
QY 601 ATCGTATTCCACTGATTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 631 ATCGTATTCCACTGATTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 690
QY 661 AGGAGCATGCTCTGCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 691 AGGAGCATGCTCTGCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 750
QY 721 TGTGTGGAATGAGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 780
DB 751 TGTGTGGAATGAGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 810
QY 781 GAGTTTCCGCGCAGCATGAAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 811 GAGTTTCCGCGCAGCATGAAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 870
QY 841 GACGAGGCTGAAGGCGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
DB 871 GACGAGGCTGAAGGCGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 930
QY 901 AGGAGGAGGAGGAGGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 960
DB 931 AGGAGGAGGAGGAGGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 990
QY 961 AAGGAAGGAGGAGGAGGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1020
DB 991 AAGGAAGGAGGAGGAGGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1050
QY 1021 GTCAACCATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1051 GTCAACCATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1110
QY 1081 AATTTCAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1111 AATTTCAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1170
QY 1141 CGTAACAGCAACGACCCCTCTGCGCCAGGTGTACCAAGTGAAGCTGTGTAAGTGT 1200
DB 1171 CGTAACAGCAACGACCCCTCTGCGCCAGGTGTACCAAGTGAAGCTGTGTAAGTGT 1230
QY 1201 ATCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1231 ATCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1290
QY 1261 CTGGCGGTGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1291 CTGGCGGTGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1350
QY 1321 TGGCTTTTCTTCTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380

Db 1351 TGCGTTTCTTCTCAGTGCATCCACCCCTTATGCTATGCTACATGCACAAGACC 1410
Qy 1351 ATTAAGAGGAATTCAGAGACATGCTGAAGAATTCTTCTGCAGAGAAAAGCCCGAAA 1440
Db 1411 ATTAAGAGGAATTCAGAGACATGCTGAAGAATTCTTCTGCAGAGAAAAGCCCGAAA 1470
Qy 1441 GAAAGTACGACCCAGACCTGCGGAAACAGAGGGTGGAGCTGAAGGCAAGTTGTCCCT 1500
Db 1471 GAAAGTACGACCCAGACCTGCGGAAACAGAGGGTGGAGCTGAAGGCAAGTTGTCCCT 1530
Qy 1501 TCCCTAGATTGCTACTTTCTTCTTGA 1527
Db 1531 TCCCTAGATTGCTACTTTCTTCTTGA 1557

RESULT 8
ACCS8886
ID ACCS8886 standard; cDNA; 4718 BP.
ACCS8886;
ACCS8886;
22-SEP-2003 (first entry)
XX Human G-protein coupled receptor OM_10 cDNA.
DE
XX G-protein coupled receptor; OM_10; human; receptor; cardiac;
KW hypertensive; hypotensive; antidiagonal; cytosolic; antiparietal;
KW analgesic; gynaecological; antidepressant; antidiabetic; osteoporotic;
KW neurologic; tranquilizer; nephrotoxic; antitumor; antiallergic;
KW neurologic; anticonvulsant; neuroprotective; antiparkinsonian;
KW gene therapy; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 332..1858
FT CDS /tag= a
FT /product= "OM_10"
XX
XX MO200304162-A2.
XX
XX 30-MAY-2003.
XX
XX 12-NOV-2002; 2002MO-US036204.
XX
XX 16-NOV-2001; 2001US-0332110P.
XX
XX (AMHP) WYETH.
XX
XX Blatcher M, Paulsen JE, Bates BG;
XX
XX WPI; 2003-449811/42.
XX
XX P-PsDB; ABR42865.
XX
XX
XX New polynucleotides encoding G-protein coupled receptor, i.e. OM-10 and
XX UP-11 polypeptides, useful for diagnosing, preventing and treating, e.g.
XX Parkinson's disease, acute heart failure, hypertension, cancer or
XX osteoporosis.
XX
XX Claim 49; Page 174-178; 190pp; English.
XX
XX The present sequence is that of cDNA encoding a novel human G-protein
XX coupled receptor (GPCR) termed OM_10. This orphan GPCR was identified
XX from a genome database search using the human 5-HT6 receptor sequence.
XX Identified regions of genomic DNA were used to predict full-length genes,
XX and these gene predictions were used to isolate the present sequence from
XX a cDNA library. OM_10 is predominantly expressed in the putamen and
XX caudate nucleus. OM_10 and UP_11 polypeptides, polynucleotides, agonists
XX and antagonists of the invention are useful in drug screening assays,
XX pharmacogenomics, monitoring of effects during clinical trial, or for
XX diagnosing, preventing and treating diseases associated with enhanced or
XX inhibited GPCR activity, e.g. acute heart failure, hypertension,
XX hypertension, angina pectoris, myocardial infarction, hyperproliferative

CC diseases such as cancers and psoriasis, apoptotic diseases, pain,
CC endometriosis, anorexia, bulimia, asthma, osteoporosis, schizophrenia,
CC delirium, depression, anxiety, urinary retention, ulcer, allergies,
CC dyskinesias such as Huntington's disorder or Gilles de la Tourette's
CC syndrome, Alzheimer's disease, or Parkinson's disease
XX
SQ Sequence 4718 BP; 1359 A; 1078 C; 1060 G; 1221 T; 0 U; 0 Other;
Query Match 100.0%; Score 1527; DB 9; Length 4718;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAGTCCACCTGACCAACAGACAGCGGAGAGTAACAGACAGCAAGTGCATGCCCC 60
Db 332 ATGAGTCCACCTGACCAACAGACAGCGGAGAGTAACAGACAGCAAGTGCATGCCCC 391
Qy 61 CTCTCAAAATGCCATCAGCTGAGCCAGGAGCATCATCGCTCAACCGTGGTTATC 120
Db 392 CTCTCAAAATGCCATCAGCTGAGCCAGGAGCATCATCGCTCAACCGTGGTTATC 451
Qy 121 TTCTCGCGGCTCTTTTGTGCGCAACATAGTGTGGCTAGTGTGACGCGAAGCCG 180
Db 452 TTCTCGCGGCTCTTTTGTGCGCAACATAGTGTGGCTAGTGTGACGCGAAGCCG 511
Qy 181 CAGCTGCTGAGTGAACCAACCGTTTATCTTTAACCCTGCTGACCGACCTGCTGAG 240
Db 512 CAGCTGCTGAGTGAACCAACCGTTTATCTTTAACCCTGCTGACCGACCTGCTGAG 571
Qy 241 ATTTGCTGAGGCGGCGGCTGGGTGGGCACTGTGCTGCTCTTGTGCGCCCTCAAC 300
Db 572 ATTTGCTGAGGCGGCGGCTGGGTGGGCACTGTGCTGCTCTTGTGCGCCCTCAAC 631
Qy 301 AGCCATTCTGACAGCGGCGGCTGTTAGCTCAACCAACCTGTTGCGCTTGGCAGCGTCAAC 360
Db 632 AGCCATTCTGACAGCGGCGGCTGTTAGCTCAACCAACCTGTTGCGCTTGGCAGCGTCAAC 691
Qy 361 ACCATTGCTTGGTGTACGTGATGCTACTTGTTCATCATCAACCTCTCTCTCAACCG 420
Db 692 ACCATTGCTTGGTGTACGTGATGCTACTTGTTCATCATCAACCTCTCTCTCAACCG 751
Qy 421 TCCAGATGACCAAGCGCGGCTTACCTGCTCTTATGAGCACTGAGATTGGCCATC 480
Db 752 TCCAGATGACCAAGCGCGGCTTACCTGCTCTTATGAGCACTGAGATTGGCCATC 811
Qy 481 CTGAGAGCACTCTCTCACTTACGCTGAGGCGCAAGCTGCTTGTATGAGCGCAATGCT 540
Db 812 CTGAGAGCACTCTCTCACTTACGCTGAGGCGCAAGCTGCTTGTATGAGCGCAATGCT 871
Qy 541 CTCTGCTCATGATGTGGGGGGCCAGCCCAAGCTACATATTCTCAAGGTGTCTTC 600
Db 872 CTCTGCTCATGATGTGGGGGGCCAGCCCAAGCTACATATTCTCAAGGTGTCTTC 931
Qy 601 ATGCTATTCCATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 932 ATGCTATTCCATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 991
Qy 661 AGGAGCAATGCTCTGCTGTATCAATGTCAAGAGACACAGCTTGAAGTGCAGTCAAGAC 720
Db 992 AGGAGCAATGCTCTGCTGTATCAATGTCAAGAGACACAGCTTGAAGTGCAGTCAAGAC 1051
Qy 721 TGTGTGAATAGAGATGAAG 780
Db 1052 TGTGTGAATAGAGATGAAG 1111
Qy 781 GAGTTTCCCGCAGACATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
Db 1112 GAGTTTCCCGCAGACATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1171
Qy 841 GAGGAG 900
Db 1172 GAGGAG 1231
Qy 901 AGGGAG 960

Db 1232 AGGGGAGGAGAGGCTAGAGAGACAGACGCTGGCCAGCAGCAGCATGAGGGT 1291
 961 AAGGAAGGAGAGCCAAAGTTGGAGAGACAGATGAAGGAGCAAGGGTGGCAGAGG 1020
 1292 AAGGAAGGAGAGCCAAAGTTGGAGAGACAGATGAAGGAGCAAGGGTGGCAGAGG 1351
 1021 GTCAACCAAGTGCAGATTGATCTGGTGAAGATGATGAGAGTTGGTGAAGAGCAGATC 1080
 1352 GTCAACCAAGTGCAGATTGATCTGGTGAAGATGATGAGAGTTGGTGAAGAGCAGATC 1411
 1081 AATTTCAGTGAAGATGATGATGAGAGGAGTGAACATCCCGAGAGCTCCCAAGCTGCT 1140
 1412 AATTTCAGTGAAGATGATGATGAGAGGAGTGAACATCCCGAGAGCTCCCAAGCTGCT 1471
 1141 CCTAACAGAGAGAGCAACCTCTCTGAGGAGTGTACAGAGAGAGAGTGTAAAGT 1200
 1472 CGTAAACAGAGAGCAACCTCTCTGAGGAGTGTACAGAGAGAGAGTGTAAAGT 1531
 1201 ATCTTCATCATATTTCTCTATGATGATATCCCTGGAGGCTTCTTTTGAAGATC 1260
 1532 ATCTTCATCATATTTCTCTATGATGATATCCCTGGAGGCTTCTTTTGAAGATC 1591
 1261 CTGGCCGTGTGGGTGATGATGAGAACCCAGTACCCAGTGGTATCAACATATATC 1320
 1592 CTGGCCGTGTGGGTGATGATGAGAACCCAGTACCCAGTGGTATCAACATATATC 1651
 1321 TGGCTTTTCTCTGAGAGTGTGATCCACCCCTATGATGATGATGATGATGATGATG 1380
 1652 TGGCTTTTCTCTGAGAGTGTGATCCACCCCTATGATGATGATGATGATGATGATG 1711
 1381 ATTAAGAGAGAGATCCAGAGCATGATGATGATGATGATGATGATGATGATGATG 1440
 1712 ATTAAGAGAGAGATCCAGAGCATGATGATGATGATGATGATGATGATGATGATG 1771
 1441 GAAGATAGCCAGCCAGACCTGCCCCGAGAGAGAGTGGAGCTGAGAGAGAGATGTCCT 1500
 1772 GAAGATAGCCAGCCAGACCTGCCCCGAGAGAGAGTGGAGCTGAGAGAGAGATGTCCT 1831
 1501 TCTTACGATTTGCTACTTTTCTTGA 1527
 1832 TCTTACGATTTGCTACTTTTCTTGA 1858
 Db
 RESULT 9
 AAS42857
 ID AAS42857 standard; cDNA, 1527 BP.
 XX
 AC AAS42857;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human G Protein-Coupled Receptor (GPCR) cDNA #52.
 XX
 XX Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia;
 XX attention deficit disorder; anxiety; depression; bipolar disorder; ss;
 XX neurological disorder; Huntington's disease; dementia; obesity; anorexia;
 XX metabolic disorder; Parkinson's disease; Tourette's syndrome; Chromoblasts;
 XX type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer;
 XX cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV;
 XX viral infection; immunosuppressant; neuroleptic; nootropic; tranquiliser;
 XX antidepressant; anorectic; PCR primer; gene therapy.
 OS Homo sapiens.
 XX
 PN WO200162797-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001MO-US005676.
 XX
 XX 23-FEB-2000; 2000US-0184247P.
 PR 23-FEB-2000; 2000US-0184303P.
 PR

PR 23-FEB-2000; 2000US-0184304P.
 PR 23-FEB-2000; 2000US-0184305P.
 PR 23-FEB-2000; 2000US-0184307P.
 PR 02-MAR-2000; 2000US-0186457P.
 PR 03-MAR-2000; 2000US-0186810P.
 PR 09-MAR-2000; 2000US-0186804P.
 PR 13-MAR-2000; 2000US-0188880P.
 PR 03-APR-2000; 2000US-0194344P.
 PR 23-JUN-2000; 2000US-0213861P.
 PR 11-JUL-2000; 2000US-0217369P.
 PR 11-JUL-2000; 2000US-0217370P.
 PR 14-JUL-2000; 2000US-0218337P.
 PR 20-JUL-2000; 2000US-0218492P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PT Vogel G, Wood LS, Parodi LA, Lind P;
 XX
 DR MPI; 2001-570628/64.
 DR P-PSDB; AAU25605.
 XX
 PT New isolated nucleic acid encoding a new G-protein coupled receptor
 PT polypeptide for detecting receptor modulators that can treat mental
 PT disorders, such as schizophrenia, anxiety, depression, or obesity.
 XX
 PS Claim 4; Page 89-90; 279pp; English.
 XX
 CC Sequences AAS42806-AAS42926 represent cDNA molecules and PCR primers for
 CC cDNA molecules encoding human G-protein coupled receptor (GPCR)
 CC polypeptides. The protein and DNA sequences of the invention can be used
 CC to identify compounds which bind to GPCR polypeptides and in screening
 CC for compounds that modulate GPCR activity. By screening a human subject
 CC for the presence of mutations in GPCR DNA, a GPCR-related disorder or a
 CC genetic predisposition can be diagnosed. The sequences can also be used
 CC for treatment and prevention of mental disorders such as schizophrenia,
 CC attention deficit disorder, anxiety, depression, dementia and bipolar
 CC disorder, neurological disorders such as Huntington's disease,
 CC Parkinson's disease and Tourette's syndrome, metabolic disorders such as
 CC obesity, anorexia and type 2 diabetes, cardiovascular disorders such as
 CC thrombosis, myocardial infarction, cardiomyopathy and atherosclerosis,
 CC viral infections caused by HIV and cancers
 XX
 SQ Sequence 1527 BP; 347 A; 439 C; 420 G; 321 T; 0 U; 0 Other;
 Query Match 99.9%; Score 1525.4; DB 4; Length 1527;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 ATGACGTCCACCTGACCAACAGACAGCGCGAGAGTAAAGAGAGCCAGCGATGCC 60
 1 ATGACGTCCACCTGACCAACAGACAGCGCGAGAGTAAAGAGAGCCAGCGATGCC 60
 61 CTCTCCAAATAGCCATCAGCTGAGCCAGCGAGATCATCCGCTCAACGGTGTATC 120
 61 CTCTCCAAATAGCCATCAGCTGAGCCAGCGAGATCATCCGCTCAACGGTGTATC 120
 121 TTCTCTGCGCGCTCTTTGCTGGCAACATAGTGTGGCTGTGTTGAGCGCCAGCGG 180
 121 TTCTCTGCGCGCTCTTTGCTGGCAACATAGTGTGGCTGTGTTGAGCGCGCGG 180
 121 TTCTCTGCGCGCTCTTTGCTGGCAACATAGTGTGGCTGTGTTGAGCGCGCGG 180
 181 CAGCTGCTCAGAGTGACCAACGGTTTATCTTTAACTCTGTCACGACCTGTGAG 240
 181 CAGCTGCTCAGAGTGACCAACGGTTTATCTTTAACTCTGTCACGACCTGTGAG 240
 181 CAGCTGCTCAGAGTGACCAACGGTTTATCTTTAACTCTGTCACGACCTGTGAG 240
 241 ATTTGCTGTGAGCGCCCTGAGTGTGAGCCACTGTGCTCTTCTTGGCCCTCAAC 300
 241 ATTTGCTGTGAGCGCCCTGAGTGTGAGCCACTGTGCTCTTCTTGGCCCTCAAC 300
 301 AGCACTTTGTGACAGCGCCCTGTGTAGCTTACCAACCACTTTGGCTTGGCCAGCTCAAC 360
 301 AGCACTTTGTGACAGCGCCCTGTGTAGCTTACCAACCACTTTGGCTTGGCCAGCTCAAC 360
 361 ACCATTGTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 420


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Db 361 ACCATTGCTGTTGTTGCTGATGATGCTACTTGTCCATCATCACCTCTCTCCACCG 420
Qy 421 TCCAGATGATACCAGCCGCGCGTTAACTGTCTCTATGAGCACTGTGATGGCCATC 480
Db 421 TCCAGATGATACCAGCGCGCGTTAACTGTCTCTATGAGCACTGTGATGGCCATC 480
Qy 481 CTGCGAGACATCTCTCTCACTCTACGGCTGGGGCCAGGCTGCTTTGATGAGCGCAATGCT 540
Db 481 CTGCGAGACATCTCTCACTCTACGGCTGGGGCCAGGCTGCTTTGATGAGCGCAATGCT 540
Qy 541 CTCTGCTCATGATCTGGGGGGCCAGCCCGACGTCACATATCTCAAGCTGGTCTTC 600
Db 541 CTCTGCTCATGATCTGGGGGGCCAGCCCGACGTCACATATCTCAAGCTGGTCTTC 600
Qy 601 ATCGTCATTCCACTGATTTGTCTATGATTTGCTCTACTCCGCTGTTCTGTGAGCCCG 660
Db 601 ATCGTCATTCCACTGATTTGTCTATGATTTGCTCTACTCCGCTGTTCTGTGAGCCCG 660
Qy 661 AGGCGACATGCTCTGTCTGATCAATGTCAAGAGACACAGCTTGAAAGTGGAGTCAAGAC 720
Db 661 AGGCGACATGCTCTGTCTGATCAATGTCAAGAGACACAGCTTGAAAGTGGAGTCAAGAC 720
Qy 721 TGTGTGAGATGATGATGATGAGGAGGAGAGAAAGAGAGAGAGTTCAGGATGAGT 780
Db 721 TGTGTGAGATGATGATGATGAGGAGGAGAGAAAGAGAGAGAGTTCAGGATGAGT 780
Qy 781 GAGTTTCGCGCGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db 781 GAGTTTCGCGCGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Qy 841 GAGTTTCGCGCGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 841 GAGTTTCGCGCGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Qy 901 AGGGCAGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 901 AGGGCAGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Qy 961 AAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 961 AAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy 1021 GTCAACCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1021 GTCAACCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Qy 1081 AATTTCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Db 1081 AATTTCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Qy 1141 CGTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db 1141 CGTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Qy 1201 ATCTTCATCATGATTTTCTCTATGATGATGATGATGATGATGATGATGATGATGAT 1260
Db 1201 ATCTTCATCATGATTTTCTCTATGATGATGATGATGATGATGATGATGATGATGAT 1260
Qy 1261 CTGGCCGTGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Db 1261 CTGGCCGTGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Qy 1321 TGGCTTTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
Db 1321 TGGCTTTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
Qy 1381 ATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 ATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Qy 1441 GAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Db 1441 GAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
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Db 1441 GAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Qy 1501 TCTTACGATTTCTGCTACTTTTCTTTGA 1527
Db 1501 TCTTACGATTTCTGCTACTTTTCTTTGA 1527

RESULT 10
AAS07942 ID AAS07942 standard; cDNA, 1527 BP.
XX
AC AAS07942;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human cDNA encoding G-protein coupled receptor, hrup15.
XX
KW Human; G-protein coupled receptor; GPCR; hrup15; agonist;
XX inverse agonist; lung cancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1527
FT /tag= a
FT /product= "hrup15"
XX
PN WO200136471-A2.
XX
PD 25-MAY-2001.
XX
PF 16-NOV-2000; 2000WO-US031509.
XX
PR 17-NOV-1999; 99US-0166088P.
XX
PR 17-NOV-1999; 99US-0166099P.
XX
PR 17-NOV-1999; 99US-0166369P.
XX
PR 23-DEC-1999; 99US-0171900P.
XX
PR 23-DEC-1999; 99US-0171901P.
XX
PR 23-DEC-1999; 99US-0171902P.
XX
PR 11-FEB-2000; 2000US-0181749P.
XX
PR 14-MAR-2000; 2000US-0189258P.
XX
PR 14-MAR-2000; 2000US-0189259P.
XX
PR 10-APR-2000; 2000US-0195898P.
XX
PR 10-APR-2000; 2000US-0195899P.
XX
PR 10-APR-2000; 2000US-0196078P.
XX
PR 28-APR-2000; 2000US-0200419P.
XX
PR 12-MAY-2000; 2000US-0203630P.
XX
PR 12-JUN-2000; 2000US-0210741P.
XX
PR 12-JUN-2000; 2000US-0210982P.
XX
PR 21-AUG-2000; 2000US-0226760P.
XX
PR 26-SEP-2000; 2000US-0235418P.
XX
PR 26-SEP-2000; 2000US-0235779P.
XX
PR 20-OCT-2000; 2000US-0242332P.
XX
PR 20-OCT-2000; 2000US-0242343P.
XX
PR 24-OCT-2000; 2000US-0243019P.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Chen R, Dang HT, Lowitz KP;
XX
DR MPI: 2001-355616/37.
XX
DR P-PSDB; AAN04369.
XX
PT Endogenous and non-endogenous versions of human G-protein coupled
PT receptors for direct identification of candidate compounds as agonists,
PT inverse agonists or partial agonists for use as therapeutic agents.
XX
PS Claim 31; Page 102; 160pp; English.
XX
CC The sequence encodes a human G-protein coupled receptor (GPCR), hrup15.
CC The endogenous and non-endogenous, constitutively activated versions of
CC human G-protein coupled receptors (GPCR), are useful for direct
CC identification of candidate compounds as receptor agonists, inverse
```


CC agonists or partial agonists having applicability as therapeutic agents
CC for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous
CC version of human GPCRs are also utilized in research settings and in
CC vitro and in vivo system, incorporating GPCRs can be utilized to
CC elucidate and understand the roles these receptors play in the human
CC condition, both normal and diseased

XX Sequence 1527 BP; 347 A; 439 C; 420 G; 321 T; 0 U; 0 Other;

Query Match 99.9%; Score 1525.4; DB 5; Length 1527;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 ATGAGCTTCACCTGACCAACACGCGGAGAGTAACAGACCAACGTCATGCC 60
DB 1 ATGAGCTTCACCTGACCAACACGCGGAGAGTAACAGACCAACGTCATGCC 60
QY 61 CTCTCCAAAATGCCATCAGCCCTGGCCACGGGATATCGCTCAACCGTGTATTC 120
DB 61 CTCTCCAAAATGCCATCAGCCCTGGCCACGGGATATCGCTCAACCGTGTATTC 120
QY 121 TTCCTGCGCGCCTCTTTCGTGGCAACATAGTGTGGCTAGTGTGGAGGCAAGCCG 180
DB 121 TTCCTGCGCGCCTCTTTCGTGGCAACATAGTGTGGCTAGTGTGGAGGCAAGCCG 180
QY 181 CAGCTGCTGCAAGTGAACCAACCGTTTATCTTTTAACTCTCTGTCACCGACTGTGAC 240
DB 181 CAGCTGCTGCAAGTGAACCAACCGTTTATCTTTTAACTCTCTGTCACCGACTGTGAC 240
QY 241 ATTTGCTGTGGCCCCCTGGGTGGTGGCACTCTGTGCTTCTTGGCCCCCTAAC 300
DB 241 ATTTGCTGTGGCCCCCTGGGTGGTGGCACTCTGTGCTTCTTGGCCCCCTAAC 300
QY 301 AGCAATTTGCAACGCGCGCTGTAGCTCAACCACTGTGCTTCCGCAAGCTCAAC 360
DB 301 AGCAATTTGCAACGCGCGCTGTAGCTCAACCACTGTGCTTCCGCAAGCTCAAC 360
QY 361 ACCATTGTGTGGTGTCAAGTATCGCTACTTGTCCATATCCACCTCTCTCTACCG 420
DB 361 ACCATTGTGTGGTGTCAAGTATCGCTACTTGTCCATATCCACCTCTCTCTACCG 420
QY 421 TCCAAAGATACCAAGCGCGGCTTACCTGTCTCTATGGCACTGGATTGTGGCCATC 480
DB 421 TCCAAAGATACCAAGCGCGGCTTACCTGTCTCTATGGCACTGGATTGTGGCCATC 480
QY 481 CTGCAAGACATCTCTCACTCTACGCTGGGCGCAGGCTGCTTATAGCGGCATATGCT 540
DB 481 CTGCAAGACATCTCTCACTCTACGCTGGGCGCAGGCTGCTTATAGCGGCATATGCT 540
QY 541 CTCTGCTCATGATCTGGGGGGGCAAGCCAGCTACATATTTCTACGCGTGTCTTTC 600
DB 541 CTCTGCTCATGATCTGGGGGGGCAAGCCAGCTACATATTTCTACGCGTGTCTTTC 600
QY 601 ATCGTCATTCACCTGATATGATGATGCTGCTACTCCGTGGTGTCTGTGACCGCCG 660
DB 601 ATCGTCATTCACCTGATATGATGATGCTGCTACTCCGTGGTGTCTGTGACCGCCG 660
QY 661 AGGAGCATGCTCTGTGTACAATGTCAGAGACACAGCTGGAATGGCAAGTCAAGAC 720
DB 661 AGGAGCATGCTCTGTGTACAATGTCAGAGACACAGCTGGAATGGCAAGTCAAGAC 720
QY 721 TGTGTGAGAAATGAGATGAAGAGGAGAGAGAGAGAGAGAGTTCAGATGAGAT 780
DB 721 TGTGTGAGAAATGAGATGAAGAGGAGAGAGAGAGAGAGAGTTCAGATGAGAT 780
QY 781 GAGTTTCCGCGCCAGCATGAAGTGAAGTCAAGGCGCAAGATGGAAGCCAA 840
DB 781 GAGTTTCCGCGCCAGCATGAAGTGAAGTCAAGGCGCAAGATGGAAGCCAA 840
QY 841 GACGGAGGCTGAAGGCAAGAGAGAGAGAGAGAGAGAGAGAGTGTGAGAGGCC 900
DB 841 GACGGAGGCTGAAGGCAAGAGAGAGAGAGAGAGAGAGAGAGTGTGAGAGGCC 900
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QY 901 AGGAGGAGGAGAGGTCAGAGAGACAGACGCTGGCCAGCGCAGCATGAGGGT 960
DB 901 AGGAGGAGGAGAGGTCAGAGAGACAGACGCTGGCCAGCGCAGCATGAGGGT 960
QY 961 AAGGAAGGAGAGCAAAATTGAGAGAAACAGATTAAGGAGAGAGAGTGGCAGAG 1020
DB 961 AAGGAAGGAGAGCAAAATTGAGAGAAACAGATTAAGGAGAGAGTGGCAGAG 1020
QY 1021 GTCAACCATGTCAGATTTGCTGATGAGTATGATGATGATGATGATGATGATG 1080
DB 1021 GTCAACCATGTCAGATTTGCTGATGAGTATGATGATGATGATGATGATGATG 1080
QY 1081 AATTTGAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
DB 1081 AATTTGAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1141 CTTAAGAGCAACAGCAACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
DB 1141 CTTAAGAGCAACAGCAACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1201 ATCTTCATCATATTTTCTCTATGATGATGATGATGATGATGATGATGATGATG 1260
DB 1201 ATCTTCATCATATTTTCTCTATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1261 CTGGCCGTGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
DB 1261 CTGGCCGTGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 TGGCTTTTCTTCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1380
DB 1321 TGGCTTTTCTTCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1380
QY 1381 ATTTAAGAAAGAAATCCAGGACATGCTGAAGAAAGTTCTTGAAGGAAAGCCCG 1440
DB 1381 ATTTAAGAAAGAAATCCAGGACATGCTGAAGAAAGTTCTTGAAGGAAAGCCCG 1440
QY 1441 GAAGATAGCACCACAGACCTGCGCGGAGAGAGTGGAGATGAAGCAAGATTGTCC 1500
DB 1441 GAAGATAGCACCACAGACCTGCGCGGAGAGAGTGGAGATGAAGCAAGATTGTCC 1500
QY 1501 TCCTAGATTCGTGCTACTTTTCTTTGA 1527
DB 1501 TCCTAGATTCGTGCTACTTTTCTTTGA 1527

RESULT 11
AA18899
ID AA18899 standard; cDNA; 1527 BP.
XX
XX AA18899;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Human cDNA encoding alpha1a adrenergic receptor-1-like GPCR.
DE
XX
XX Human; ss; alpha1a adrenergic receptor; G protein-coupled receptor; GPCR;
KW peripheral nervous system disease; central nervous system disease;
KW urinary incontinence; benign prostatic hypertrophy; infection;
KW HIV infection; human immunodeficiency virus; pain; cancer; anorexia;
KW bulimia; asthma; Parkinson's disease; obesity; acute heart failure;
KW hypertension; urinary retention; osteoporosis;
KW angina pectoris; myocardial infarction; ulcer; allergy; psychosis;
KW neurological disorder; anxiety; schizophrenia; manic depression;
KW delirium; dementia; severe mental retardation; dyskinesia;
KW Huntington's disease; Tourette's syndrome.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1.1527
FT CDS /tag= a
FT /product= "Alpha1a adrenergic receptor"
XX
```

PN WO200188126-A2.
XX 22-NOV-2001.
XX 11-MAY-2001; 2001WO-BP005383.
PE 15-MAY-2000; 2000US-0204145P.
XX 04-DEC-2000; 2000US-0250505P.
PR (FARB) BAYER AG.
XX
XX Ramakrishnan S;
XX WPI; 2002-106124/14.
DR P-PSDB; AAU11764.
PT New polynucleotide, useful for treating pain, cancer, Parkinson's
PT diseases, obesity, hypertension, asthma, schizophrenia, encodes an alpha
PT (1a) adrenergic receptor-like G-protein coupled receptor (GPCR).
XX
XX Claim 1; Fig 2; 123pp; English.
XX
XX The invention relates to an isolated polynucleotide encoding an alpha
CC adrenergic receptor-like G-protein coupled receptor (GPCR) polypeptide,
CC the encoded polypeptide, fragments, derivatives and allelic variants.
CC Also include are an expression vector comprising the polynucleotide, a
CC host cell containing the vector, screening for therapeutic agents which
CC decrease or increase the activity of the receptor by binding a test agent
CC to the protein and determining whether the activity is decreased or
CC increased. A modulator of the receptor is useful for treating alpha
CC adrenergic receptor-like GPCR disorder such as peripheral or central
CC nervous system disease, urinary incontinence or benign prostatic
CC hypertrophy. The receptor, polynucleotide or modulator is useful for
CC treating disorders such as bacterial, fungal, protozoan, and viral
CC infections, particularly those caused by HIV (human immunodeficiency
CC virus), pain, cancer, anorexia, bulimia, asthma, Parkinson's diseases,
CC obesity, acute heart failure, hypotension, hypertension, urinary
CC retention, osteoporosis, angina pectoris, myocardial infarction, ulcer,
CC allergy, benign prostatic hypertrophy, and psychotic and neurological
CC disorders, including anxiety, schizophrenia, manic depression, delirium,
CC dementia, severe mental retardation, and dyskinesias, such as
CC Huntington's disease and Tourette's syndrome. The polynucleotide is
CC useful in diagnostic assays for detecting diseases and abnormalities or
CC susceptibility to disease and abnormalities related to the presence of
CC mutations in the gene. The protein is useful to identify test compounds
CC which may act as agonists or antagonists, and for raising antibodies
CC which can block the receptor and effectively prevent ligand binding. The
CC present sequence is the cDNA encoding the alpha adrenergic receptor-
CC like GPCR
XX
XX Sequence 1527 BP; 347 A; 439 C; 420 G; 321 T; 0 U; 0 Other;
SQ
Query Match 99.9%; Score 1525.4; DB 6; Length 1527;
Beef Local Similarity 99.9%; Pred. No. 0;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAGCTCCACCTGCAACCAAGACGCGGAGAGTAAGACGACACGTCGATGCC 60
DB 1 ATGAGCTCCACCTGCAACCAAGACGCGGAGAGTAAGACGACACGTCGATGCC 60
QY 61 CTCTCCAAATGCCATCAGCTGCGCCACGCGCATCATCCGCTCAACCGTGTGTTATC 120
DB 61 CTCTCCAAATGCCATCAGCTGCGCCACGCGCATCATCCGCTCAACCGTGTGTTATC 120
QY 122 TTCCTCGCGGCTTTTCTGTCGGCAACATAGTGTGCGCTAGTGTGTCAGCGCCAGCCG 180
DB 122 TTCCTCGCGGCTTTTCTGTCGGCAACATAGTGTGCGCTAGTGTGTCAGCGCCAGCCG 180
QY 121 TTCCTCGCGGCTTTTCTGTCGGCAACATAGTGTGCGCTAGTGTGTCAGCGCCAGCCG 180
DB 121 TTCCTCGCGGCTTTTCTGTCGGCAACATAGTGTGCGCTAGTGTGTCAGCGCCAGCCG 180
QY 181 CAGCTGCTCAGAGTGACCAACGTTTATCTTAACTCTCGTCAACCACTGTCGAG 240
DB 181 CAGCTGCTCAGAGTGACCAACGTTTATCTTAACTCTCGTCAACCACTGTCGAG 240
QY 241 ATTTCGCTGTGGCCCTGTGGGTGTGGCCACTGTGTGCTCTCTTTCGCGCCCTCAAC 300

DB 241 ATTTCGCTGTGGCCCTGTGGGTGTGGCCACTGTGTGCTCTCTTTCGCGCCCTCAAC 300
QY 301 AGCCACTTCTGCAAGGCGCTGTGTTAGCTCAACCCACTGTTGCGCTTGCAGAGCTCAAC 360
DB 301 AGCCACTTCTGCAAGGCGCTGTGTTAGCTCAACCCACTGTTGCGCTTGCAGAGCTCAAC 360
QY 361 ACCATTGTCTGTGTGTCAAGTGCATCTGTTTCATCATCATCCCTCTCTCTCAACCG 420
DB 361 ACCATTGTCTGTGTGTCAAGTGCATCTGTTTCATCATCATCCCTCTCTCTCAACCG 420
QY 421 TCCAAATGATCCCAAGCGCGGTTAACTGCTCTCTTAATGCACTGATGTGGCCATC 480
DB 421 TCCAAATGATCCCAAGCGCGGTTAACTGCTCTCTTAATGCACTGATGTGGCCATC 480
QY 481 CTGCAAGACACTCTCCACTCAAGCTGAGGCGCCAGGCTGCTTGTATGAGCGCAATCT 540
DB 481 CTGCAAGACACTCTCCACTCAAGCTGAGGCGCCAGGCTGCTTGTATGAGCGCAATCT 540
QY 541 CTGCTCTCATGATCTGAGGGGGCCAGCCCAAGCTCACTATTCTCAGCGTGTCTTC 600
DB 541 CTGCTCTCATGATCTGAGGGGGCCAGCCCAAGCTCACTATTCTCAGCGTGTCTTC 600
QY 601 ATTCGATTCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 601 ATTCGATTCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 AGGCAAGATGCTCTGCTGCTCAATGTCAGAGACACAGCTTGAAGTCCGATCAAGAC 720
DB 661 AGGCAAGATGCTCTGCTGCTCAATGTCAGAGACACAGCTTGAAGTCCGATCAAGAC 720
QY 721 TGTGTGGAATGAGATGAGATGAGAGGAGCAGAGAGAGAGAGAGTTCAGATGAGAT 780
DB 721 TGTGTGGAATGAGATGAGATGAGAGGAGCAGAGAGAGAGAGTTCAGATGAGAT 780
QY 781 GAGTTTCCGCGCAGACATGAAAGTGAAGTCAAGGCCAAGAGGCGAAGATGAACCAAG 840
DB 781 GAGTTTCCGCGCAGACATGAAAGTGAAGTCAAGGCCAAGAGGCGAAGATGAACCAAG 840
QY 841 GAGGCGAGCTGAAAGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 GAGGCGAGCTGAAAGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 AGGCGCAGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 960
DB 901 AGGCGCAGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 960
QY 961 AAGGAAGCAGACCAAGATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 AAGGAAGCAGACCAAGATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 GTCAACAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 GTCAACAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 AATTTCAGTAGAGATGAGTGTGAGGCAAGTGAACATCCGAGAGAGCTCCCAACAGTCT 1140
DB 1081 AATTTCAGTAGAGATGAGTGTGAGGCAAGTGAACATCCGAGAGAGCTCCCAACAGTCT 1140
QY 1141 CGTAACAG 1200
DB 1141 CGTAACAG 1200
QY 1201 ATCTTCATCATATTTTCTCTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 1260
DB 1201 ATCTTCATCATATTTTCTCTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 1260
QY 1261 CTGGCCGTGTGGGTGATGTGAAAACCAAGTATCCCAAGTGGGTATCATCAATATCATC 1320
DB 1261 CTGGCCGTGTGGGTGATGTGAAAACCAAGTATCCCAAGTGGGTATCATCAATATCATC 1320
QY 1321 TGGCTTTTCTTCTGAGTGTGATCAACCCCTATATGCTATATGCTATATGCAAGAGCC 1380

QY	1021	GTCAACCAAGTCACAGTTGACTGCTGGGCGTAAGAAATGACATGAGAGTTTGGGAAAGAGACATC	1080
Db	1021	GTCACCAAGTCAGCAATTGACTTGGGTGTAABATGACATGAGAGTTTGGTGAAGACACATC	1080
QY	1081	AATTTCAAGTAGAGTAGACGTGAGGCAAGTGAACATCCCGAAGACCTTCCACCCAGTCGT	1140
Db	1081	AATTTCAAGTAGAGTAGACGTGAGGCAAGTGAACATCCCGAAGACCTTCCACCCAGTCGT	1140
QY	1141	CGTAAACAGCAACAGAACCCCTCCCTGCGCCAGGTGCTACGATGCGAAACGTGCTAAAGTG	1200
Db	1141	CGTAAACAGCAACAGAACCCCTCTCTGCGCCAGGTGCTACGATGCGAAACGTGCTAAAGTG	1200
QY	1201	ATCTTCATCATCATTTTCTCCATGTGCTATCCCTGGGCCCCTACTGCTTTTATGACAGTC	1260
Db	1201	ATCTTCATCATCATTTTCTCCATGTGCTATCCCTGGGCCCCTACTGCTTTTATGACAGTC	1260
QY	1261	CTGGCGCGTGTGGGTGAGATGTGGAAACCCAGGTACCCCAAGTGGGTGATACATATATCATC	1320
Db	1261	CTGGCGCGTGTGGGTGAGATGTGGAAACCCAGGTACCCCAAGTGGGTGATACATATATCATC	1320
QY	1321	TGGCTTTTCTTCTCTGACGTGCTGATCCACCCCTATGTCTATGGGTACATGACAAAGCC	1380
Db	1321	TGGCTTTTCTTCTCTGACGTGCTGATCCACCCCTATGTCTATGGGTACATGACAAAGCC	1380
QY	1381	ATTAAAGAGAAATCCAGACATGCTGAAGAAATTCTTCTGACAGAAAGACCCCGGAA	1440
Db	1381	ATTAAAGAGAAATCCAGACATGCTGAAGAAATTCTTCTGACAGAAAGACCCCGGAA	1440
QY	1441	GAAGATAGACCAACCCAGACCTGCGCCGGAACAGAGGGTGGGACTGAAGCAAGATTGTCCCT	1500
Db	1441	GAAGATAGACCAACCCAGACCTGCGCCGGAACAGAGGGTGGGACTGAAGCAAGATTGTCCCT	1500
QY	1501	TCCTTAGATTCGTACTATTTTCTTTGA	1527
Db	1501	TCCTTAGATTCGTACTATTTTCTTTGA	1527

RESULT 13
AB242914
ID AB242914 standard; DNA; 1527 BP.
XX
XX
AC AB242914;
XX
DT 06-MAR-2003 (first entry)
XX
DE Human GPCR polynucleotide SEQ ID NO 89.
XX
XX Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
KW drug development; gustatory; taste; fragrance; gene; ds.
XX
CS Homo sapiens.
XX
PN WO200216548-A2.
XX
PD 28-FEB-2002.
XX
PF 30-JUL-2001; 2001WO-IB001446.
XX
PR 04-AUG-2000; 2000JP-00237818.
XX
PR 13-FEB-2001; 2001JP-00034434.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Haga T, Takeda S, Mitaku S;
XX
XX WPI; 2002-304118/34.
DR P-PSDB; ABP95640.
XX
XX Database global search for G protein-coupled receptors, proteins and
PT encoded genes for studying in vivo signal transduction mechanism and
PT identifying targets for drug development.
PS
PS Claim 9; SEQ ID NO 89; 97pp + Sequence listing; Japanese.

XX	CC	The invention relates to a method for screening G protein-coupled
CC	receptor (GPCR) genes (AB242870-AB243216) and/or GPCR proteins (AB955596-	
CC	ABP95942) by extracting open-reading frames containing 6-8 transmembrane	
CC	domains with 250-1000 amino acid residues to give a gene homologous with	
CC	a known GPCR gene. The receptor proteins and encoded genes are useful for	
CC	studying in vivo signal transduction mechanism and identifying targets	
CC	for drug development e.g. based on olfactory and gustatory receptors in	
CC	form of agonists and antagonists by screening intrinsic and extrinsic	
CC	ligands as bitter taste inhibitors, taste enhancers and fragrance	
CC	improvers. Note: The sequence data for this patent did not form part of	
CC	the printed specification, but was obtained in electronic format directly	
CC	from WIPO at ftp://pub.int/pub/published_pct_sequences	
XX	Sequence 1527 BP, 347 A; 439 C; 420 G; 321 T; 0 U; 0 Other;	
XX	Query Match 99.9%; Score 1525.4; DB 6; Length 1527;	
XX	Best Local Similarity 99.9%; Pred. No. 0;	
XX	Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
QY	1 ATGAGCTCCACCTGTGACCAACAGACGCGCGAGAGTAAACAGCAGCCACACGTGATGCC 60	
DB	1 ATGAGCTCCACCTGTGACCAACAGACGCGCGAGAGTAAACAGCAGCCACGTGATGCC 60	
QY	61 CTCTCCAAAATGCCATCATGCTGGGCCAAGGCATCATCCGCTAAACGCTGATATAC 120	
DB	61 CTCTCCAAAATGCCATCATGCTGGGCCAAGGCATCATCCGCTGATATAC 120	
QY	121 TTCCTCGCGCCTCTTTCGTGCGCAACATAGTGTGCGCTATGTTTCAGCGCAAGCGG 180	
DB	121 TTCCTCGCGCCTCTTTCGTGCGCAACATAGTGTGCGCTATGTTTCAGCGCAAGCGG 180	
QY	181 CAGCTGTGACAGTGAACCAACCGTTTATCTTTAACTCTCTGTCAACGCACTGCTGCAG 240	
DB	181 CAGCTGTGACAGTGAACCAACCGTTTATCTTTAACTCTCTGTCAACGCACTGCTGCAG 240	
QY	241 ATTGGCTGTGCGCCCTCTGGTGTGTGCGCACTGTGTGCTCTTTCGGGCCCTCAAC 300	
DB	241 ATTGGCTGTGCGCCCTCTGGTGTGTGCGCACTGTGTGCTCTTTCGGGCCCTCAAC 300	
QY	301 AGCCACTTCTGACGGGCCCTGGTTAGCCTACACCCACTGTTGGCCTTGGCCAGCGTCAAC 360	
DB	301 AGCCACTTCTGACGGGCCCTGGTTAGCCTACACCCACTGTTGGCCTTGGCCAGCGTCAAC 360	
QY	361 ACCATTGTCTTGGTGTCAGTGATGCTATCTTGTCCATCATCAACCTCTCTCTTAACCG 420	
DB	361 ACCATTGTCTTGGTGTCAGTGATGCTATCTTGTCCATCATCAACCTCTCTCTTAACCG 420	
QY	421 TCCAAGATGACCCAGCGCGCGGTTAAGCTGCTCTCTATAGCACTGGAATTTGGCCATC 480	
DB	421 TCCAAGATGACCCAGCGCGCGGTTAAGCTGCTCTCTATAGCACTGGAATTTGGCCATC 480	
QY	481 CTGCAGAGACCTTCCTCACTATGAGGCTGGGGCCAGGCGCTTTGATAGGCGAATGCT 540	
DB	481 CTGCAGAGACCTTCCTCACTATGAGGCTGGGGCCAGGCGCTTTGATAGGCGAATGCT 540	
QY	541 CTCTGCTCCATGATCTGGGGGGCCAGCCCACTACATATTCAGCGTGTGTCTTTC 600	
DB	541 CTCTGCTCCATGATCTGGGGGGCCAGCCCACTACATATTCAGCGTGTGTCTTTC 600	
QY	601 ATGCTCATTCACATGATTTGTCAATGATTTGCTCTCTACCTCGTGTGTTCTGTCCAGCCCG 660	
DB	601 ATGCTCATTCACATGATTTGTCAATGATTTGCTCTCTACCTCGTGTGTTCTGTCCAGCCCG 660	
QY	661 AGGCAAGACGCTCTGCTGTACAAATGCAAGACACACAGTTTGAAGTGGAGTCAAGGAC 720	
DB	661 AGGCAAGACGCTCTGCTGTACAAATGCAAGACACACAGTTTGAAGTGGAGTCAAGGAC 720	
QY	721 TGTGTGAGAAATGAGATGAAGAGGAGCAGAGAAAGAGAGATTCAGAGTATGAGAT 780	
DB	721 TGTGTGAGAAATGAGATGAAGAGGAGCAGAGAAAGAGAGATTCAGAGTATGAGAT 780	
QY	781 GAGTTTCGCCGACAGATGAGTGAAGTCAAGGCCAAGAGGCGCAATGAGAACCAAG 840	

Db	781	GAGTTTCGCCCCCAGCATGAAAGTGAGTCAAGGCCAAGAGGCGAGATGGAAGCCAG	840
Qy	841	GACGGCAGCCTTGAAAGGCCAAGAAAGAAAGCAACGGGACCAAGTGAAGTGTGAAGGCC	900
Db	841	GACGGCAGCCTTGAAAGGCCAAGAAAGAAAGCAACGGGACCAAGTGAAGTGTGAAGGCC	900
Qy	901	AGGGGCGACCGAGAGGTCTAGAGACAGACGACCGTGGCCACGACCGACAGATGAGAGGT	960
Db	901	AGGGGCGACCGAGAGGTCTAGAGAGCAGCACGGTGGCCACGACCGACAGATGAGAGGT	960
Qy	961	AAGGAAGCGACACCAAAAGTTGAGAGAGAAACAGATGAAGCGACGAACAAAGGTCGCACAG	1020
Db	961	AAGGAAGCGACACCAAAAGTTGAGAGAGAAACAGATGAAGCGACGAACAAAGGTCGCACAG	1020
Qy	1021	GTCAACCACTGCAGCATTGACTTTGGGTGAAGATGACATGAGTTTGGTGAAGACGACATC	1080
Db	1021	GTCAACCACTGCAGCATTGACTTTGGGTGAAGATGACATGAGTTTGGTGAAGAGACATC	1080
Qy	1081	AAATTCAGTGAAGATGACGTGAGGCGAGTGAACATCCCGAGAGCCTCCACCCAGTCGT	1140
Db	1081	AAATTCAGTGAAGATGACGTGAGGCGAGTGAACATCCCGAGAGCCTCCACCCAGTCGT	1140
Qy	1141	CGTAACAGCAACAGCAACCTCTCTTGCACCAGTGCTAACAGTGCACAAAGCTGTAAAGTG	1200
Db	1141	CGTAACAGCAACAGCAACCTCTCTTGCACCAGTGCTAACAGTGCACAAAGCTGTAAAGTG	1200
Qy	1201	ATCTTCATCATCATTTTCTCCTATGTGTATTCCTGGGGGCCCTACTGCTTTTATAGCAGTC	1260
Db	1201	ATCTTCATCATCATTTTCTCCTATGTGTATTCCTGGGGGCCCTACTGCTTTTATAGCAGTC	1260
Qy	1261	CTGGCCCGTGGGTGATGTGAAACCAGAGTACCCCACTGGGTGATACCATATATCATC	1320
Db	1261	CTGGCCCGTGGGTGATGTGAAACCAGAGTACCCCACTGGGTGATACCATATATCATC	1320
Qy	1321	TGCGCTTTCTTCTCGACGTGCTGCATCCACCCCTATGTCTATGTGCTACATGACAAAGCC	1380
Db	1321	TGCGCTTTCTTCTCGACGTGCTGCATCCACCCCTATGTCTATGTGCTACATGACAAAGCC	1380
Qy	1381	ATTAAAGAAAGAAATTCAGAGACATGCTGAAGAAAGTTCTTCTGCAAGGAAAGCCCCCGAAA	1440
Db	1381	ATTAAAGAAAGAAATTCAGAGACATGCTGAAGAAAGTTCTTCTGCAAGGAAAGCCCCCGAAA	1440
Qy	1441	GAAAGTACCAACCCAGACCTGCGCCGGAAACAGGGGTGGGACTGAAGCGCAAGATTGTCCCT	1500
Db	1441	GAAAGTACCAACCCAGACCTGCGCCGGAAACAGGGGTGGGACTGAAGCGCAAGATTGTCCCT	1500
Qy	1501	TCCTACGATTCGTGCTACTTTTCTCTTGA	1527
Db	1501	TCCTACGATTCGTGCTACTTTTCTCTTGA	1527

RESULT 14	
ABZ42550	
ID	ABZ42550 standard; DNA, 1527 BP.
XX	
AC	ABZ42550;
XX	
XX	
DT	04-MAR-2003 (first entry)
XX	
DE	
XX	Human G protein-coupled receptor GPR101 nucleotide SEQ ID NO:582.
XX	
KM	G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KM	G protein-coupled receptor modulator; antibody; immune-related disease;
KM	growth-related disease; cell regeneration-related disease; AIDS; cancer;
KM	immunological-related cell proliferative disease; autoimmune disease;
KM	Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy
KM	osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KM	graft versus host disease; Parkinson's disease; multiple sclerosis; pain
KM	psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KM	mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KM	hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KM	ulcer; gene; ds.

XX Homo sapiens.
OS
XN MO200261087-A2.
FN
XX 08-AUG-2002.
PD
XX
PF 19-DEC-2001; 2001MO-US050107.
PE
PR 19-DEC-2000; 2000US-0257144P.
XX
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Butner GC, Roush CL, Brown JF;
DR WPI; 2003-046718/04.
DR P-PADB; ABP81704.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

CC The present invention describes antigenic peptides (1) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP93619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting and
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related diseases, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ4523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention

	Query Match	Best Local Similarity	Score 15.25, 4	DB 8	Length 1527	99.9%	Pred. 15.25, 4	Mismatches 0	Indels 0	Gaps 0
	Matches 1526	Conservative	0	1	0	0	0	0	0	0
QY	1	ATGAGCTGCACCTGCACCAACAGCAGCAGCGGAGAGGTAA	CAGCAGCCACCTGCATGCC	60						
DB	1	ATGAGCTGCACCTGCACCAACAGCAGCGGAGAGGTAA	CAGCAGCCACCTGCATGCC	60						
QY	61	CTCTCCAAAATAGCCCATCAGCTGGCCCAAGGCAATCGGCTCAACCGGTCGTGTTATC		120						
DB	61	CTCTCCAAAATAGCCCATCAGCTGGCCCAAGGCAATCGGCTCAACCGGTCGTGTTATC		120						
QY	121	TTCTCTCGCGCGCTCTTTTGTGTGGGCAACAATAGTGTGGCTAGTGTTCACGCGCAAGCCG		180						
DB	121	TTCTCTCGCGCGCTCTTTTGTGTGGGCAACAATAGTGTGGCTAGTGTTCACGCGCAAGCCG		180						
QY	181	CAGCTGTGTGACAGGTGACCAACCGTTTATCTTTTAACTCTCTCGTACCGACACTGTGTGAG		240						
DB	181	CAGCTGTGTGACAGGTGACCAACCGTTTATCTTTTAACTCTCTCGTACCGACACTGTGTGAG		240						

QY	241	ATTTCGCTCGAGGCCCCCTGGGTGGTGGCACTCTGAGCCCTCTTTCTGGCCCCCTCAAC	300
Db	241	ATTTCGCTCGAGCCCCCTGGGTGGTGGCACTCTGAGCCCTCTTTCTGGCCCCCTCAAC	300
QY	301	AGCCACTTCTGCA CGG CCTGGTTAGCTCAACCCACTGTTCCGCTTCGCACGGTCAAC	360
Db	301	AGCCACTTCTGCA CGG CCTGGTTAGCTCAACCCACTGTTCCGCTTCGCACGGTCAAC	360
QY	361	ACCATTTGTCCTGGTGTCA GTGATCGTACTTTGTCAATCAACCCCTCTCTCTACCCG	420
Db	361	ACCATTTGTCCTGGTGTCA GTGATCGTACTTTGTCAATCAACCCCTCTCTCTACCCG	420
QY	421	TCCAAAGATGACCCAGCGCGCGGTTAACTGTCTCTCTATGCGCACTGGAATTGTGGCATC	480
Db	421	TCCAAAGATGACCCAGCGCGCGGTTAACTGTCTCTCTATGCGCACTGGAATTGTGGCATC	480
QY	481	CTGCAGAGCACTCTCCCACTCTACGGCTGGGGCCAGCGTGCCTTTGATGACGGCAATGCT	540
Db	481	CTGCAGAGCACTCTCCCACTCTACGGCTGGGGCCAGCGTGCCTTTGATGACGGCAATGCT	540
QY	541	CTTGCTCCATGATCTGGGGGGGCCAGGCCCAAGCTACATATTCTTCA GCGTGTCTTC	600
Db	541	CTTGCTCCATGATCTGGGGGGGCCAGGCCCAAGCTACATATTCTTCA GCGTGTCTTC	600
QY	601	ATCGGCATTTCCACTCATATTGTCA TGA TTTGCTGTCTACTCCGCGGTGTTCTGTGCAACCCCG	660
Db	601	ATCGGCATTTCCACTCATATTGTCA TGA TTTGCTGTCTACTCCGCGGTGTTCTGTGCAACCCCG	660
QY	661	AGCGAGCATGCTCTGTCTGTCAATGTC AAGAGACACACACTTTGGAAGTGCAGTCAAGGAC	720
Db	661	AGCGAGCATGCTCTGTCTGTCAATGTC AAGAGACACACACTTTGGAAGTGCAGTCAAGGAC	720
QY	721	TGTGTGAGAAATGAGGATGAAGGGAGCAGAGAAAGAGAGATTCCAGGATGAGAGT	780
Db	721	TGTGTGAGAAATGAGGATGAAGGGAGCAGAGAAAGAGAGATTCCAGGATGAGAGT	780
QY	781	GAGTTTCCCGCCGACAGTGAAGAGTGA GGTCAAGGCCCAAGAGGGCGAATAAGAACCAAG	840
Db	781	GAGTTTCCCGCCGACAGTGAAGAGTGA GGTCAAGGCCCAAGAGGGCGAATAAGAACCAAG	840
QY	841	GACGGCAGCTTAAGGCCAAGGAAGAAAGCA CCGGGACCAAGTAGAGTGTGAGAGCC	900
Db	841	GACGGCAGCTTAAGGCCAAGGAAGAAAGCA CCGGGACCAAGTAGAGTGTGAGAGCC	900
QY	901	AGGGCGAGCGAGGAGGTCA GAGAGACAGCA CGTGTGGCCAGCGACGGCAGCATGGAGGT	960
Db	901	AGGGCGAGCGAGGAGGTCA GAGAGACAGCA CGTGTGGCCAGCGACGGCAGCATGGAGGT	960
QY	961	ANGAAGGCA GCA CCAAA GTTAGAGAA CACATGAAGGCAAGACAGAGGTTCGCA CAGAG	1020
Db	961	ANGAAGGCA GCA CCAAA GTTAGAGAA CACATGAAGGCAAGACAGAGGTTCGCA CAGAG	1020
QY	1021	GTCAACCACTGACAGTCTGGGTGAAGTGA CTA GGAATTGTGGAAGACGACATC	1080
Db	1021	GTCAACCACTGACAGTCTGGGTGAAGTGA CTA GGAATTGTGGAAGACGACATC	1080
QY	1081	AATTTTCAGTGAAGATGACGTTCGAGGCA GTGAACATCCCGAGAGGCTCCACCCAGTGT	1140
Db	1081	AATTTTCAGTGAAGATGACGTTCGAGGCA GTGAACATCCCGAGAGGCTCCACCCAGTGT	1140
QY	1141	CGTAAACGCAACAGCA CCGCTCTCTCTGCGCCAGGTCTACACAGTGCCTTAAAGTG	1200
Db	1141	CGTAAACGCAACAGCA CCGCTCTCTCTGCGCCAGGTCTACACAGTGCCTTAAAGTG	1200
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Db	1201	ATCTTCATCATATTTTCTCCATGTGCTATCC TGGGGCCCTTACGTGCTTTTACAGATC	1260
QY	1261	CTGGCCGTGTGGGTGATGTGAAACCCAGGTACCCCAAGTGGGTATCA CCAATAATCATC	1320
Db	1261	CTGGCCGTGTGGGTGATGTGAAACCCAGGTACCCCAAGTGGGTATCA CCAATAATCATC	1320
QY	1321	TGGCTTTTCTTCCTGCA GTGCA TCCACCCCTATGTCTATAGCTACATGCACAAGAC	1380

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Db	1381	ATTAAGAGAGAAATCCAGGACATGCTGTAAGAGTTCTTCTGCAGAGAAAAGCCCCGAGAA	1440
Qy	1441	GAAAGTAGCCACCCGAGACCTGCCCGGAAACAGAGGGGTGGAGCTGAAGGCAGATTGTCCCT	1500
Db	1441	GAAAGTAGCCACCCGAGACCTGCCCGGAAACAGAGGGGTGGAGCTGAAGGCAGATTGTCCCT	1500
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RESULT 15			
ID	ABV73366	standard; DNA; 1527 BP.	
XX	ABV73366;		
AC			
XX			
XX			
XX	22-JAN-2003	(first entry)	
DT			
DE	Human TGR36 polypeptide encoding DNA.		
XX			
KW	G-protein coupled receptor; GPCR; antipsoriatic; antiinflammatory;		
KW	antihypertensive; neurotrophic; neuroprotective; antianemic; antifungal;		
XX	antiparkinsonian; antihypertensive; TGR36; gene; de.		
OS	Homo sapiens.		
XX			
FX	Key	Location/Qualifiers	
FT	CDS	1..1527	
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FT		/product= "TGR36"	
FT		/note= "GPCR polypeptide"	
PN	WO200277001-A2.		
PD			
XX	03-OCT-2002.		
XX			
XX	08-MAR-2002; 2002MO-US007171.		
PR			
PR	09-MAR-2001; 2001US-00802803.		
PR	16-MAR-2001; 2001US-0276649P.		
XX			
PA	(TULSA-) TULARIX INC.		
XX			
PI	Tian H, Zhao J, Chen J, Cutler G;		
DR	WPI: 2003-018881/01.		
XX	P-PSDB; ABB82501.		
XX			
PT	New G-protein coupled receptor polypeptides and polynucleotides useful		
PT	for identifying compounds for treating a TGR-associated disorder, e.g.		
PT	psoriasis, inflammatory bowel disease, hyperlipidemia, Parkinson's		
XX	disease, anemia.		
PS	Claim 6; Page 64-65; 87pp; English.		
XX			
CC	The invention relates to G-protein coupled receptor (GPCR) polypeptides		
CC	and encoding polynucleotides selected from TGR20, TGR35, TGR36, TGR183,		
CC	TGR341, TGR211, TGR216 and TGR79. The polypeptides and nucleic acids are		
CC	useful for identifying compounds for treating a TGR-associated disorder,		
CC	such as psoriasis, inflammatory bowel disease, hyperlipidemia,		
CC	Parkinson's disease, Huntington's disease, anemia, immune and blood		
CC	disorders, ulcerative colitis, Crohn's disease or spleen enlargement.		
CC	They are also useful for identifying cells such as kidney, liver,		
CC	hypothalamus, colon, adipose, or spleen cells, for forensics and		
CC	paternity determination, diagnosing diseases and examining signal		
CC	transduction. The present sequence represents a human TGR36 polypeptide		
CC	encoding DNA		

XX Sequence 1527 BP, 347 A, 439 C, 420 G, 321 T, 0 U, 0 Other;
SQ
Query Match 99.9%; Score 1525.4; DB 8; Length 1527;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 ATGACGTCCACCTGCAACCAACGACGCGGAGAGTAACAGACGCCACAGTGCATGCC 60
QY 61 CTCTCCAAATATGCCCATCAGCCTTGGCCCAAGGATATCCTGCTCAACCGTGTGTTATC 120
DB 61 CTCTCCAAATATGCCCATCAGCCTTGGCCCAAGGATATCCTGCTCAACCGTGTGTTATC 120
QY 121 TTCCTGCGCGCCCTTTTCGTGGCAACATATGCTGCGCTAGTGTGACGCGCAAGCG 180
DB 121 TTCCTGCGCGCCCTTTTCGTGGCAACATATGCTGCGCTAGTGTGACGCGCAAGCG 180
QY 181 CAGCTGCTCAGGTGACCAACCGTTTATCTTTTAACTCTCGTCAACCGACTGTGAC 240
DB 181 CAGCTGCTCAGGTGACCAACCGTTTATCTTTTAACTCTCGTCAACCGACTGTGAC 240
QY 241 ATTTCCCTGTGGCCCCCTGTGGGTGGCCACTCTGTGCTCTTCTTGGCCCCCTCAAC 300
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DB 661 AGGCAAGCATGCTCTGCTGTAACAATGTCAGAGACACAGCTTGGAAAGTGGAGTCAAGAC 720
QY 721 TGTGTGAAGATGAGGATGAAGGAGGAGAGAGAAAGAGAGATTCCAGATGAGAT 780
DB 721 TGTGTGAAGATGAGGATGAAGGAGGAGAGAGAAAGAGAGATTCCAGATGAGAT 780
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DB 781 GAGTTTTCGCGCCAGCATGAGGTGAGGTCAAGGCCAAGGAGGAGAAATGAAAGCCAAAG 840
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DB 841 GACGCAAGCTTGAAGGCCAAAGAGAGACGCGGACCAAGTGAAGTGTGAGAGCC 900
QY 901 AGGGGAGAGAGAGGTCAAGAGAGACAGCAGTGGCCAGCAGCAGCATGAGAGGT 960
DB 901 AGGGGAGAGAGAGGTCAAGAGAGACAGCAGTGGCCAGCAGCAGCATGAGAGGT 960
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DB 961 AAGGAAGGAGACCAAAAGTTGAGAGAAACAGCATGAAGGAGAGCAAGGTCGACAGAG 1020

DB 961 AAGGAAGGAGACCAAAAGTTGAGAGAAACAGCATGAAGGAGAGCAAGGTCGACAGAG 1020
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DB 1021 GTCAACCAAGTGAAGCATTTGACTTGGGTGAAGTACATGAGAGTTTGGTGAAGACGACATC 1080
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DB 1141 CGTAAAGAGAACAGCAACCTCCTGCGCAGAGTGTACAGATGCAAAAGCTGTAAGTG 1200
QY 1201 ATCTTCATCATATTTTCTCTATGTCATCCCTGAGGCCCTTACCTGCTTTTATGACATC 1260
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QY 1261 CTGGCCGTGTGGGTGAGTGTGAACCCAGGTACCCCAAGTGGGTGATCAACATATCATC 1320
DB 1261 CTGGCCGTGTGGGTGAGTGTGAACCCAGGTACCCCAAGTGGGTGATCAACATATCATC 1320
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DB 1501 TCTTACGATTCTGTCTACTTTTCTTGA 1527

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Job time : 665 secs

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OM nucleic - nucleic search, using sw model

Run on: December 10, 2005, 00:09:47 ; Search time 214 Seconds
(without alignments)

12663.816 Million cell updates/sec

Title: US-10-712-615-1

Perfect score: 1527

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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Maximum DB seq length: 200000000

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1522.4	99.7	2781	3	US-10-314-048A-103
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6	98.4	6.4	1776	2	US-08-722-001-29
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8	98.4	6.4	2140	2	US-08-334-698-1
9	98.4	6.4	2140	2	US-08-228-932-1
10	98.4	6.4	2140	2	US-08-468-939-1
11	98.4	6.4	2140	2	US-08-406-855A-1
12	98.4	6.4	2140	2	US-08-722-190-1
13	98.4	6.4	2140	3	US-08-244-354-1
14	98.4	6.4	2140	3	US-09-206-899-1
15	98.4	6.4	2140	3	US-09-444-783-1
16	98.4	6.4	2140	3	US-09-688-415-1
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18	98.4	6.4	2140	6	PCT-US95-04203-1
19	97.7	6.4	1382	2	US-09-364-425B-22
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21	97.2	6.0	1584	3	US-09-016-434-284
22	92.2	6.0	1047	3	US-08-540-650B-6
23	92.2	6.0	1050	3	US-09-826-509-502
24	92.2	6.0	1053	3	US-09-016-434-1423

25	92.2	6.0	1882	3	US-08-540-650B-11	Sequence 11, Appl
26	92.2	6.0	3083	3	US-08-693-308-1	Sequence 1, Appl
27	90.4	5.9	1050	3	US-09-762-661A-1	Sequence 1, Appl
28	86.4	5.7	2481	2	US-08-467-568-1	Sequence 1, Appl
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44	84	5.5	2004	2	US-08-722-001-11	Sequence 11, Appl
45	84	5.5	2290	3	US-09-016-434-1368	Sequence 1368, Ap

ALIGNMENTS

RESULT 1
US-10-314-048A-15
Sequence 15, Application US/10314048A
Patent No. 6902902
GENERAL INFORMATION:
APPLICANT: Unetl, David J.
APPLICANT: Chen, Ruoping
APPLICANT: Richman, Jeremy
APPLICANT: Connolly, Daniel
APPLICANT: Dang, Huong T.
APPLICANT: Choi, Bryan
APPLICANT: Leonard, James
APPLICANT: Hakak, Yaron
APPLICANT: Liaw, Chen
APPLICANT: Lowitz, Kevin P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
FILE REFERENCE: 22, US6, CIP
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: US/10/314,048A
PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 10/096,511
PRIOR FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 09/995,543
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 60/399,917
PRIOR FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 60/404,761
PRIOR FILING DATE: 2002-09-13
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 1527
TYPE: DNA
ORGANISM: Homo sapiens
US-10-314-048A-15
Query Match 99.9%; Score 1525.4; DB 3; Length 1527;
Best Local Similarity 99.9%; Pred No. 0;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 ATGAGCTGCACTGCAACCAAGCAGCGCCGAGAGTAAACAGACCAACGCTGATGCC 60
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 Oy 361 ACCATTTGCTGTGAGCGCCCTGTGGTGTGGCAGCTGTGTGCTCTCTTGTGCGCCCTCAAC 420
 Db 361 ACCATTTGCTGTGAGCGCCCTGTGGTGTGGCAGCTGTGTGCTCTCTTGTGCGCCCTCAAC 420
 Oy 421 TTCAAAGATGACCCAGCGCCGCTTAACTGTCTCTATGAGCACTGTGAGTTGTGCGCATC 480
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 Db 541 CTCTGCTCATGATCTGAGGCGCGCCAGCGCCAGCTCACTATTTCTAGGCTGTGCTTTC 600
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RESULT 2
 US-10-314-048A-103
 ; Sequence 103, Application US/10314048A
 ; Patent No. 6902902
 ; GENERAL INFORMATION:
 ; APPLICANT: Unetec, David J.
 ; APPLICANT: Chen, Ruoping
 ; APPLICANT: Richman, Jeremy
 ; APPLICANT: Connolly, Daniel
 ; APPLICANT: Dang, Huong T.
 ; APPLICANT: Choi, Bryan
 ; APPLICANT: Leonard, James
 ; APPLICANT: Hakak, Yaron
 ; APPLICANT: Liaw, Chen
 ; APPLICANT: Lowitz, Kevin P.
 ; APPLICANT: Behan, Dominic P.
 ; APPLICANT: Chalmers, Derek T.
 ; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
 ; FILE REFERENCE: 22, US6, CIP
 ; CURRENT APPLICATION NUMBER: US/10/314, 048A
 ; CURRENT FILING DATE: 2002-12-06
 ; PRIOR APPLICATION NUMBER: 10/096, 511
 ; PRIOR FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: 09/995, 543
 ; PRIOR FILING DATE: 2001-11-27
 ; PRIOR APPLICATION NUMBER: 60/399, 917
 ; PRIOR FILING DATE: 2002-07-29
 ; PRIOR APPLICATION NUMBER: 60/404, 761
 ; PRIOR FILING DATE: 2002-08-19
 ; PRIOR APPLICATION NUMBER: 60/410, 747
 ; PRIOR FILING DATE: 2002-09-13
 ; NUMBER OF SEQ ID NOS: 161
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 103
 ; LENGTH: 2781
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens and Rat
 ; US-10-314-048A-103

Query Match 99.7%; Score 1522.4; DB 3; Length 2781;
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 1523; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	1	ATGAGCTCACCTGACCAAGACGCGGAGAGTAACAGCAGCCACAGTCATGCCC	60	
DB	1	ATGAGCTCACCTGACCAAGACGCGGAGAGTAACAGCAGCCACAGTCATGCCC	60	
QY	61	CTCTCCAAATGCGCCATCAGCCTGGCCCAAGGCATATCCGCTCAACCGTGTGTTATC	120	
DB	61	CTCTCCAAATGCGCCATCAGCCTGGCCCAAGGCATATCCGCTCAACCGTGTGTTATC	120	
QY	121	TTCTCTGCGCGCTCTTTCTGCGCAATATGCTGGCGCTATGTTTGAAGCCAGCCG	180	
DB	121	TTCTCTGCGCGCTCTTTCTGCGCAATATGCTGGCGCTATGTTTGAAGCCAGCCG	180	
QY	181	CAGCTGCTCAGGTGACCAACGTTTATCTTAACTCTGCTGACCGACCTGCTGACG	240	
DB	181	CAGCTGCTCAGGTGACCAACGTTTATCTTAACTCTGCTGACCGACCTGCTGACG	240	
QY	241	ATTTGCTGTGGCCCCCTGGGTGGGCACTGTGTGCTCTTCTGGCCCCCTCAAC	300	
DB	241	ATTTGCTGTGGCCCCCTGGGTGGGCACTGTGTGCTCTTCTGGCCCCCTCAAC	300	
QY	301	AGCCATTCTGACGCGCCCTGTGTTAGCTTCACTCCTGTGGCTTCCGACGCTCAAC	360	
DB	301	AGCCATTCTGACGCGCCCTGTGTTAGCTTCACTCCTGTGGCTTCCGACGCTCAAC	360	
QY	361	ACCATTTCTGTGTGTCATGATGCTGCTCTTGTCCATATCCACCTCTCTCAACCG	420	
DB	361	ACCATTTCTGTGTGTCATGATGCTGCTCTTGTCCATATCCACCTCTCTCAACCG	420	
QY	421	TCCAAAGATGACCGACGCGCGGTATCTGCTCTCTATGAGCACTGATTTGTGGCANTC	480	
DB	421	TCCAAAGATGACCGACGCGCGGTATCTGCTCTCTATGAGCACTGATTTGTGGCANTC	480	
QY	481	CTGCGAGAGCACTCTCCTCACTTACGCGCTGGGCGCAGGCTGCTTATGAGCCCAATGCT	540	
DB	481	CTGCGAGAGCACTCTCCTCACTTACGCGCTGGGCGCAGGCTGCTTATGAGCCCAATGCT	540	
QY	541	CTCTGCTCATGATCTGGGGGCGCAGCCGACGTAACATACTTCAAGCGTGTGCTTCT	600	
DB	541	CTCTGCTCATGATCTGGGGGCGCAGCCGACGTAACATACTTCAAGCGTGTGCTTCT	600	
QY	601	ATCGTCACTTCACTGATGATGATGCTGCTACTCCGCTGCTTCTGTGACGCGCG	660	
DB	601	ATCGTCACTTCACTGATGATGATGCTGCTACTCCGCTGCTTCTGTGACGCGCG	660	
QY	661	AGGACGATGCTCTGCTGTATCAATGTCAAGAGACACAGCTTGGAGTGCAGTCAAGAC	720	
DB	661	AGGACGATGCTCTGCTGTATCAATGTCAAGAGACACAGCTTGGAGTGCAGTCAAGAC	720	
QY	721	TGTGTGGAATATGAGATGAAAGGAGCAGAGAAAGAGAGATTTCCAGATGAGACT	780	
DB	721	TGTGTGGAATATGAGATGAAAGGAGCAGAGAAAGAGAGATTTCCAGATGAGACT	780	
QY	781	GAGTTTCCGCGCAGCATGAAAGGTGAGGTCAAGGCCAAGAGGGCAGATGAAAGCAAG	840	
DB	781	GAGTTTCCGCGCAGCATGAAAGGTGAGGTCAAGGCCAAGAGGGCAGATGAAAGCAAG	840	
QY	841	GACGCGAGCTTGAAGCCCAAGAAAGCAAGGAGCAAGTGAAGTGTATGAGGCC	900	
DB	841	GACGCGAGCTTGAAGCCCAAGAAAGCAAGGAGCAAGTGAAGTGTATGAGGCC	900	
QY	901	AGGGGCGAGGAGAGGTCAAGAGAGCAGCAGTGTGCGCAGCGCAGCATGAGAGGT	960	
DB	901	AGGGGCGAGGAGAGGTCAAGAGAGCAGCAGTGTGCGCAGCGCAGCATGAGAGGT	960	
QY	961	AAGGAAGGCGACCAAAAGTTGAGAGAAAGCAGTGAAGGCGACAAAGGTTCGACAGAG	1020	
DB	961	AAGGAAGGCGACCAAAAGTTGAGAGAAAGCAGTGAAGGCGACAAAGGTTCGACAGAG	1020	
QY	1021	GTCACCAAGTGCAGCATTTGACTTGGGTGAAGATGACATGAGTTTGTGAAGACGACATC	1080	
DB	1021	GTCACCAAGTGCAGCATTTGACTTGGGTGAAGATGACATGAGTTTGTGAAGACGACATC	1080	

QY	1081	AATTTCAGTGAGATGACCTGAGGCAAGTGAACATCCCGAGAGCCTCCACCACTGCT	1140	
DB	1081	AATTTCAGTGAGATGAGCTGAGGCAAGTGAACATCCCGAGAGCCTCCACCACTGCT	1140	
QY	1141	CGTAACAGCAACAGCAACCTCTCTGCGCAGGTGCTACAGTGCAGAACTGTAAAGT	1200	
DB	1141	CGTAACAGCAACAGCAACCTCTCTGCGCAGGTGCTACAGTGCAGAACTGTAAAGT	1200	
QY	1201	ATCTTCATCATATTTTCTTATGATGCTATCCCTGGGGCCCTAAGCTTTTATGAGATC	1260	
DB	1201	ATCTTCATCATATTTTCTTATGATGCTATCCCTGGGGCCCTAAGCTTTTATGAGATC	1260	
QY	1261	CTGGCCGTGTGGGTGATGTCAGAACCCAGGTACCCCAAGTGGGTATCCATATATC	1320	
DB	1261	CTGGCCGTGTGGGTGATGTCAGAACCCAGGTACCCCAAGTGGGTATCCATATATC	1320	
QY	1321	TGGCTTTTCTTCTGACAGTGTGATCCACCCCTATGTCTATGAGCTACATGACAGACC	1380	
DB	1321	TGGCTTTTCTTCTGACAGTGTGATCCACCCCTATGTCTATGAGCTACATGACAGACC	1380	
QY	1381	ATTAAAGAAATCCAGGACATGCTGAAGAGTTCTTGAAGGAAAGCCCCGAAA	1440	
DB	1381	ATTAAAGAAATCCAGGACATGCTGAAGAGTTCTTGAAGGAAAGCCCCGAAA	1440	
QY	1441	GAAATAGGCAACCAAGACCTGCCCCGGAACAGAGGTGGAGCTGAAGCAAGATTGCTCT	1500	
DB	1441	GAAATAGGCAACCAAGACCTGCCCCGGAACAGAGGTGGAGCTGAAGCAAGATTGCTCT	1500	
QY	1501	TCCTACGATTCGTACTTTTCTT	1524	
DB	1501	TCCTACGATTCGTACTTTTCTT	1524	

RESULT 3
US-10-314-048A-91
Sequence 91, Application US/10314048A
Patent No. 6902902
GENERAL INFORMATION:
APPLICANT: Unetel, David J.
APPLICANT: Chen, Kuoping
APPLICANT: Richman, Jeremy
APPLICANT: Connolly, Daniel
APPLICANT: Dang, Huang T.
APPLICANT: Choi, Bryan
APPLICANT: Leonard, James
APPLICANT: Hakak, Yaron
APPLICANT: Liaw, Chen
APPLICANT: Lowitz, Kevin P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
FILE REFERENCE: 22 US6, CIP
CURRENT APPLICATION NUMBER: US/10/314, 048A
PRIOR FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: 10/096, 511
PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/995, 543
PRIOR FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/399, 917
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 60/404, 761
PRIOR FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 60/410, 747
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn version 3.1
SEQ ID NO 91
LENGTH: 1527
TYPE: DNA
ORGANISM: Homo sapiens

US-10-314-048A-91

Query Match 99.6%; Score 1520.6; DB 3; Length 1527;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1523; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 ATGAGTTCACCTGACCAACGACGCGGAGATGACAGCCACACGTCGATGCC 60
DB 1 ATGAGTTCACCTGACCAACGACGCGGAGATGACAGCCACACGTCGATGCC 60
QY 61 CTCTCAAAATGCCATCAGCTGGGCGGACGATCATCGCTCAACGGCTGGTTATC 120
DB 61 CTCTCAAAATGCCATCAGCTGGGCGGACGATCATCGCTCAACGGCTGGTTATC 120
QY 121 TTCTCGCGCGCTCTTTCGTGCGCAACATAGTGTGCGCGTAGTGTGCGCAAGCGG 180
DB 121 TTCTCGCGCGCTCTTTCGTGCGCAACATAGTGTGCGCGTAGTGTGCGCAAGCGG 180
QY 181 CAGCTGTGCAAGTGAACCAACCGTTTATCTTTAACCTTCTGTCACGACCTGTCGAG 240
DB 181 CAGCTGTGCAAGTGAACCAACCGTTTATCTTTAACCTTCTGTCACGACCTGTCGAG 240
QY 241 ATTTGGCTGTGCGCGCGGTTGAGTGTGCGACCTGTGTCCTGTTCTGGCGCCGTCAC 300
DB 241 ATTTGGCTGTGCGCGCGGTTGAGTGTGCGACCTGTGTCCTGTTCTGGCGCCGTCAC 300
QY 301 AGCCACTTGTGACGCGCCCTGTGTTAGCTTACCCACCTGTTGCGCTTCCGACGCTCAAC 360
DB 301 AGCCACTTGTGACGCGCCCTGTGTTAGCTTACCCACCTGTTGCGCTTCCGACGCTCAAC 360
QY 361 ACCATTGTGTGTGTGATGATGCTATCTTGTGATGATGATGATGATGATGATGATGATG 420
DB 361 ACCATTGTGTGTGTGATGATGCTATCTTGTGATGATGATGATGATGATGATGATGATG 420
QY 421 TCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 421 TCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 481 CTGACAGACGCTCTCTCACTCTTACCGGCTGCGGCGCAGCTGCTTGTGATGAGCGCATGCT 540
DB 481 CTGACAGACGCTCTCTCACTCTTACCGGCTGCGGCGCAGCTGCTTGTGATGAGCGCATGCT 540
QY 541 CTCTGTCTCATATATCTGCGGCGGCGCAGCCGACGTCATATCTTCTGAGCTGTGCTTTC 600
DB 541 CTCTGTCTCATATATCTGCGGCGGCGCAGCCGACGTCATATCTTCTGAGCTGTGCTTTC 600
QY 601 ATGCTCATTTCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
DB 601 ATGCTCATTTCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 661 AGGCAAGCATGCTCTGTGTATCAATGTCAAGAGACACAGCTTGGAGTGCAGTCAAGAC 720
DB 661 AGGCAAGCATGCTCTGTGTATCAATGTCAAGAGACACAGCTTGGAGTGCAGTCAAGAC 720
QY 721 TGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
DB 721 TGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 781 GAGTTTCGCGCGGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
DB 781 GAGTTTCGCGCGGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 841 GACGCGACGCTGAAGGCAAGGACGAGGACGAGGACGAGTGTGAGTGTGAGGCGC 900
DB 841 GACGCGACGCTGAAGGCAAGGACGAGGACGAGGACGAGTGTGAGTGTGAGGCGC 900
QY 901 AGGCGGACGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
DB 901 AGGCGGACGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
QY 961 AAGGAAGGACGACCAAAATGTTGAGGAAACAGATGATGATGATGATGATGATGATGATGATG 1020
DB 961 AAGGAAGGACGACCAAAATGTTGAGGAAACAGATGATGATGATGATGATGATGATGATGATG 1020
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QY 1021 GTCAACGATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
DB 1021 GTCAACGATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1081 AATTTCACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
DB 1081 AATTTCACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1141 CGTAACAGCAACAGCAACCTCTCTGCGCAGGTGTCTACAGTGCMAAGCTGTAAAGTG 1200
DB 1141 CGTAACAGCAACAGCAACCTCTCTGCGCAGGTGTCTACAGTGCMAAGCTGTAAAGTG 1200
QY 1201 ATCTTCATCATATTTTCTCTATGTGTATCTCTGCGGCGCTTACTGCTTTTATGACATC 1260
DB 1201 ATCTTCATCATATTTTCTCTATGTGTATCTCTGCGGCGCTTACTGCTTTTATGACATC 1260
QY 1261 CTGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
DB 1261 CTGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
QY 1321 TGGCTTTTCTTCTGCAAGTGTGATCCACCCCTATGTCTATGCTATCATGACACAAAGCC 1380
DB 1321 TGGCTTTTCTTCTGCAAGTGTGATCCACCCCTATGTCTATGCTATCATGACACAAAGCC 1380
QY 1381 ATTAAGAGAAATTCAGGACATGCTGAAGAGTTCTTTCGAAGAAAGCCCCCGAAA 1440
DB 1381 ATTAAGAGAAATTCAGGACATGCTGAAGAGTTCTTTCGAAGAAAGCCCCCGAAA 1440
QY 1441 GAAGATACCAACCCAGACCTCCCGGAAACAGAGGTTGGGACTGAAGGCAAGATTGTCCCT 1500
DB 1441 GAAGATACCAACCCAGACCTCCCGGAAACAGAGGTTGGGACTGAAGGCAAGATTGTCCCT 1500
QY 1501 TCCTAGATTCGTACTTTTCTTGA 1527
DB 1501 TCCTAGATTCGTACTTTTCTTGA 1527

RESULT 4
US-08-233-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZGPT-F15
US-08-232-463-14

Query Match 6.8%; Score 103.8; DB 2; Length 7218;
Best Local Similarity 3.8%; Pred. No. 2,4e-16;
Matches 15; Conservative 264; Mismatches 116; Indels 0; Gaps 0;

QY 686 TCAGAGACACAGCTTGGAAGTCCAGTCAAGAGCTGTGTGAGAAATGAGATGAAGAG 745
DB 1458 TAAAGAGATAGAAATTTGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1399
QY 746 GAGCAGAGAGAGAGAGAGATTCCAGATGAGAGTTCGCCGCCAGCATGAAGTG 805
DB 1398 RRR 1339
QY 806 AGTCAGAGCCAGAGAGAGAGATGAGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 865
DB 1338 RRR 1279
QY 866 GAGCAGAGAGAGAGAGAGAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 925
DB 1278 RRR 1219
QY 926 GAGCAG 985
DB 1218 RRR 1159
QY 986 AGAAGCAGTGAAG 1045
DB 1158 RRR 1099
QY 1046 GTGAAGATGACATGAGATTGTGAGAGAGACATC 1080
DB 1098 RRR 1064

RESULT 5
US-08-722-001-13
; Sequence 13, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huft, Joel R.
; APPLICANT: Neerberg, Jennie B.
; APPLICANT: Lee, Hee-Yoon
; APPLICANT: Bell, Ian M.
; TITLE OF INVENTION: ALPHALIC ADRENALINIC RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,001

FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,276
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19169Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3462
TELEFAX: (908) 594-4720
TELEX: 138825
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULAR TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-722-001-13

Query Match 6.4%; Score 98.4; DB 2; Length 1621;
Best Local Similarity 50.7%; Pred. No. 3e-15;
Matches 293; Conservative 276; Mismatches 276; Indels 9; Gaps 2;

QY 85 GCCCAGGATATCCGCTCAACCGTGTGTTATCTCTCGCCGCTTTCTGTCGC 144
DB 209 GCGCAGGGGCTGGGGGCGTCTTCCGAGAGCCCTTATGAGCCCTGAGAGT 268
QY 145 AACATAGTCTGCGCTAGTGTGACAGGAGCCGAGCTGAGTGACCAACGT 204
DB 269 AACCTGTTGTATCTCTCAAGTGGCTGCAACCGCAGCTTCAAGCTTCACTAT 328
QY 205 TTATCTTAACTCTCTGTCACGAGCTGTGAGATTTGCTGAGCCCTCGAGTG 264
DB 329 TTATCTGTAACCTGCGGTGCGGAGCTGCTGAGGCGACCGTACTGAGCTTCTG 388
QY 265 GTGGCAGCTCTGTGCTCTCTTCTGAGCCCTCAACAGCACTTGTGACGCGCTGTT 324
DB 389 GCCACATGAGAGTTCTGGGCTTCTGGGCTTGGCCGCTTCTGCGACGTATGAGGCC 448
QY 325 AGCCACCCACCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 384
DB 449 GCCGTGAGAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 508
QY 385 CGCTACTGTCCATGATCCACCTCTCTCTCAACCGCTCCAGATGACCGAGCGCGGT 444
DB 509 CGGTACGTGGGCTGCGGACCTCACTCAAGTACCAAGCATATGACGAGCGCAAGGG 568
QY 445 TACTGCTCTCTATAGCAGCTGATGATGAGGATCTGAGAGAGACTTCTCACTTAC 504
DB 569 GCCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 628
QY 505 GCGTGGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 564
DB 629 GCGTGGAGAGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 683
QY 565 AGCCGAGTCACTATTTCTGAGCGTGTGCTTCAATGATTCATTCATGATTCATGATTCATG 624
DB 684 -----CGGCTAGGCTGTCTTCTCTCCGCTGCTGCTCTTCTACTGCTGCTGCTGCTGCT 739
QY 625 ATGCTGCTACTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 662
DB 740 GTGTCACTACTGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777

RESULT 6
US-08-722-001-29
; Sequence 29, Application US/08722001
; Patent No. 5760054

GENERAL INFORMATION:
APPLICANT: Thompson, Wayne J.
APPLICANT: Huff, Joel R.
APPLICANT: Nerenberg, Jennie B.
APPLICANT: Lee, Hee-yeon
APPLICANT: Ball, Ian M.
TITLE OF INVENTION: ALPHALC ADRENERGIC RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,001
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,276
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19169Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3462
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-722-001-29

Query Match 6.4%; Score 98.4; DB 2; Length 1776;
Best Local Similarity 50.7%; Pred. No. 3.1e-15;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;
QY 85 GCCACGGCATCATCGCTCAACCGGCTGATTATCTTCCTGCGCCCTCTTTCGTGGC 144
DB 337 GCGCAGGGGCTGGGCGCTGCTCTTCTGCGAGCTTATCTTATGCGCGTGGAGGT 396
QY 145 AACATAGTGTGCGCTAGTGTGACGCGCAAGCCGACGCTGTGAGGTGACCAACCGT 204
DB 397 AACGTGCTGTATCTCTCAAGTGGCGTCAACCGCACCTGAGACCGTCAACCACTAT 456
QY 205 TTTATCTTAACTCTCTGTCAACCGACGCTGTGCAATTTGGTGTGGCCCTTGGGGT 264
DB 457 TTCATCGTGAACCTGGCCGTGGCCGACCTGTGCTAGAGCGCACCTACTGTGCTTCTG 516
QY 265 GTGGCCACTGTGTGCTCTCTTCTGGGCGCCCTCAACGAGCACTTTCGACGCGCGTGT 324
DB 517 GCCACATGAGAGTTTGGGCTTCTGGGCTTGGCGCGCTTCTGCACTGATGGGCC 576
QY 325 AGCCTACCCACCTGTTCGCTTTCGCGACGCTCAACACCATTTGTGTTGTCAGTGGAT 384
DB 577 GCGGTGAGAGTGTGTGCTGACGAGGCTTCATCTCAGCTTCGACACATCTTCGTGAGC 636
QY 385 GCGTACTTGTTCATCATCAACCTCTCTCTCAACCGCTTCAAGATGACCAAGCGCGCGGT 444
DB 637 CGGTACGTGGGCGTGGCGCACTCACTCAAGTACCCAGCATCATGACGAGCGCAGGCG 696

QY 445 TACTGTCTCTATAGCACTGATTTGSCCATCTGCAAGACATCTTCACCTTAC 504
DB 697 GCCGCATCTGAGCCCTCTGCTGGGTGATGAGTGTGTCGATGAGGCGCCCTGCTG 756
QY 505 GCGTGGGCGCGGCTGCTTGTGATGAGGCAATGTCTCTGCTCCATGATCTGGGGGCC 564
DB 757 GCGTGAAGAGAGCCGTCGCCCCCTGA--CGAGCGCTTCTCGGTATACCGAGAGG-- 811
QY 565 AGCCCACTACATATTCTGAGCGTGTGCTTTCATGTCATTCATTCATGATTGTATG 624
DB 812 ----CGGCTAGCGTGTCTTCTCCGCTGTGCTCTTCTACCTGCACTGAGCGGTATC 867
QY 625 ATTGCTCTACTCCGCTGTGTTCTGTGACGCCGCGAG 662
DB 868 GTGTCAATGATGCGCGGTGATCGTGTGCGGCGAG 905

RESULT 7
US-09-016-434-1172
Sequence 1172, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Selhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1172:
SEQUENCE CHARACTERISTICS:
LENGTH: 2002 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g177806
US-09-016-434-1172
Query Match 6.4%; Score 98.4; DB 3; Length 2002;
Best Local Similarity 50.7%; Pred. No. 3.3e-15;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;
QY 85 GCCACGGCATCATCGCTCAACCGTGTGATTATCTTCGCGCCCTCTTTCGTGGC 144
DB 209 GCGCAGGGGCTGGGCGTGGCGCTTCTCTGCGAGCTTATCTTATGAGCCGTGCAAGT 268

Oy	145	AACATAGTCTGGCGCTAGTGTGGACGCGAACCCGAGCTGCTGGACAGGTACCAACCGT	204
Db	269	AACCTGCTGTATCTCTTCAGTGGCTGCACCCGACCTTGACAGACCTTCACCACTAT	328
Oy	205	TTTATCTTTAACTCTCTCGTCAACCGACTGCTGCAGATTTGCTGTGGCCCCCTGGGTG	264
Db	329	TTCAATGTGAACCTGGCCGCGTGGCGAAGCTGTCTAGAGCGCCACACGTACTGCCCCCTCG	388
Oy	265	GTGGCCACTCTGTGCTCTCTTTGTGGCCCCCTCAACAGCCATTCTTGACAGGCCCTTGTT	324
Db	389	GCCACCATGAGAGTTCCTGGGCTCTTGCGGCTTGCGCGCGCCTTCTGCGACGATAGGAGCC	448
Oy	325	AAGCTCACCCACTCTGTGCGCTTTCGGCTTCCGACAGGTCAACACATTTGTCTTGGTGTCAATGAT	384
Db	449	GCGGTGAAGTGTCTGTGCTGCACAGGCGCTTCATCTCAGCCTCTGCACCACTCTCCGTGGAC	508
Oy	385	CGCTACTTGTCAATATTCACCCCTCTCTCCACCCGTCGAAGTGAACCCAGCGCCGGGCT	444
Db	509	CGGTAGTGGGGGTGGCGCCACTTACTACAGTACCCAGCAATCAATGACCGAGCCGCAAGGCG	568
Oy	445	TACCTGCTCTCTATGAGCACTGATTTGTGGCATCTCTGCAGAGCACTCTTCACATCTAC	504
Db	569	GCGCGCATCTGGCCCTGCTCTGGGTGTGAAGCCCTGTGTGTTCGTGAGGCCCCCTGCTG	628
Oy	505	GCGTGGGGGCGACAGCTGCGCTTTGATGAAGCGCAATGCTCTGTCTGCATGATCTGGGGGGCC	564
Db	629	GCGTGAAGAGACCCGTCGCCCTTGA---GAGCGCTTCTTGGCGGTATCAACGAGGAGG--	683
Oy	565	AGCCCAAGTAACTATTTCTCAAGCGGTGTCTCTTATGTGTCAATTTGCACCTGATTTGTATG	624
Db	684	----GGGGTACGCTGTCTTCTCTCCGATGTCTCTTACCTGCCCCATGCGCGTATC	739
Oy	625	ATTGCTGTACTCCGGTGAGTTCTGTGACGCCGGAG	662
Db	740	GTGTATATACTGCCCGCGTACAGTGTGCGCCGAG	777

RESULT 8
US-08-334-698-1
Sequence 1, Application US/08334698
Patent No. 5556755
GENERAL INFORMATION:
Applicant: Jonathan A. Bard et al.
Title of Invention: DNA Encoding Human Alpha 1 Adrenergic
Title of Invention: Receptors and Uses Thereof
Number of Sequences: 6
Correspondence Address:
Addresser: COOPER & DUNHAM
Street: 30 Rockefeller Plaza
City: New York
State: New York
Country: U.S.A.
Zip: 10112
COMPUTER READABLE FORM:
Medium Type: Floppy disk
Computer: IBM PC compatible
Operating System: PC-DOS/MS-DOS
Software: Patent in Release #1.24
Current Application Data:
Application Number: US/08/334,698
Filing Date:
Classification: 435
Prior Application Data:
Application Number: US/07/952,798
Filing Date:
Attorney/Agent Information:
Name: White, John P.
Registration Number: 28,678
Reference/Docket Number: 376901
Telecommunication Information:
Telephone: (212) 977-9550
Telefax: (212) 664-0525

```

?       TEXT:      (1212, 422523 COOP UT
?
?       INFORMATION FOR SEQ ID NO: 1:
?
?       SEQUENCE CHARACTERISTICS:
?
?       LENGTH:    2140 base pairs
?
?       TYPE:       nucleic acid
?
?       STRANDEDNESS: single
?
?       TOPOLOGY:   unknown
?
?       MOLECULE TYPE: DNA (genomic)
?
?       HYPOTHEICAL: N
?
?       ANTI-SENSE: N
?
?       FEATURE:
?
?       NAME/KEY:   CDS
?
?       LOCATION:   178..1893
?
?       OTHER INFORMATION:
?
US-08-334-698-1

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Query Match	6.4%	Score 98.4:	DB 2:	Length 2140;
Best Local Similarity	50.7%	Pred. No. 3	4e-15;	
Matches 293;	Conservative	0;	Mismatches 276;	Indels 9;
				Gaps 2

Oy	85	GCCACGGGATATCCGCTCAACCGTGGTATATCTCCGCGGCTCTTCGCGGC	144
Db	457	GCCAGGGGCGTGGGCGTGGGCGCTCTTCGCGAGCTTCACTTAAAGCCGTGCAAGT	516
Oy	145	AACATAGTGTGCGCTAGTGTGGACGGCGAAGCGGACGCTGTGAGTGAAACCGT	204
Db	517	AACCTCTTGATCTCTCACTGAGCTGCAACGGCCACCTGCAGACCTGACCAATAT	576
Oy	205	TTTATCTTTAACTCTCTGTCAACGACGTGTGCAGATTTTGCTGTGGCCCCGTGGGTG	264
Db	577	TTTATGTAACTGTGCGGTGGCGCACTGTGCTGAGCGGCACCGTACTGCCCCCTTCTCG	636
Oy	265	GTGGCACCCTGTGGCTCTCTTCTTGAGCCCCCTCAACAGCCACTTCTGACGGCCCTGTT	324
Db	637	GCCACCATGAGAGTTCTGGGCTTCTGGGCTTTTGCGCGGCTTCTGCAAGTATGGCC	696
Oy	325	AGCCTACCCACTGTGTGGCTTGTGCGCCAGCGTCAACACATTTGTTGTGTGATGAT	384
Db	697	GCGGTGAAGTGTGTGTGTCAGACGGCCCTCAATCCCAAGCCTCTGCAATCTCGTGGAC	756
Oy	385	CGCTACTTGTCCATATCCACCCTTCTTCATCCCGTCCAAAGATGACCAAGCCGCGGT	444
Db	757	CGGTAGTGGGCGTGGCGCACTCACTCAAGTACCAGCATCAATGACCGGACGAGCGG	816
Oy	445	TACCTGCTCCTATAGGACACTGAAATTGTGACATCCGACAGACACTCTCACTTAC	504
Db	817	GCGCCATCTGTGCGCTGTCTGTGGTGTGATGACCTGTGTGTGTGCGTAGGGCCCTGTCTG	876
Oy	505	GAGTGGGGACAGACTGCTCTTTGATGAGGCGAATGCTCTGTCTTCATGATCTGGGGGCC	564
Db	877	GGTGTGAAGAGACCGGTGCCCCCTGA---CGAGGCGTTCTGCGGTATCACCGAGAGG--	931
Oy	565	AGCCCAAGTACATATTTCTCAGCGGTGTCTTTCATCGTATTTCACTGATTTGTATG	624
Db	932	----CGGGCTACGCTGTCTTCTCTCCGCTGTGTCTCTTTCATCTGACCATGGCGGTATC	987
Oy	625	ATTGCGTACATCCGTGTGTGTTCTGTGACGCGCGAG	662
Db	988	GTGTGATGATGCTGCGCGGTGACGTGTGTGCGGCGAG	1025

RESULT 9
 US-08-228-932-1
 ; Sequence 1, Application US/08228932
 ; Patent No. 5578611
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
 ; APPLICANT: Theresa A. Brancheck, John M. Wetzel and Paul R. Hartig
 ; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
 ; TITLE OF INVENTION: PROSTATIC HYPERPLASIA
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: COOPER & DUNHAM
 ;

```
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,932
FILING DATE: 13-APR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-B/JPW/TEP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 178..1893
OTHER INFORMATION:
US-08-228-932-1

Query Match
Best Local Similarity 50.7%; Score 98.4; DB 2; Length 2140;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;
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QY 565 AGCCCACTACACTATTCTCAGCGGTGCTCTTCATCGCATTCACATGATGTCATG 624
DB 932 ----CGGCTACGCTGCTCTCTCCCTGCTGCTCTTCACTGCGCCATGCGCGTATC 987
QY 625 ATGCGCTGCTACCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 662
DB 988 GTGCTACGTACTGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1025
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RESULT 10
US-08-468-939-1
Sequence 1, Application US/08468939
Patent No. 5714381

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GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,939
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 178..1893
OTHER INFORMATION:
US-08-468-939-1
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Query Match
Best Local Similarity 50.7%; Score 98.4; DB 2; Length 2140;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;

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QY 85 GCCCAGGCATCATCCGCTCAACCGTCTGTTATCTTCTGCGCGCTCTTTGCTGCGC 144
DB 457 GCGCAGGCGGTGCGGTGCGGTCTTCTGCGAGCCTTATCTTATGCGCGTGAAGT 516
QY 145 AACATAGTCTGCGCTAGTGTGTCAGCGCAGCCAGCTGCTGAGGTGACCAACGT 204
DB 517 AACCTGCTTGTATCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 576
QY 205 TTATCTTTAACTCTCTGTCACCGACCTGCTGCAAGATTGCTGCGCGCTGCGGTG 264
DB 577 TTATCTGTAAGACCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 636
QY 265 GTGGCACTCTGTGCTCTCTTCTTCTGCGCGCTCAACGCACTTCTGCAAGGCGCTG 324
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Db 637 GCACCATGAGAGTCTGAGGCTTCTGAGGCTTGTGGCCCTTGTGCGCCCTTGTGCGACGATGAGGCC 696
Qy 325 AGCCACACCAACCTGTTGCGCTTGTGCGAGCGTCAACACATTTCTTGGTGTCAGTGGAT 384
Db 697 GCGGTGAGAGTGTGTGCTGTGCGACGCGCTTCATCTCAAGCTTGTGACCACTTCTCGTGAC 756
Qy 385 CGCTACTTGTTCATTCATCCACCTCTCTCTTACCCGTCAGATGACCCGACCGCCGCT 444
Db 757 CGGTAGTGGGGGTGGCGCACTCACTCAAGTACCGACCATATGACCGACCGCCAGGGC 816
Qy 445 TACCTGCTCTCTATGACACCTGTGATTTGGCCATCTTGACAGCACTCTCTCACTTAC 504
Db 817 GCGGCATCTGAGCCCTGCTGTGGTGATGACCCCTGTGTGTCTGTAGGGGCCCTGCTG 876
Qy 505 GGCTGGGGGCGAGCTGCTTTTATGATGAGCGCATGCTCTGCTCCATGATTTGGGGGGCC 564
Db 877 GCGTGAAGAGAGCCCTGCCCCCTGA--CGAGCGCTTGTGCGGTATCACCGAGAGG-- 931
Qy 565 AGCCCGAGCTACATATTTCTCAGCGGTGTGCTCTTATGCTATTCACCTGATTTGATG 624
Db 932 ----CGGGGTAGCGTCTTCTTCTCGGTGTGTCTCTTCTTACCTGCGCGGTCTATC 987
Qy 625 ATTGCTGCTACTCGTGTGTGTCTGTGACCGCCGAG 662
Db 988 GTGCTATGTACTGCGCGGTGTACGTGTGCGCGAG 1025

RESULT 11
US-08-406-855A-1
; Sequence 1, Application US/08406855A
; Patent No. 5861309
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,855A
; FILING DATE: 21-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2140 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 178..1893
; OTHER INFORMATION:

US-08-406-855A-1
Query Match 6.4%; Score 98.4; DB 2; Length 2140;
Best Local Similarity 50.7%; Pred. No. 3 4e-15;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;
Qy 85 GCCACGGCATCATCGCTCAACCGGTGTTATCTTCTGCGCCCTTTTCGTGCGC 144
Db 457 GCGAGGGCGGTGAGGCGGTCTTCTGTGAGCCTTATCTTATGACCGGTGAGGT 516
Qy 145 AACATAGTCTGCGCTTATGTCAGCCGACCGCAAGCCGACTCTGAGTGAACCAAGT 204
Db 517 AACCTGCTTGTATCTCTCAAGTGTGTCACCGCACTTGTCAACCGTCAACATAT 576
Qy 205 TTTATCTTAACTCTGCTGTGACCGACCTGCTGAGATTTGCTGTGAGCCCTGAGGT 264
Db 577 TTCTATGTAACTCTGAGCGGTGTGACCTGCTGTGAGGCAACGTTATGCTTCTTCTG 636
Qy 265 GTGGCCACTCTGTGTGCTCTTCTGTGAGCCCTCAACAGCCACTTGTGACAGCCCTGATT 324
Db 637 GCACCATGAGAGTCTGTGGCTTGTGGGCTTGTGGCGGCTTGTGCGACGATGAGGCC 696
Qy 325 AGCCACACCACTGTTGCGCTTGTGCGAGCGTCAACACATTTGTTGGTGTCAGTGGAT 384
Db 697 GCGGTGAGAGTGTGTGTGTGACAGCGCTTCATCTCAGCTTGTGACCACTTCTCGTGAC 756
Qy 385 CGCTACTTGTTCATATCCACCTCTCTCTTACCCGTCAGATGACCGAGGCGCGGT 444
Db 757 CGGTAGTGGGGGTGGCGCACTCACTCAAGTACCAAGCATATGACCGAGGCAAGGCG 816
Qy 445 TACCTGCTCTCTATGACACCTGATTTGGCCATCTTGCAGACGACTCTCTCACTTAC 504
Db 817 GCGGCATCTGTGGCCCTGCTGTGGGTGTGAGCGCTGTGTCTCGTAGGGCCCTGCTG 876
Qy 505 GCGTGGGGCGAGCGCTGCTTATGAGCGCAATGCTCTGCTCCATGATTTGGGGGGCC 564
Db 877 GCGTGAAGAGAGCCGTCGCCCTGA--CGAGCGCTTGTGCGGTATCACCGAGAGG-- 931
Qy 565 AGCCCGAGCTACATATTTCTCAGCGGTGTGCTCTTATGCTGATTCATTCACATGATG 624
Db 932 ----CGGGGTAGCGTCTTCTTCTCGGTGTGTCTCTTCTTACCTGCGACGCGGTCTATC 987
Qy 625 ATTGCTGCTACTCGTGTGTGTCTGTGACCGCCGAG 662
Db 988 GTGCTATGTACTGCGCGGTGTACGTGTGCGCGAG 1025

RESULT 12
US-08-722-190-1
; Sequence 1, Application US/08722190
; Patent No. 5990128
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, Carlos C. Forray, George
; APPLICANT: Chiu, Theresa A. Brancheck, John M. Wetzel and Paul R. Hartig
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
; TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,190
; FILING DATE: 4-APR-1995
; CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-D-PCT/JPM/AGL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 178..1893
OTHER INFORMATION:
US-08-722-130-1

Query Match 6.4%; Score 98.4; DB 2; Length 2140;

Best Local Similarity 50.7%; Pred. No. 3.4e-15; Mismatches 276; Indels 9; Gaps 2;

Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;

85 GCCACGCGCATATCGCTCAACCGTGTGTTATCTTCGCGCCCTCTTTCGTGGC 144
457 GCGGAGGGGCGTGGGCGTGGCGCTTCTCGGAGCCTTATCTTATGCGCGTGGAGGT 516
145 AACATAGTGTGCGCGCTAGTGTGACGCGCAACGCGGAGCTGTGAGTGAACACCGT 204
517 AACCTGCTGTATCTCTCACTGAGCTGCAACCGGACCTGACAGCCGTACCAACTAT 576
205 TTTATCTTAACTCTCTCTCAACCGGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 264
577 TTCACTGTGAACCTGCGCGTGGCGGACCTGCTGAGGCGCAACGCTACTGCTTCTCG 636
265 GTGGCCACCTGTGCGCTCTCTTGTGGCCCTCAACAGGCACTTGTGACGCGCCCTGTT 324
637 GCCACCATGAGAGTCTGAGGCTTCTGAGGCTTGTGGCGGCGCTTCTGCGACGATAGGCG 696
325 AGCTTACCCACCTGTGCGCTTGTGCGGAGCTGCAACCACTATGCTTGTGATGATGAT 384
697 GCGGTGAGAGTGTGCTGTGACGAGGCGCTCACTCTGAGCTGTGACATCTCCGTGAC 756
385 CGCTACTGTGATATCAACCTCTCTCTACCGCTTCAAGATGACCGAGGCGCGGT 444
757 CGGTAGTGGGCGTGGCGCACTCACTCAAGTACCCAGCATCATGACGAGCGCAAGGCG 816
445 TACCTGCTCTGATAGGCACTGATGAGGCACTGAGCTGCAAGGCACTCTCACTCTAC 504
817 GCGGCGATCTGCGCGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 876
505 GCGTGGGCGGAGGCTGCTTGTGAGGCGCAATGCTCTCTGCTCATGATCTGGGCGGCG 564
877 GCGTGAAGAGAGCCCTGCGCCCTGA---GAGCGCTTGTGCGGATGACCAAGAGG--- 931
565 AGCCCGAGTACATATTTCTGACGCGGTGCTTCTGATGATGATGATGATGATGATGAT 624
932 ---GCGGCTACGCTGTCTTCTCTCCGCTGCTCTTCTTACCTGCGCATGCGGCTCATC 987
625 ATTGCTGCTACTCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 662
988 GTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1025

RESULT 13
US-08-244-354-1
Sequence 1, Application US/08244354
Patent No. 6015819
GENERAL INFORMATION:

APPLICANT: Charles Gluchowski, et al.
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
TREAT BENIGN PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,354
FILING DATE: April 1, 1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-D-PCT-US/JPM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 178..1893
OTHER INFORMATION:
US-08-244-354-1

Query Match 6.4%; Score 98.4; DB 3; Length 2140;

Best Local Similarity 50.7%; Pred. No. 3.4e-15; Mismatches 276; Indels 9; Gaps 2;

Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;

85 GCCACGCGCATATCGCTCAACCGTGTGTTATCTTCGCGCCCTCTTTCGTGGC 144
457 GCGGAGGGGCGTGGGCGTGGCGCTTCTCGGAGCCTTATCTTATGCGCGTGGAGGT 516
145 AACATAGTGTGCGCGCTAGTGTGACGCGCAACGCGGAGCTGTGAGTGAACACCGT 204
517 AACCTGCTGTATCTCTCACTGAGCTGCAACCGGACCTGACAGCCGTACCAACTAT 576
205 TTTATCTTAACTCTCTCTCAACCGGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 264
577 TTCACTGTGAACCTGCGCGTGGCGGACCTGCTGAGGCGCAACGCTACTGCTTCTCG 636
265 GTGGCCACCTGTGCGCTCTCTTGTGGCCCTCAACAGGCACTTGTGACGCGCCCTGTT 324
637 GCCACCATGAGAGTCTGAGGCTTCTGAGGCTTGTGGCGGCGCTTCTGCGACGATAGGCG 696
325 AGCTTACCCACCTGTGCGCTTGTGCGGAGCTGCAACCACTATGCTTGTGATGATGAT 384
697 GCGGTGAGAGTGTGCTGTGACGAGGCTTCACTCTGAGCTGTGACATCTCCGTGAC 756
385 CGCTACTGTGATATCAACCTCTCTCTACCGCTTCAAGATGACCGAGCGCGCGGT 444
757 CGGTAGTGGGCGTGGCGCACTCACTCAAGTACCCAGCATCATGACGAGCGCAAGGCG 816
445 TACCTGCTCTGATAGGCACTGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 504

Db 817 GCCGCATCTGGCCCTGCTGCTGGGTCTAGACCCCTGCTGCTCCGTAAGGCCCCCTGCTG 876
Qy 505 GGGTGGGCGCAGGCTGCTTGTATGAGCGCAATGCTCTCTGCATCATGATCTGGGGGCC 564
Db 877 GGCTGGAAGAGCCCGGCGCCCTGA---CGAGGCTTTCGGGGTATCACCGAGAGG--- 931
Qy 565 AGCCCCAGCTACATATTTCTCAGCGGTGTCTTCTTATCGTCAATTCATGATTTGATC 624
Db 932 ----CGGGCTACCGCTGCTCTCTCTCCGTGTGCTCTTCACTGCGCATGGCGGTATC 987
Qy 625 ATGCTGTACTCCGGTGTCTGTGAGCCCGAG 662
Db 988 GTGCTATGTACTGCCCGGTGTAGTGTGCGGCGAG 1025

RESULT 14

US-09-206-899-1
Sequence 1, Application US/09206899
Patent No. 6083705
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
TITLE OF INVENTION: Receptors and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,899
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,855
FILING DATE: 21-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 178..1893
OTHER INFORMATION:
US-09-206-899-1

Query Match 6.4%; Score 98.4; DB 3; Length 2140;
Best Local Similarity 50.7%; Pired. No. 3.4e-15;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;

Qy 85 GCCCAGGATCATCCGCTGAACCGTGTATCTTCTCCGCGCTTTCTGCGC 144
Db 457 GCCCAGGCGCTGGCGCTTCTCTCTGCGACGCTTCACTTATGCGCGGAGGT 516

Qy 145 AACATAGTGTGAGCGCTAGTGTTCAGCGCAAGCCGACGCTGTGACAGTACCAACCGT 204
Db 517 AACCTCTTGTATCTCTCAAGTGCCTGCAACCGCACCTGACAGACCGTACCACTAT 576
Qy 205 TTATATTAACTCTCTGTCACCGACCTGTGAGATTTGCGTGTGCCCCCTGGGT 284
Db 577 TTATATTAACTCTGCGTGTGCGACCTGTGCTGAGCGCACCGTACTGCTTCTG 636
Qy 265 GTGGCAGCTGTGTGCTCTCTTGTGCCCCCTCAACAGCAGCTTGTGACAGCGCTGT 324
Db 637 GCCACATAGAGGTTCTGTGGGCTTCTGTGGGCTTTGGCGGCGCTTGTGACAGTATGGCC 656
Qy 325 AGCTCAGCCAGCTGTGTGCGCTTGTGCGCAGCGTCAACCAATGTCTTGTGTGATGAT 384
Db 697 GCCGTGAGAGTGTGTGTGTCAGACGCGCTCCATCTCAGCTCTGACCATCTCGTAGC 756
Qy 385 CGCTATTGTTCATATCCACCTCTCTCTCAACCGTCCAAATGATCCAGGCGCGCGT 444
Db 757 CGGTAGTGTGGCGTGGCCACTCACTCAAGTACCCAGCCATCATGACGAGCGCAAGGCG 816
Qy 445 TACCTGCTCTATGAGCAGCTGATGTGCGCATCTGACAGCACTCCCATCTAC 504
Db 817 GCCGCATCTGCGCCTGCTGTGGTGTGAGCCCTGTGTGTGCTAGGGCCCTGCTG 876
Qy 505 GGGTGGGCGCAGGCTGCTTGTATGAGCGCAATGCTCTGTCTCATGATTTGGGGGCC 564
Db 877 GGCTGGAAGAGCCCGTGGCCCCCTGA---CGAGCGTTCTGGGGTATCACCGAGAGG--- 931
Qy 565 AGCCCCAGCTACATATTTCTCAGCGGTGTCTTCTTATGCTCATTTGATTTGATC 624
Db 932 ----CGGGCTACCGCTGCTCTCTCTCCGTGTGCTCTTCACTGCGCATGGCGGTATC 987
Qy 625 ATGCTGTACTCCGGTGTCTGTGAGCCCGAG 662
Db 988 GTGCTATGTACTGCCCGGTGTAGTGTGCGGCGAG 1025

RESULT 15

US-09-444-783-1
Sequence 1, Application US/09444783
Patent No. 6420389
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, et al.
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,783
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 178..1893
OTHER INFORMATION:
US-09-444-783-1

Query Match 6.4%; Score 98.4; DB 3; Length 2140;

Best Local Similarity 50.7%; Pred. No. 3.4e-15;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;

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QY      85  GCCACGGGATCATCGGCTCAACCGTGTGCTTATCTTCGCGCGCTTTTCGTGGC 144
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      457  GCGCAGGGGCGTGGGCGTGGGCGCTTCTCTGCAAGCTTCATCTTATGCGCGTGGCAGGT 516

QY      145  AACATAGTGTGCGGTAGTGTGACGCGCAAGCCGACGCTGTGAGGTGACCAACCGT 204
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      517  AACGTGCTGTATCTCTCAAGTGGCTGCAACCGCACCTGAGACGTCACCAACTAT 576

QY      205  TTTATCTTAACTCTCTGTCACCGACTGCTGCAAGATTGCGTGGCCCCCTGGGTG 264
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      577  TTCATCGTGAACCTGGCCGTGGCCGACCTGTGCTGAGCGCACCGTACTGCGCTTCTCG 636

QY      265  GTGGCCACTGTGTGCTCTTTCTGGCCCCCTCAACAGCCACTTTCAGCGGCCCTGTT 324
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      637  GCCACCAATGAGGTTCTGGGCTTCTGGGCTTTGGCGGCGCTTCTGCAAGTATGGGCC 696

QY      325  AGCCTCACCCACTGTTGCGCTTTCGCGAGCGTCACACCATGTTGTTGTCAGTGAT 384
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      697  GCCGTGAGAGTGTGTGTGCAAGGCGCTCATCTCAGCGCTGACCAATCTCCGTGAC 756

QY      385  CGCTACTTGTCAATCATCAACCTCTCTCTCAACCGTCCAAGATGACCAAGCGCGCGT 444
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      757  CGGTAGTGGGCGTGGCCACTCACTCAATCCAGCCATCATGACCGAGCGCAAGGCG 816

QY      445  TACCTGCTCTCTATGAGCACTGATATGAGCCATCTGACAGCACTCTCCTCACTCTAC 504
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      817  GCTGCGCATCTGAGCCCTGCTCTGGGTGTAAGCCCTGTGTGTCTAGAGGCCCTGTG 876

QY      505  GGCTGGGGCCAGGCTGCTTTGATGAGCGCAATGCTCTGCTCAATGATCTGGGGGCGC 564
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      877  GGTGGAAGAGAGCCCGTGCCTCTGA--CGAGCGCTCTGGCGTATCACCGAGAGG-- 931

QY      565  AGCCCCAGTTACATATTTCTAGCGGTGTCTTTCATGTCTATTCACACTGATTGTATG 624
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      932  ---CGGGCTAGCGTGTCTTCTCCGTTGTCTCTTCTTACCTGCCCATTGGCGGTATC 987

QY      625  ATTGCTGTACTCCGTGATGTTCTGTGAGCCCGGAG 662
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      988  GTGCTATATTACTGCCGCTGTATGTTGCGCGCAG 1025
```

Search completed: December 10, 2005, 03:07:08
Job time : 218 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 06:22:00 ; Search time 113.714 Seconds
(without alignments)
1437.373 Million cell updates/sec

Title: US-10-712-615-103

Perfect score: 1967
Sequence: 1 MEHTHAHLAANSLGWSWPG.....NDSKSYQPEDAIGACVILL 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1967	100.0	372	4 AAU10067	Chemokine
2	1967	100.0	372	5 Aae18645	Human G-P
3	1967	100.0	372	6 ABR62521	Human G-P
4	1967	100.0	372	7 ADD18023	Human G-P
5	1967	100.0	372	7 ADJ87767	G-coupled
6	1967	100.0	372	8 ADI79323	ADI79323
7	1962	99.7	372	8 ADO56002	Human NOV
8	1939.5	98.6	369	6 ABR62522	Abri62522
9	1864	94.8	591	7 ADF70485	Orphan re
10	1857	94.4	353	5 AAU76416	Novel G-P
11	1857	94.4	353	5 ABU04075	Human G P
12	1857	94.4	353	5 ABB79517	Human che
13	1857	94.4	353	6 ABP98724	Human AXO
14	1857	94.4	353	6 ABR44437	Human G P
15	1857	94.4	353	6 ABB82499	Human TGR
16	1857	94.4	353	8 ADR16434	Human KOR
17	1853	94.2	353	4 AAU10068	Chemokine
18	1853	94.2	353	7 ADJ87769	G-coupled
19	1853	94.2	353	8 ADI79325	NOV11 pro
20	1853	94.2	353	8 ADO56004	Human NOV
21	1853	94.2	353	8 ADO28954	Human nov
22	1829	93.0	353	5 AAE29236	Human 7TM
23	1829	93.0	353	6 ABG71163	Novel hum
24	1829	93.0	353	6 ABU09571	Human pro

25	1741	88.5	345	6 ABB82508	Abb82508
26	1741	88.5	345	8 ADO28956	Mouse TGR
27	1628	82.8	318	7 ADJ87772	Mouse nov
28	1628	82.8	318	8 ADI79348	Adi87772 G-coupled
29	1628	82.8	318	8 ADO56027	Adi79348 NOV10b pr
30	1623	82.5	333	5 AAE17081	Ado56027 Human NOV
31	1623	82.5	333	7 ABW00814	Aae17081 Human G-P
32	1623	82.5	343	5 ABB79519	Abw00814 Human GPC
33	1623	82.5	356	5 ABB79518	Abb79519 Human che
34	1623	82.5	385	5 ABB95606	Abb79518 Human che
35	1623	82.5	388	8 ADO89946	Abb95606 Human GPC
36	1611	81.9	333	5 AAE17229	Adg89946 Antagonis
37	1471	74.8	287	4 AAU25559	Aae17229 Human tly
38	1421	72.2	321	7 ADC12696	Aau25559 Human G P
39	1317	67.0	265	6 ABR81706	Adc12696 Human GPC
40	1317	67.0	265	6 ABR62524	Abp81706 Human G P
41	912.5	46.4	313	4 AAU25556	Abri62524 Human G-P
42	742	37.7	340	8 AAU28936	Aau25556 Human G P
43	742	37.7	348	6 ABR82431	Ado28936 Mouse nov
44	737	37.5	374	5 ABU04070	Abri82431 Murine is
45	737	37.5	374	5 AAM49155	Abj04070 Human G P
					Aam49155 Human G P

ALIGNMENTS

RESULT 1	AAU10067	standard; protein; 372 AA.
ID	AAU10067	
AC	AAU10067	
XX		
XX		
DT	14-FEB-2002	(first entry)
XX		
DE	Chemokine receptor family related protein, NOV10.	
XX		
XX	NOV; cytostatic; psoriasis; noctropic; neuroprotectant;	
KW	cerebroprotective; hepatic; antiinflammatory; diabetes; anaemia;	
KW	haemostatic; atherosclerosis; gene therapy; neurogenesis; motility;	
KW	differentiation; proliferation; haematopoiesis; wound healing;	
KW	angiogenesis; cystic fibrosis; congenital myotonia; acute pancreatitis;	
KW	haemophilia; allergy; Peridred syndrome; skeletal dysplasia;	
KW	ischaemic injury; neuroepithelial disorder; hepatitis; heart failure;	
KW	chemokine receptor; chromosome 1.	
XX		
OS	Homo sapiens.	
XX		
XX		
EH	Key	Location/Qualifiers
FT	Peptide	1..47
FT		/label= Signal_peptide
FT	Protein	48..372
FT		/note= "Mature chemokine receptor related protein, NOV10"
XX		
XX	WO200170978-A2.	
XX		
XX	27-SEP-2001.	
XX		
XX	20-MAR-2001; 2001WO-US000993.	
XX		
XX	20-MAR-2000; 2000US-0190768P.	
XX	20-MAR-2000; 2000US-0190835P.	
XX	22-MAR-2000; 2000US-0190972P.	
XX	22-MAR-2000; 2000US-0191199P.	
XX	24-MAR-2000; 2000US-0191947P.	
XX	24-MAR-2000; 2000US-0192657P.	
XX	28-MAR-2000; 2000US-0192664P.	
XX	28-MAR-2000; 2000US-0192665P.	
XX	28-MAR-2000; 2000US-0192984P.	
XX	29-MAR-2000; 2000US-0192836P.	
XX	31-MAR-2000; 2000US-0193843P.	
XX		
XX	(CURA-) CURAGEN CORP.	
XX		
XX		

PI Taupier RJ, Majumder K, Spaderna SK, Smithson G, Mezes PS;
PI Vernet CAM;
XX MPI; 2001-639127/73.
DR N-PSDB; AAS15730.
XX Polypeptides and nucleic acids related to chloride channel, insulin-like
FT growth factor family of proteins, useful for diagnosing and treating
PT cancer, cystic fibrosis, acute pancreatitis and Alzheimer's disease.
XX
XX
PS Claim 1; Page 42; 151pp; English.
XX
XX The invention describes isolated NOVX (NOVX-11) polypeptides. NOVX
CC polypeptides are useful for treating pathology associated with NOVX
CC polypeptide, determining the presence of or predisposition to a disease
CC associated with altered levels of NOVX, identifying agents binding to
CC NOVX and treatment of disorders associated with altered expression of
CC members of chloride channel-associated proteins e.g. cystic fibrosis and
CC congenital myotonia. NOVX proteins are useful in treatment of disorders
CC including psoriasis, cancer, diabetes, metabolic disorders of pancreas,
CC e.g. acute pancreatitis, abnormal growth and accumulation of mast cells
CC in one or more organs (e.g. haemophilia, anaemia), Pendered syndrome,
CC skeletal dysplasias, disorders characterised by altered cell shape,
CC motility, and apoptosis, ischaemic injury, hepatitis, neuroepithelial
CC disorders, hepatic disorders (e.g. cryptogenic cirrhosis) and in the
CC treatment of disorders of vascular smooth muscle cell differentiation,
CC (e.g. heart failure, stroke). NOVX nucleic acids and polypeptides are
CC useful to screen for molecules which inhibit or enhance NOVX activity or
CC function and are useful as targets for the identifying small molecules,
CC that modulate or inhibit e.g. neurogenesis, proliferation, motility, cell
CC differentiation, haematopoiesis, wound healing and angiogenesis. NOV
CC sequences are also useful for: identifying a cell or tissue type in a
CC biological sample; amplifying DNA sequences from very small biological
CC samples e.g. hair or skin or body fluids and as primers and probes to
CC identify and/or clone NOVX homologues. NOVX proteins are useful
CC immunogens to generate antibodies to monitor protein levels and modulate
CC NOVX activity. Cells comprising the nucleic acids are useful for
CC producing transgenic animals, for studying the function and/or activity
CC of NOVX protein and identifying and/or evaluating modulators of NOVX
CC protein activity. This sequence is the NOV10 amino acid sequence (gene
CC located on chromosome 1) related to the chemokine receptor family of
CC proteins, one of 12 NOV polypeptides described in the method of the
CC invention
CC
XX
SQ Sequence 372 AA;

Query Match 100.0%; Score 1967; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.4e-209;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTAHHLAANSLSWSPGSAAGLGFVAVVYVYLLCTGLPANILTVIILSQLVARQK 60
DB 1 MEHTAHHLAANSLSWSPGSAAGLGFVAVVYVYLLCTGLPANILTVIILSQLVARQK 60
QY 61 SSYNVTLALAAADIVLFFTVVDFLLEDFILNMQMPQVDPKIIIEVLEFSSIHSTIWTV 120
DB 61 SSYNVTLALAAADIVLFFTVVDFLLEDFILNMQMPQVDPKIIIEVLEFSSIHSTIWTV 120
QY 121 PTTIRAYAVCHPLKYHTMSYPARTKRVSVYITICFLTSIYVWMPNWTEDYSTSVH 180
DB 121 PTTIRAYAVCHPLKYHTMSYPARTKRVSVYITICFLTSIYVWMPNWTEDYSTSVH 180
QY 181 HVLWIHCTVTVLVPCSIFFIINSIIYVTLARRKSNRLRGYSTGKTTALFTITSFATL 240
DB 181 HVLWIHCTVTVLVPCSIFFIINSIIYVTLARRKSNRLRGYSTGKTTALFTITSFATL 240
QY 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALINTAINFLYCFISKRFRMAAATL 300
DB 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALINTAINFLYCFISKRFRMAAATL 300
QY 301 KAFRCQOPQOPFYTNHNSITSSPWISPANSHCTIMLVYQYDKNGKPKSRNDSKSSYQ 360
DB 301 KAFRCQOPQOPFYTNHNSITSSPWISPANSHCTIMLVYQYDKNGKPKSRNDSKSSYQ 360

QY 361 FEDAIACVITL 372
DB 361 FEDAIACVITL 372

RESULT 2
AAE18645
ID AAE18645 standard; protein, 372 AA.
XX
XX AAE18645;
AC
XX
XX 17-MAY-2002 (first entry)
DT
XX
XX Human G-protein coupled receptor (GCR6C-6).
DE
XX
XX Human; G-protein coupled receptor; GCR6C-6; cell proliferative disorder;
KW neurological; cardiovascular; gastrointestinal; autoimmune; inflammatory;
KW metabolic; hepatitis; psoriasis; cancer; epilepsy; Alzheimer's disease;
KW Pick's disease; Huntington's disease; Parkinson's disease; hypertension;
KW atherosclerosis; myocardial infarction; gastritis; cirrhosis; cytostatic;
KW osteoporosis; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW anaemia; asthma; rheumatoid arthritis; diabetes; obesity; drug screening;
KW transgenic animal; allergy; gene therapy; hepatotropic; anticonvulsant;
KW nocotropic; neurotrophic; cardiac; immunosuppressive; anorectic;
KW vitruide; receptor.
XX
XX Homo sapiens.
OS
XX
XX
XX
XX
XX Key Location/Qualifiers
FH 1..47
FT Peptide /label= Signal_peptide
FT Domain /label= Signal_peptide
FT Domain /note= "Transmembrane domain"
FT Protein 48..372
FT Domain /label= Human_mature_GCR6C-6
FT Domain 74..100
FT Domain /note= "Transmembrane domain"
FT Domain 184..208
FT Domain /note= "Transmembrane domain"
XX
XX MO200210387-A2.
XX
XX
XX
XX 07-FEB-2002.
XX
XX
XX 25-JUL-2001; 2001WO-US023433.
XX
XX 27-JUL-2000; 2000US-0231478P.
PR 03-AUG-2000; 2000US-023268P.
PR 21-AUG-2000; 2000US-02327054P.
PR 08-SEP-2000; 2000US-0231121P.
PR 13-SEP-2000; 2000US-023243P.
PR 15-SEP-2000; 2000US-0232691P.
PR 22-SEP-2000; 2000US-0235146P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Thornton M, Patterson C, Lal P, Burford N, Yue H, Gandhi AR;
PI Elliot VS, Ramkumar J, Baughn MR, Kallick DA, Wajia NK, Hatalla AJA;
PI Yao MG, Lu Y, Tribouley CM, Policky JL, Kearney L, Graul RC;
PI Warren BA, Lee EA, Ding L;
XX
XX MPI; 2002-188744/24.
DR N-PSDB; AAD29672.
XX
XX New human G-protein coupled receptor polypeptide for diagnosis,
PT prevention and treatment of cell proliferative, neurological,
PT cardiovascular, gastrointestinal, autoimmune/inflammatory, and metabolic
PT disorders.
XX
XX
XX Claim 1; Page 120; 150pp; English.
XX
XX The invention relates to novel human G-protein coupled receptors (GCR6C)

CC and their encoding polynucleotides. GCRC is useful as an immunogen for
 CC preparing monoclonal and polyclonal antibodies. GCRC is useful for
 CC diagnosing, treating and preventing a cell proliferative disorder (e.g.,
 CC hepatitis, psoriasis, cancer), a neurological disorder (e.g., epilepsy,
 CC Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's
 CC disease), a cardiovascular disorder (e.g., atherosclerosis, hypertension,
 CC myocardial infarction), gastrointestinal disorder (e.g., gastritis,
 CC cirrhosis, Crohn's disease), an autoimmune/ inflammatory disorder (e.g.,
 CC acquired immunodeficiency syndrome (AIDS), allergy, anaemia, asthma,
 CC rheumatoid arthritis), a metabolic disorder (e.g., diabetes, obesity,
 CC osteoporosis), and viral infections. GCRC is useful in a number of drug
 CC screening techniques, and to analyse the proteome of a tissue or cell
 CC type. GCRC is useful for creating knockin humanised animals or
 CC transgenic animals to model human diseases, in somatic or germline gene
 CC therapy, to generate a transcript image of a tissue or cell type, for
 CC detecting differences in the chromosomal location due to translocation,
 CC inversion, etc., among normal, carrier or affected individuals, and as
 CC hybridisation probes for mapping naturally occurring genomic sequences.
 CC GCRC is useful in Southern or northern analysis, dot blot or other
 CC membrane-based technologies, in PCR technologies, in digestick, pin,
 CC microarray enzyme linked immunosorbant (ELISA)-like assays, and in
 CC microarrays utilising fluids or tissues from patients to detect altered
 CC GCRC expression. The present sequence is human GCRC-6

XX Sequence 372 AA;

Query Match 100.0%; Score 1967; DB 5; Length 372;

Best Local Similarity 100.0%; Pred. No. 1,4e-209; Indels 0; Gaps 0;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTAHLANSSLSWSWSPGACGFGFVYVYVYSLLCGLPANILVTIILSQLVARQK 60

DB 1 MEHTAHLANSSLSWSWSPGACGFGFVYVYVYSLLCGLPANILVTIILSQLVARQK 60

QY 61 SSVNYLLAAADILVLPFIVPDELLEBPILMOMPOVPDKIIVLESSIHITSWTV 120

DB 61 SSVNYLLAAADILVLPFIVPDELLEBPILMOMPOVPDKIIVLESSIHITSWTV 120

QY 121 PLTIDRYIAVCHPLKHTVSYPARTRKIVSVYITCFLTSIPYMMPNWTEDYISTSVH 180

DB 121 PLTIDRYIAVCHPLKHTVSYPARTRKIVSVYITCFLTSIPYMMPNWTEDYISTSVH 180

QY 181 HVLWIMHCFVYLVPCSIFFILNSIIVYKLRKSNRLRGYSTGKTTAIFTTISFATL 240

DB 181 HVLWIMHCFVYLVPCSIFFILNSIIVYKLRKSNRLRGYSTGKTTAIFTTISFATL 240

QY 241 WAPRIIMILYHLYGAPIQNRMLVHMSDIANMLALNTAINPFLYCFISKRFPTMAATL 300

DB 241 WAPRIIMILYHLYGAPIQNRMLVHMSDIANMLALNTAINPFLYCFISKRFPTMAATL 300

QY 301 KAPFKOKOPVOPTMHNSTSSPWPISPNASHCIRMVYOVOKNKPISKRNDSKSYO 360

DB 301 KAPFKOKOPVOPTMHNSTSSPWPISPNASHCIRMVYOVOKNKPISKRNDSKSYO 360

QY 361 FEDATGACVITL 372

DB 361 FEDATGACVITL 372

RESULT 3

ABR62521

ID ABR62521 standard; protein; 372 AA.

XX ABR62521;

XX 06-NOV-2003 (first entry)

DE Human G-protein coupled receptor HGRPMY34.

XX HGRPMY34; G-protein coupled receptor; receptor; GPCR-P14; GPCR-145;

KW human; neuroprotective; nootropic; tranquilizer; antinigraine;

KW neuroleptic; antianemic; antidepressant; anticonvulsant; antiparkinsonian;

KW cytoskeletal; cardiant; hypotensive; antidiagonal; analgesic; anorectic;

KW anti-HIV; antiasthmatic; osteopathic; uropathic; antitumor; antiallergic;

XX gene therapy.

OS Homo sapiens.

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Claim 5; Fig 1A-B; 112pp; English.

The present sequence is the protein sequence of human HGRPMY34, a newly
 identified G-protein coupled receptor (GPCR) belonging to the group of
 'Class A' GPCRs and showing homology to the Pfam model 7 transmembrane
 receptor, rhodopsin family. HGRPMY34, also referred to as GPCR-P14
 and/or GPCR-145, is highly expressed in brain (especially in the
 CC amygdala, caudate nucleus, corpus callosum, hippocampus, thalamus,
 CC substantia nigra), spinal cord and pituitary, indicating an association
 CC in neurological systems and conditions. It is also expressed in the bone
 CC marrow and testis. The invention provides HGRPMY34 polynucleotides,
 CC polypeptides and antibodies, expression vectors, host cells and antisense
 CC molecules, methods for screening for modulators of HGRPMY34 activity
 CC and/or function, and methods for diagnosing, treating, preventing and
 CC screening for disorders and diseases associated with abnormal HGRPMY34
 CC activity, including: a disorder related to aberrant G-protein coupled
 CC signalling; a disorder related to aberrant cell cycle regulation;
 CC neurological disorders; anxiety; headache; migraine; schizophrenia;
 CC depression; delirium; dementia; severe mental retardation and
 CC dyskinesias, such as Huntington's disease or Gilles de la Tourette's
 CC syndrome; Parkinson's disease; brain disorders; spinal cord disorders;
 CC affective disorders; neoplastic disorders; cardiovascular disorders;
 CC acute heart failure; hypotension; hypertension; angina pectoris;
 CC myocardial infarction; an immunological disorder; immune-related
 CC disorders; endocrinal diseases; growth disorders; neuropathic pain;

CC obesity; anorexia; HIV infections; cancers; bulimia; asthma; osteoporosis
 CC ; psychosis; metabolic disorders; pituitary disorders; urinary retention;
 CC ulcers; allergies; or benign prostatic hypertrophy (all claimed)
 XX
 SQ Sequence 372 AA;

Query Match 100.0%; Score 1967; DB 6; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.4e-209;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTAHLAANSSLSWSPGACGFPVYVYSSLLCLGIPANILTVIISQLVAROK 60
 DB 1 MEHTAHLAANSSLSWSPGACGFPVYVYSSLLCLGIPANILTVIISQLVAROK 60
 QY 61 SSYNVLLAAADIVLFFIVDFLEDFILNMQMPQVPDKIEVLEFSSIHSTIWTIV 120
 DB 61 SSYNVLLAAADIVLFFIVDFLEDFILNMQMPQVPDKIEVLEFSSIHSTIWTIV 120
 QY 121 PLTIRYIAVCHPLKHYTVSPARTKRVIVSVYITCFLTSIPYWMPIWTEGYISTSVH 180
 DB 121 PLTIRYIAVCHPLKHYTVSPARTKRVIVSVYITCFLTSIPYWMPIWTEGYISTSVH 180
 QY 181 HVLWIHGFYTVLVPCSFIFLINSIIYVKLRKSNFRLGYSTGKTALIFTITSIFATL 240
 DB 181 HVLWIHGFYTVLVPCSFIFLINSIIYVKLRKSNFRLGYSTGKTALIFTITSIFATL 240
 QY 241 WAPRIIMLYLHGYAPIONRWLVHMSDIANMLALNTAINFLYCFISKPRRTMAAATL 300
 DB 241 WAPRIIMLYLHGYAPIONRWLVHMSDIANMLALNTAINFLYCFISKPRRTMAAATL 300
 QY 301 KAFKCOQOPVQFYTNHNSITSSPWISPAISHCIKMLVYQYDKGKPIKSRNDSKSSYQ 360
 DB 301 KAFKCOQOPVQFYTNHNSITSSPWISPAISHCIKMLVYQYDKGKPIKSRNDSKSSYQ 360
 QY 361 FEDAIACVYIIL 372
 DB 361 FEDAIACVYIIL 372

RESULT 4
 ADD18023
 ID ADD18023 standard; protein; 372 AA.
 XX
 AC ADD18023;
 DT 15-JAN-2004 (first entry)
 DE Human G-protein coupled receptor (GPCR) sequence Seq ID19.
 XX
 KW G protein coupled receptor; GPCR; signal transduction pathway; G protein;
 KW Alzheimer's disease; Parkinson's disease; diabetes; dwarfism;
 KW colour blindness; retinal pigmentosa; asthma; depression; schizophrenia;
 KW sleeplessness; hypertension; anxiety; stress; renal failure;
 KW cardiovascular disorder; neural disorder; oncology disorder;
 KW immune disorder; neuroprotective; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 347..351 /note="Encoded by AAAGTC"
 FT
 PN W02003016478-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 15-AUG-2002; 2002W0-US026017.
 XX
 PR 20-AUG-2001; 2001US-0313658P.
 PR 12-SEP-2001; 2001US-0313675P.
 PR 30-OCT-2001; 2001US-0340703P.
 PR 26-NOV-2001; 2001US-0333417P.
 PR 06-DEC-2001; 2001US-0338367P.

PR 06-FEB-2002; 2002US-0355596P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Feder JN, Ramanathan CS, Gopal S, Mintier GA;

XX MPI, 2003-278558/27.

XX N-PSDB; ADD18120.

PT New nucleic acid, useful for manufacturing a medicament for preventing,
 PT treating or ameliorating a medical condition e.g., neural disorder.

PS Example 1; SEQ ID NO 19; 251bp. English.

CC This invention relates to novel G protein coupled receptors (GPCRs) and
 CC their encoding nucleotide sequences. Many medically significant
 CC biological processes are mediated by proteins participating in signal
 CC transduction pathways involving G proteins. GPCRs are one of the largest
 CC receptor superfamilies known. These receptors are biologically important
 CC and malfunction of these receptors results in diseases such as
 CC Alzheimer's, Parkinson's, diabetes, dwarfism, colour blindness, retinal
 CC pigmentosa and asthma. They are also involved in depression,
 CC schizophrenia, sleeplessness, hypertension, anxiety, stress, renal
 CC failure and other cardiovascular, neural, oncology and immune disorders.
 CC A modulator of the GPCRs of the invention may have neuroprotective
 CC activity whilst the sequences of the invention may be useful for gene
 CC therapy. The invention may also be useful for manufacturing a medicament
 CC for preventing, treating or ameliorating a medical condition. The present
 CC sequence is the amino acid sequence of a human GPCR of the invention.

XX Sequence 372 AA;

Query Match 100.0%; Score 1967; DB 7; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.4e-209;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTAHLAANSSLSWSPGACGFPVYVYSSLLCLGIPANILTVIISQLVAROK 60
 DB 1 MEHTAHLAANSSLSWSPGACGFPVYVYSSLLCLGIPANILTVIISQLVAROK 60
 QY 61 SSYNVLLAAADIVLFFIVDFLEDFILNMQMPQVPDKIEVLEFSSIHSTIWTIV 120
 DB 61 SSYNVLLAAADIVLFFIVDFLEDFILNMQMPQVPDKIEVLEFSSIHSTIWTIV 120
 QY 121 PLTIRYIAVCHPLKHYTVSPARTKRVIVSVYITCFLTSIPYWMPIWTEGYISTSVH 180
 DB 121 PLTIRYIAVCHPLKHYTVSPARTKRVIVSVYITCFLTSIPYWMPIWTEGYISTSVH 180
 QY 181 HVLWIHGFYTVLVPCSFIFLINSIIYVKLRKSNFRLGYSTGKTALIFTITSIFATL 240
 DB 181 HVLWIHGFYTVLVPCSFIFLINSIIYVKLRKSNFRLGYSTGKTALIFTITSIFATL 240
 QY 241 WAPRIIMLYLHGYAPIONRWLVHMSDIANMLALNTAINFLYCFISKPRRTMAAATL 300
 DB 241 WAPRIIMLYLHGYAPIONRWLVHMSDIANMLALNTAINFLYCFISKPRRTMAAATL 300
 QY 301 KAFKCOQOPVQFYTNHNSITSSPWISPAISHCIKMLVYQYDKGKPIKSRNDSKSSYQ 360
 DB 301 KAFKCOQOPVQFYTNHNSITSSPWISPAISHCIKMLVYQYDKGKPIKSRNDSKSSYQ 360
 QY 361 FEDAIACVYIIL 372
 DB 361 FEDAIACVYIIL 372

RESULT 5

ID ADJ87767 standard; protein; 372 AA.

XX ADJ87767;

DT 06-MAY-2004 (first entry)

DE G-coupled protein receptor-related protein #56.
 XX novel protein; G-coupled protein receptor-related protein;
 XX cardiomyopathy; atherosclerosis; cell signal processing-related disorder;
 KM metabolic pathway modulation-related disorder; diabetes; cancer; stroke;
 KM Huntington's disease; epilepsy; anxiety; pain; hypercholesterolaemia;
 KM obesity; hypertension; Crohn's disease; systemic lupus erythematosus;
 KM viral infections; bacterial infection; parasitic infection;
 KM hyperthyroidism; hypothyroidism; Von Hippel-Lindau syndrome;
 KM Alzheimer's disease; tuberosus sclerosis; hypercalcaemia; cerebral palsy.
 XX
 OS Unidentified.
 XX
 PN WO2002102321-A2.
 XX
 XX 27-DEC-2002.
 PD
 XX
 PF 18-JUN-2002; 2002WO-US019522.
 XX
 XX 18-JUN-2001; 2001US-0298994P.
 PR 18-JUN-2001; 2001US-0299134P.
 PR 04-OCT-2001; 2001US-00972446.
 PR 06-JUN-2002; 2002US-00299134.
 PR 07-JUN-2002; 2002US-00298994.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX
 PI Anderson DW, Guo X, Gusev VY, Herrmann JL, Li L, Mezes PS;
 PI Pena CER, Spaderna SK, Zhong M;
 DR WPI; 2003-167441/16.
 XX
 XX N-PSDB; ADJ87766.
 XX
 PT New MOX polypeptides and polynucleotides, useful in gene therapy,
 PT particularly for treating or preventing e.g. cardiomyopathy,
 PT atherosclerosis, diabetes, adenoma, brain tumor, breast cancer, prostate
 PT cancer, stroke or pain.
 XX
 PS Claim 1; SEQ ID NO 202; 378bp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of novel G-
 CC coupled protein receptor-related (MOL) proteins. The DNA and protein
 CC sequences of the invention are useful for treating or preventing a MOL-
 CC associated disorder, such as: cardiomyopathy, atherosclerosis, disorders
 CC associated with cell signal processing and metabolic pathway modulation,
 CC or diabetes. The DNA and protein sequences are also useful for the
 CC treatment of: cancer, stroke, Huntington's disease, epilepsy, anxiety,
 CC pain, hypercholesterolaemia, obesity, hypertension, Crohn's disease,
 CC systemic lupus erythematosus, viral infections, bacterial infections,
 CC parasitic infections, hyperthyroidism, hypothyroidism, Von Hippel-Lindau
 CC syndrome, Alzheimer's disease, tuberosus sclerosis, hypercalcaemia, or
 CC cerebral palsy. The present amino acid sequence represents a MOL protein
 CC of the invention.
 CC
 SQ Sequence 372 AA;

Query Match 100.0%; Score 1967; DB 7; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.4e-209;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTAHNLANSLSMSWSPGACGLFVPUVYVYLLCGCLPANILTVIILISQVARRQK 60
 DB 1 MEHTAHNLANSLSMSWSPGACGLFVPUVYVYLLCGCLPANILTVIILISQVARRQK 60
 QY 61 SSYNYLLALAAADILVLFPIVDFLEDFILNMQMPQVDPDKIIEVLFSSIHSTIWTIV 120
 DB 61 SSYNYLLALAAADILVLFPIVDFLEDFILNMQMPQVDPDKIIEVLFSSIHSTIWTIV 120
 QY 121 PLTIORXIVAVCHPKLKHVTSYPAKTRKXVVSVYITCEFLSIPYMMWPNITWEDYISTSVH 180
 DB 121 PLTIORXIVAVCHPKLKHVTSYPAKTRKXVVSVYITCEFLSIPYMMWPNITWEDYISTSVH 180
 QY 181 HVLIMHCFVTVLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240

DB 181 HVLIMHCFVTVLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
 QY 241 WAPRIMLYLHYGAPIONRMVLVHIMSIPANLALNTAINFLYCFISKRRRTMAAATL 300
 DB 241 WAPRIMLYLHYGAPIONRMVLVHIMSIPANLALNTAINFLYCFISKRRRTMAAATL 300
 QY 301 KAFPRCQOPQVQFYNNHFSITSSPWISPAHSHCIKMLVYOYDKNGKPIKSRNDSKSSYO 360
 DB 301 KAFPRCQOPQVQFYNNHFSITSSPWISPAHSHCIKMLVYOYDKNGKPIKSRNDSKSSYO 360
 QY 361 FEDAIGACVITL 372
 DB 361 FEDAIGACVITL 372

RESULT 6
 ADI79323 standard; protein; 372 AA.
 ID ADI79323

AD179323;

DT 22-APR-2004 (first entry)

DE NOVI0a protein sequence, SEQ ID 20.

XX Cytostatic; Immunosuppressive; Anti-allergic; Antimicrobial; Vasotropic;
 KM Respiratory; Hepatotropic; Virucide; Gastrointestinal; Antidiabetic;
 KM Ophthalmological; Antiproliferative; Neuroprotective; Nocotropic;
 KM Antiarteriosclerotic; Hypotensive; Cardiant; Cerebroprotective;
 KM Gene Therapy; NOX; human; cancer; myelogenous leukaemia;
 KM congenital neonatal autoimmune thrombocytopaenia; immunological disorder;
 KM allergy; infection; asthma; lung disease; reproductive disorder;
 KM haemangioma; deafness; liver cirrhosis; hepatitis C; gastric disorder;
 KM diabetic retinopathy; psoriasis; multiple sclerosis; atherosclerosis;
 KM hypertension; stroke; heart failure; chromosome 1; NOVI0a;
 KM chemokine receptor.
 XX

OS Homo sapiens.

PN WO2004009635-A2.

PD 29-JAN-2004.

PF 04-OCT-2001; 2001WO-US031292.

PR 20-MAR-2001; 2001US-00813432.

PA (CURA-) CURAGEN CORP.

PI Taupier RJ, Majumder K, Spaderna SK, Smithson G, Mezes PS;
 PI Vernet CAM;

DR WPI; 2004-123380/12.

XX N-PSDB; ADI79322.

PS Claim 1; Page 41; 158bp; English.

CC The present invention relates to novel NOX proteins and their coding
 CC sequences (ADI79304-ADI79327). The sequences are useful for the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease associated with the protein, or for diagnosing and treating
 CC disorders associated with the NOX protein, such as cancer, myelogenous
 CC leukaemia, congenital neonatal autoimmune thrombocytopaenia,
 CC immunological disorders, allergy and infection, asthma, lung diseases,
 CC reproductive disorders, male and female reproductive diseases,
 CC haemangioma, deafness, liver cirrhosis, hepatitis C, gastric disorders,
 CC diabetic retinopathy, psoriasis, multiple sclerosis, atherosclerosis,
 CC hypertension, stroke and heart failure. NOVI0a represents a new member of
 CC the chemokine receptor family and the gene is located on chromosome 1.
 CC
 SQ Sequence 372 AA;

Query Match 100.0%; Score 1967; DB 8; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.4e-209;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTHAHLAANSSLSWSPSGACGAFVPPVYYSLLCGLGPANILTVIILSOLVARROK 60
 |||||||
 DB 1 MENTHAHLAANSSLSWSPSGACGAFVPPVYYSLLCGLGPANILTVIILSOLVARROK 60
 |||||||

QY 61 SSYNVLLAAADILVLFPIVDFLEDFILNMQMPQVDPKIIIEVLEFSSIHISIMITV 120
 |||||||
 DB 61 SSYNVLLAAADILVLFPIVDFLEDFILNMQMPQVDPKIIIEVLEFSSIHISIMITV 120
 |||||||

QY 121 PLTIDRYIAVCHPLKHYTVSPARTRKIVSVYITCFLTSPYWMWPIMWEDYISTSVH 180
 |||||||
 DB 121 PLTIDRYIAVCHPLKHYTVSPARTRKIVSVYITCFLTSPYWMWPIMWEDYISTSVH 180
 |||||||

QY 181 HVLIMHCFITYVLPVCSIFILNSIIYVKLRKSNFRLGYSTGKTTAIFTTISIFATL 240
 |||||||
 DB 181 HVLIMHCFITYVLPVCSIFILNSIIYVKLRKSNFRLGYSTGKTTAIFTTISIFATL 240
 |||||||

QY 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFPLYCFISKRFRTMAAATL 300
 |||||||
 DB 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFPLYCFISKRFRTMAAATL 300
 |||||||

QY 301 KAFKCCQKQVQVPTNNHFSITSSPWSIPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
 |||||||
 DB 301 KAFKCCQKQVQVPTNNHFSITSSPWSIPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
 |||||||

QY 361 FEDAIGACVIIL 372
 |||||||
 DB 361 FEDAIGACVIIL 372
 |||||||

RESULT 7
 ADO56002
 ID ADO56002 standard; protein; 372 AA.
 XX
 AC ADO56002;
 DT 15-JUL-2004 (first entry)
 XX
 DE Human NOVI0 polypeptide.
 XX
 KW human; cancer; obesity; diabetic nephropathy; acute pancreatitis; stroke;
 KM multiple sclerosis.
 XX
 OS Homo sapiens.
 XX
 PN US2004058862-A1.
 XX
 PD 25-MAR-2004.
 XX
 PF 18-SEP-2002; 2002US-00246583.
 XX
 PR 18-SEP-2002; 2002US-00246583.
 XX
 PA (MAJU/) MAJUMDER K.
 XX
 PI Majumder K;
 XX
 DR WPI, 2004-268835/25.
 XX
 DR N-PSDB; ADO56001.
 XX
 PT Novel NOVX polypeptides, useful for treating cancer, obesity, diabetic
 XX nephropathy, acute pancreatitis, strokes and multiple sclerosis.
 XX
 PS Claim 1; Page 27; 87pp; English.
 XX
 CC The invention relates to novel isolated NOVX nucleic acids and encoded
 CC polypeptides. The nucleic acids, polypeptides and antibodies raised
 CC against the polypeptides are useful for preventing or treating diseases
 CC associated with aberrant NOVX expression or activity e.g., cancer,
 CC obesity, diabetic nephropathy, acute pancreatitis, stroke, multiple

CC sclerosis. The present sequence represents a NOVX polypeptide of the
 CC invention.
 XX
 SQ Sequence 372 AA;

Query Match 99.7%; Score 1962; DB 8; Length 372;
 Best Local Similarity 99.7%; Pred. No. 4.9e-209;
 Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENTHAHLAANSSLSWSPSGACGAFVPPVYYSLLCGLGPANILTVIILSOLVARROK 60
 |||||||
 DB 1 MENTHAHLAANSSLSWSPSGACGAFVPPVYYSLLCGLGPANILTVIILSOLVARROK 60
 |||||||

QY 61 SSYNVLLAAADILVLFPIVDFLEDFILNMQMPQVDPKIIIEVLEFSSIHISIMITV 120
 |||||||
 DB 61 SSYNVLLAAADILVLFPIVDFLEDFILNMQMPQVDPKIIIEVLEFSSIHISIMITV 120
 |||||||

QY 121 PLTIDRYIAVCHPLKHYTVSPARTRKIVSVYITCFLTSPYWMWPIMWEDYISTSVH 180
 |||||||
 DB 121 PLTIDRYIAVCHPLKHYTVSPARTRKIVSVYITCFLTSPYWMWPIMWEDYISTSVH 180
 |||||||

QY 181 HVLIMHCFITYVLPVCSIFILNSIIYVKLRKSNFRLGYSTGKTTAIFTTISIFATL 240
 |||||||
 DB 181 HVLIMHCFITYVLPVCSIFILNSIIYVKLRKSNFRLGYSTGKTTAIFTTISIFATL 240
 |||||||

QY 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFPLYCFISKRFRTMAAATL 300
 |||||||
 DB 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFPLYCFISKRFRTMAAATL 300
 |||||||

QY 301 KAFKCCQKQVQVPTNNHFSITSSPWSIPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
 |||||||
 DB 301 KAFKCCQKQVQVPTNNHFSITSSPWSIPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
 |||||||

QY 361 FEDAIGACVIIL 372
 |||||||
 DB 361 FEDAIGACVIIL 372
 |||||||

RESULT 8
 ABR62522
 ID ABR62522 standard; protein; 369 AA.
 XX
 AC ABR62522;
 DT 06-NOV-2003 (first entry)
 XX
 DE Human G-protein coupled receptor HGRBM734 variant.
 XX
 KW HGRBM734; G-protein coupled receptor; receptor; GPCR-P14; GPCR-145;
 KM human; neuroprotective; nootropic; tranquilizer; antigraine;
 KW neuroleptic; anti manic; antidepressant; anticonvulsant; antiparkinsonian;
 KW cyostatic; cardiac; hypotensive; antianginal; analgesic; anorectic;
 KM anti-HIV; antiashtmatic; osteopathic; uropathic; antulcer; antiallergic;
 XX gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key
 XX
 FH Domain
 FT 16..37
 FT /label= TM1
 FT /note= "transmembrane domain 1"
 FT 65..87
 FT /label= TM2
 FT /note= "transmembrane domain 2"
 FT 109..131
 FT /label= TM3
 FT /note= "transmembrane domain 3"
 FT 148..166
 FT /label= TM4
 FT /note= "transmembrane domain 4"
 FT 182..208
 FT /label= TM5
 FT /note= "transmembrane domain 5"

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FT      Domain      227..249
FT      /label= TM6
FT      /note= "transmembrane domain 6"
FT      Domain      269..288
FT      /label= TM7
FT      /note= "transmembrane domain 7"
XX
XX      WO2003050256-A2.
XX
XX      19-JUN-2003.
XX
XX      06-DEC-2002; 2002WO-US039290.
XX
XX      06-DEC-2001; 2001US-0338371P.
XX
XX      (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX      Feder JN, Gopal S, Mintier GA, Ramanathan CS;
XX
XX      WPI; 2003-577295/54.
XX      N-PSDB; ACF05276.
XX
XX      New nucleic acid molecule encoding a human G-protein coupled receptor,
XX      HGRPMY34, useful for diagnosing, preventing or treating diseases
XX      involving the receptor, for example Parkinson's disease, dementia,
XX      asthma, hypertension or cancer.
XX
XX      Claim 5; Fig 2A-B; 112pp; English.
XX
XX      The present sequence is the protein sequence of a variant of human
XX      HGRPMY34 (see ABR62521) containing a deletion of 3 amino acids but
XX      expected to share at least some of the expression patterns and function
XX      of HGRPMY34. HGRPMY34 is a newly identified G-protein coupled receptor
XX      (GPCR) belonging to the group of 'Class A' GPCRs and showing homology to
XX      the Pfam model 7 transmembrane receptor, rhodopsin family. HGRPMY34 (or
XX      GPCR-P14, GPCR-145) is highly expressed in brain (amygdala, caudate
XX      nucleus, corpus callosum, hippocampus, thalamus, substantia nigra),
XX      spinal cord and pituitary, indicating an association in neurological
XX      systems and conditions. It is also expressed in the bone marrow and
XX      testis. The invention provides HGRPMY34 polynucleotides, polypeptides
XX      and antibodies, expression vectors, host cells and antisense molecules,
XX      methods for screening for modulators of HGRPMY34 activity and/or
XX      function, and methods for diagnosing, treating, preventing and screening
XX      for disorders and diseases associated with abnormal HGRPMY34 activity,
XX      including: a disorder related to aberrant G-protein coupled signalling; a
XX      disorder related to aberrant cell cycle regulation; neurological
XX      disorders; anxiety; headache; migraine; schizophrenia; manic depression;
XX      delirium; dementia; severe mental retardation and dyskinesias, such as
XX      Huntington's disease or Gilles de la Tourette's syndrome; Parkinson's
XX      disease; brain disorders; spinal cord disorders; affective disorders;
XX      neoplastic disorders; cardiovascular disorders; acute heart failure;
XX      hypotension; hypertension; angina pectoris; myocardial infarction; an
XX      immunological disorder; immune-related disorders; endocrine diseases;
XX      growth disorders; neuropathic pain; obesity; anorexia; HIV infections;
XX      cancers; bulimia; asthma; osteoporosis; psychosis; metabolic disorders;
XX      pituitary disorders; urinary retention; ulcers; allergies; or benign
XX      prostatic hypertrophy (all claimed)
XX
XX      Sequence 369 AA;
SQ
Query Match      98.8%; Score 1939.5; DB 6; Length 369;
Best Local Similarity 99.2%; Pred. No. 1.5e-206;
Matches 369; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY      1 MERTHAHLAANSLSWSPGACGAGFVPPVYVYSLICGLPANNITVTIISQVARROK 60
DB      1 MERTHAHLAANSLSWSPGACGAGFVPPVYVYSLICGLPANNITVTIISQVARROK 60
QY      61 SSVNYLALAAADIIILVFPFVDFPDLLEDFILMMQMPQVDPDKIIEVLESSHSITSMITWY 120
DB      61 SSVNYLALAAADIIILVFPFVDFPDLLEDFILMMQMPQVDPDKIIEVLESSHSITSMITWY 120
QY      121 PLTIDRYIAVCHPLKXHTVSYPARTRKVIYSYITCFLTSIPYMPNPINTEDYISTSVH 180

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DB      121 PLTIDRYIAVCHPLKXHTVSYPARTRKVIYSYITCFLTSIPYMPNPINTEDYISTSVH 180
QY      181 HYLWIFHCFTYVLPVPCISPFILNISTIVYLARKSNRFLRGYSGKTAILEFTTSIFATL 240
DB      181 HYLWIFHCFTYVLPVPCISPFILNISTIVYLARKSNRFLRGYSGKTAILEFTTSIFATL 240
QY      241 MAPRIIMILYHLYGAPIQNRWLHIMSIDIANNALNTAINFPLCYCFISKRPRYMAAATL 300
DB      241 MAPRIIMILYHLYGAPIQNRWLHIMSIDIANNALNTAINFPLCYCFISKRPRYMAAATL 300
QY      301 KAFPKQKQPVQVQFYTNHNSITSSPWSIPANSHCTKMLVYQYDKGKPKISRNDSSSQ 360
DB      301 KAFPKQKQPVQVQFYTNHNSITSSPWSIPANSHCTKMLVYQYDKGKPKISRNDSSSQ 357
QY      361 FEDATGACVITL 372
DB      358 FEDATGACVITL 369

RESULT 9
ADF70485
ID      ADF70485 standard; protein; 591 AA.
XX
XX      ADF70485;
XX
XX      12-FEB-2004 (first entry)
XX
XX      Orphan receptor ligand-related human protein SegID108.
XX
XX      ligand; orphan receptor protein; fusion protein; fluorescent protein;
XX      cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
XX      GFPuv; Enhanced GFP; EGFP; human.
XX
XX      Homo sapiens.
XX
XX      WO2003071272-A1.
XX
XX      28-AUG-2003.
XX
XX      21-FEB-2003; 2003WO-JP001901.
XX
XX      22-FEB-2002; 2002JP-00045728.
XX      23-JUL-2002; 2002JP-00213949.
XX      11-OCT-2002; 2002JP-00298237.
XX
XX      (TAKE ) TAKEBA CHEM IND LTD.
XX
XX      Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;
XX
XX      WPI; 2003-697654/66.
XX      N-PSDB; ADF70587.
XX
XX      Transformation of cells with a fusion protein of an orphan receptor
XX      protein with a fluorescent protein useful for identification of ligands
XX      to the orphan receptor.
XX
XX      Disclosure; SEQ ID NO 108; 594pp; Japanese.
XX
XX      This invention relates to a novel method of identifying ligands to an
XX      orphan receptor protein which comprises transforming cells with DNA
XX      encoding a fusion protein of the orphan receptor with a fluorescent
XX      protein, so that the fusion protein is expressed in the cells (or cell
XX      membranes isolated from them) and contacting the cells with the potential
XX      ligand to be tested. A suitable fluorescent protein for incorporation in
XX      the fusion protein is green fluorescent protein (GFP), for example GFP-1,
XX      wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the
XX      identification of ligands binding to an orphan receptor protein.
XX
XX      Sequence 591 AA;
SQ
Query Match      94.8%; Score 1864; DB 7; Length 591;
Best Local Similarity 96.7%; Pred. No. 7.5e-198;

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Matches 353; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 1 MENTHAHLAANSSLSWSPGACGIFVPPVYVYLLCLGLPANILTYIIISQVARRQK 60
DB 1 MENTHAHLAANSSLSWSPGACGIFVPPVYVYLLCLGLPANILTYIIISQVARRQK 60
QY 61 SSYNVLLAALADIVLFEIVFDLDFILNMQMPQVDPKIIIEVLEFSSIHSTIWTV 120
DB 61 SSYNVLLAALADIVLFEIVFDLDFILNMQMPQVDPKIIIEVLEFSSIHSTIWTV 120
QY 121 PLTIDRYAVCHPLKXHTVSPARTRKIVSVYITCFLTSPYWMWPNIMTEDYISTSVH 180
DB 121 PLTIDRYAVCHPLKXHTVSPARTRKIVSVYITCFLTSPYWMWPNIMTEDYISTSVH 180
QY 181 HVLIMHCFVTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
DB 181 HVLIMHCFVTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
QY 241 WAPRIIMLYLHYGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKRFRTMAAATL 300
DB 241 WAPRIIMLYLHYGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKRFRTMAAATL 300
QY 301 KAFKCKQKQPVQFTNNHFSITSSPWISPAHSGCIKMLVYQYDKNGKPIKVSPPSKGSEL 360
DB 301 KAFKCKQKQPVQFTNNHFSITSSPWISPAHSGCIKMLVYQYDKNGKPIKVSPPSKGSEL 360
QY 361 FEDAI 365
DB 361 FTGVV 365

RESULT 10
AAU76416
ID AAU76416 standard; protein; 353 AA.
XX
AC AAU76416;
XX
DT 08-MAY-2002 (first entry)
XX
DE Novel G-protein coupled receptor TGR8.
XX
KM G-protein coupled; receptor; cardiovascular; immunomodulator; TGR8;
KM cytosolic; antiinflammatory; antidiarr; fetal brain;
KM central nervous system disease; circulatory organ disorder; cancer;
KM metabolic disease; immunological disease; gastrointestinal disease;
KM gene therapy; transgenic animal; human.
XX
OS Homo sapiens.
XX
FN WO200194582-A1.
XX
PD 13-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-JP004643.
XX
PR 02-JUN-2000; 2000JP-00170446.
XX
PR 23-JUN-2000; 2000JP-00194926.
XX
PA (TAKEDA ) TAKEDA CHEM IND LTD.
XX
PI Terao Y, Matsui H, Shintani Y;
XX
DR WPI; 2002-164317/21.
XX
DR N-PSDB; ABK15562, ABK15563.
XX
PT Human fetal brain-originated G protein-coupled receptor protein TGR8 and
PT encoding DNA, for developing drugs to treat e.g. diseases of the central
PT nervous system or circulatory organs, cancer, and metabolic diseases.
XX
PS Claim 1; Fig 2; 102pp; Japanese.
XX
CC The invention describes a human fetal brain-originated G protein-coupled
CC receptor protein, or its salt. The protein and encoded DNA are useful for
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CC developing drugs to treat e.g. diseases of the central nervous system or
CC circulatory organs, cancer, metabolic diseases, immunological diseases
CC and gastrointestinal diseases. The invention also describes creation of a
CC probe for gene therapy and construction of a transgenic animal. This is
CC the amino acid sequence of the novel G-protein coupled receptor TGR8,
CC described in the method of the invention
XX
SQ Sequence 353 AA;
XX
Query Match 94.4%; Score 1857; DB 5; Length 353;
Beet Local Similarity 100.0%; Pred. No. 2.2e-197;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MENTHAHLAANSSLSWSPGACGIFVPPVYVYLLCLGLPANILTYIIISQVARRQK 60
DB 1 MENTHAHLAANSSLSWSPGACGIFVPPVYVYLLCLGLPANILTYIIISQVARRQK 60
QY 61 SSYNVLLAALADIVLFEIVFDLDFILNMQMPQVDPKIIIEVLEFSSIHSTIWTV 120
DB 61 SSYNVLLAALADIVLFEIVFDLDFILNMQMPQVDPKIIIEVLEFSSIHSTIWTV 120
QY 121 PLTIDRYAVCHPLKXHTVSPARTRKIVSVYITCFLTSPYWMWPNIMTEDYISTSVH 180
DB 121 PLTIDRYAVCHPLKXHTVSPARTRKIVSVYITCFLTSPYWMWPNIMTEDYISTSVH 180
QY 181 HVLIMHCFVTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
DB 181 HVLIMHCFVTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
QY 241 WAPRIIMLYLHYGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKRFRTMAAATL 300
DB 241 WAPRIIMLYLHYGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKRFRTMAAATL 300
QY 301 KAFKCKQKQPVQFTNNHFSITSSPWISPAHSGCIKMLVYQYDKNGKPIK 350
DB 301 KAFKCKQKQPVQFTNNHFSITSSPWISPAHSGCIKMLVYQYDKNGKPIK 350

RESULT 11
ABJ04075
ID ABJ04075 standard; protein; 353 AA.
XX
AC ABJ04075;
XX
DT 11-OCT-2002 (first entry)
XX
DE Human G protein coupled receptor hRUP35.
XX
KM Human; G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31;
KM hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37.
XX
OS Homo sapiens.
XX
FN WO200242461-A2.
XX
PD 30-MAY-2002.
XX
PF 26-NOV-2001; 2001WO-US044386.
XX
PR 27-NOV-2000; 2000US-0253404P.
XX
PR 12-DEC-2000; 2000US-0253366P.
XX
PR 20-FEB-2001; 2001US-0270266P.
XX
PR 20-FEB-2001; 2001US-0270286P.
XX
PR 06-APR-2001; 2001US-0282032P.
XX
PR 06-APR-2001; 2001US-0282356P.
XX
PR 06-APR-2001; 2001US-0282358P.
XX
PR 06-APR-2001; 2001US-0282365P.
XX
PR 14-MAY-2001; 2001US-0290917P.
XX
PR 31-JUL-2001; 2001US-0309208P.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
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XX DX MPI, 2002-566565/60.
DR N-PSDB; ABT04873.
XX PT Novel endogenous and non-endogenous versions of G protein-coupled
XX PT receptor useful for identification of candidate compounds as receptor
XX PT agonists or antagonists for use as therapeutic agents.
XX PS Claim 29; Page 70-72; 84pp; English.
XX CC The present invention provides the protein and coding sequences of
XX CC several human G-protein coupled receptors (GPCRs). These can be used in
XX CC the identification of candidate compounds as receptor agonists or inverse
XX CC agonists having applicability as therapeutic agents. The present sequence
XX CC is a GPCR protein of the invention
XX SQ Sequence 353 AA;
XX
XX Query Match 94.4%; Score 1857; DB 5; Length 353;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-197;
XX Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHTAHLAANSSLSWSPGACGLGFVPPVYVYSLLCGLPANILTVIILSQLVAROK 60
DB 1 MEHTAHLAANSSLSWSPGACGLGFVPPVYVYSLLCGLPANILTVIILSQLVAROK 60
QY 61 SSVNYLLAAADIIIVLPFIVDFLEDFILNMOMPOVPDKIIEVLEFSSIHSTSWITV 120
DB 61 SSVNYLLAAADIIIVLPFIVDFLEDFILNMOMPOVPDKIIEVLEFSSIHSTSWITV 120
QY 121 PLTIDRYIAVCHPLKXHTVSPARTRKIVSVYITCFLSIPYMWPNMTEDYISTSVH 180
DB 121 PLTIDRYIAVCHPLKXHTVSPARTRKIVSVYITCFLSIPYMWPNMTEDYISTSVH 180
QY 181 HVLIMHCTFTVYLVPCSIFFILNSIIYVKLRKSNFRLGYSTGKTTALFTTTSIFATL 240
DB 181 HVLIMHCTFTVYLVPCSIFFILNSIIYVKLRKSNFRLGYSTGKTTALFTTTSIFATL 240
QY 241 WAPRIIMILYHLYGAPIQRWLVIHMSDIANMLALNTAINPFLYCFISKRRTMAAATL 300
DB 241 WAPRIIMILYHLYGAPIQRWLVIHMSDIANMLALNTAINPFLYCFISKRRTMAAATL 300
QY 301 KAFPKCQKOPVOFYTNHNFSTSSPWIISPANSHCIKMLVYQYDKNGKPIK 350
DB 301 KAFPKCQKOPVOFYTNHNFSTSSPWIISPANSHCIKMLVYQYDKNGKPIK 350
XX
XX RESULT 12
XX ABB79517
XX ID ABB79517 standard; protein; 353 AA.
XX AC ABB79517;
XX DT 23-SEP-2002 (first entry)
XX DE Human chemokine-like receptor.
XX KM Chemokine-like receptor; G-protein coupled receptor; receptor; human;
XX KM HIV infection; cardiovascular disease; asthma;
XX KM chronic obstructive pulmonary disease; cardiac; antiasthmatic;
XX KM vasodilator; hypotensive; antiarrhythmic; thrombolytic; anticoagulant;
XX KM antiinflammatory; antiallergic; immunomodulator; gene therapy.
XX OS Homo sapiens.
XX PN WO200248358-A2.
XX PD 20-JUN-2002.
XX PF 12-DEC-2001; 2001WO-EP014571.
XX PR 14-DEC-2000; 2000US-0255150P.
XX PR 02-APR-2001; 2001US-0280110P.
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PR 21-JUN-2001; 2001US-0299474P.
XX PA (FARB ) BAYER AG.
XX PI Smolyar A, Zhu Z, Encinas J, Watanabe S, Okigami H;
XX DR MPI, 2002-547858/58.
XX DR N-PSDB; ABN84269, ABN84273.
XX PT New isolated polynucleotide encoding a chemokine-like receptor
XX PT polypeptide for treating e.g. asthma, myocardial infarction, human
XX PT immunodeficiency virus infection, or chronic obstructive pulmonary
XX PS disease.
XX PS Claim 25; Fig 2; 114pp; English.
XX
XX CC The present sequence is the protein sequence of a novel human chemokine-
XX CC like receptor of 353 amino acids. The chemokine-like receptor has 7
XX CC putative transmembrane domains, consistent with the structure of a G-
XX CC protein coupled receptor. Its closest human homologue is C-C chemokine
XX CC receptor 3. The novel receptor is expressed at low levels in most
XX CC tissues. It is expressed at a high level in phytohemagglutinin-
XX CC stimulated CD8+ cells, but in none of the other immune cells tested. It
XX CC may act as a receptor of chemottractant molecules on activated
XX CC lymphocytes and be involved in cell trafficking and homing to sites of
XX CC infection, inflammation or tissue injury. Regulation of activity of the
XX CC novel receptor can therefore be used to treat cardiovascular,
XX CC immunological and inflammatory diseases, including asthma and chronic
XX CC obstructive pulmonary disease (COPD). The receptor may also be a target
XX CC for viruses that reside in the nervous system. Regulating the binding of
XX CC ligands, e.g. chemottractant molecules or virus particles, to the
XX CC receptor can therefore be used to modulate the immune response to inhibit
XX CC viral infections, including HIV infection. A claimed method of reducing
XX CC activity of the receptor involves contacting a cell with a reagent
XX CC (preferably an antibody, antisense oligonucleotide or ribozyme) to a
XX CC product (preferably RNA or a polypeptide) encoded by a polynucleotide
XX CC encoding the human chemokine-like receptor in vivo or in vitro. A claimed
XX CC method of treating a chemokine-like receptor dysfunction related disease
XX CC selected from HIV infection, a cardiovascular disorder, asthma or COPD
XX CC uses a reagent that modulates a function of the receptor
XX SQ Sequence 353 AA;
XX
XX Query Match 94.4%; Score 1857; DB 5; Length 353;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-197;
XX Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHTAHLAANSSLSWSPGACGLGFVPPVYVYSLLCGLPANILTVIILSQLVAROK 60
DB 1 MEHTAHLAANSSLSWSPGACGLGFVPPVYVYSLLCGLPANILTVIILSQLVAROK 60
QY 61 SSVNYLLAAADIIIVLPFIVDFLEDFILNMOMPOVPDKIIEVLEFSSIHSTSWITV 120
DB 61 SSVNYLLAAADIIIVLPFIVDFLEDFILNMOMPOVPDKIIEVLEFSSIHSTSWITV 120
QY 121 PLTIDRYIAVCHPLKXHTVSPARTRKIVSVYITCFLSIPYMWPNMTEDYISTSVH 180
DB 121 PLTIDRYIAVCHPLKXHTVSPARTRKIVSVYITCFLSIPYMWPNMTEDYISTSVH 180
QY 181 HVLIMHCTFTVYLVPCSIFFILNSIIYVKLRKSNFRLGYSTGKTTALFTTTSIFATL 240
DB 181 HVLIMHCTFTVYLVPCSIFFILNSIIYVKLRKSNFRLGYSTGKTTALFTTTSIFATL 240
QY 241 WAPRIIMILYHLYGAPIQRWLVIHMSDIANMLALNTAINPFLYCFISKRRTMAAATL 300
DB 241 WAPRIIMILYHLYGAPIQRWLVIHMSDIANMLALNTAINPFLYCFISKRRTMAAATL 300
QY 301 KAFPKCQKOPVOFYTNHNFSTSSPWIISPANSHCIKMLVYQYDKNGKPIK 350
DB 301 KAFPKCQKOPVOFYTNHNFSTSSPWIISPANSHCIKMLVYQYDKNGKPIK 350
XX
XX RESULT 13
```

ABP98724
ID ABP98724 standard; protein; 353 AA.
XX
AC ABP98724;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human AXOR-57 protein.
XX
KW Antibacterial; antifungal; antiviral; antiparasitic; analgesic;
KW cytoskeletal; antidiabetic; anorectic; anabolic; antitachycardic; antiparkinsonian; cardiac; hypotensive; hypertensive; nephrotropic;
KW osteoporotic; antianalgesic; antileuc; antiallergic; antimigraine; agonist;
KW antiemetic; nootropic; tranquilizer; neuroprotective; antidepressant;
KW vaccinal; gene therapy; G-protein coupled receptor; receptor; infection;
KW pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; stroke;
KW parkinson's disease; osteoporosis; angina pectoris; ulcer; allergy;
KW vomiting; schizophrenia; depression; dementia; Huntington's disease.
XX
OS Homo sapiens.
XX
PN GB2365009-A.
XX
PD 13-FEB-2002.
XX
PF 11-APR-2001; 2001GB-00009018.
XX
PR 11-APR-2001; 2001GB-00009018.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Elehoubagy N, Gattu M, Michalovich D, Shabon U;
XX
DR WPI; 2003-203569/20.
XX N-PsDB; ACC44115.
XX
PT New G-protein coupled receptor, AXOR 57, for diagnosing and treating
XX diseases, such as, pain, cancer, diabetes, obesity, anorexia, asthma,
XX parkinson's disease, hypotension, hypertension, urinary retention, and
XX osteoporosis.
XX
PS Claim 1; Page 27-28; 32pp; English.
XX
CC The invention relates to the isolation of a novel G-protein coupled (7TM)
CC receptor AXOR 57 (this sequence) or a DNA fragment encoding a polypeptide
CC having at least 95% identity with AXOR-57 protein. The protein has been
CC shown to have homology to the human chromosome 16 clone C17B-H1 036A2
CC (AC008785). The protein and polynucleotides encoding the protein are used
CC in screening for compounds that stimulate or inhibit the function or
CC level of the polypeptide or polynucleotides, such as, agonists and
CC antagonists. The protein, polynucleotides, and antibodies to the protein
CC are used in diagnostic kits, to diagnose a disease. Polynucleotides
CC encoding the protein are used for chromosome localization studies, or for
CC tissue expression studies. The protein and nucleic acids encoding the
CC protein are used in vaccines for treating diseases such as, bacterial,
CC fungal, protozoal, and viral infections, pain, cancer, diabetes, obesity,
CC anorexia, bulimia, asthma, parkinson's disease, acute heart failure,
CC hypertension, hypertension, urinary retention, osteoporosis, angina
CC pectoris, myocardial infection, stroke, ulcer, allergy, benign prostatic
CC hyper trophy, migraine, vomiting, anxiety, schizophrenia, depression,
CC delirium, dementia, severe mental retardation, or Huntington's disease
XX
SQ Sequence 353 AA;

Qy	6	SSNNVLLAALAADILVLPFIVVDLLEDFILNMQMPVPRKIEVLEFSSIHSMITV	120
Qy	6	SSNNVLLAALAADILVLPFIVVDLLEDFILNMQMPVPRKIEVLEFSSIHSMITV	120
Db	61	SSNNVLLAALAADILVLPFIVVDLLEDFILNMQMPVPRKIEVLEFSSIHSMITV	120
Qy	121	PLTIDRYIANVCHPLKXHTVSYPARTRKIVSVSYITCFLTJSPYYWMENIWTEDYISTVH	180
Db	121	PLTIDRYIANVCHPLKXHTVSYPARTRKIVSVSYITCFLTJSPYYWMENIWTEDYISTVH	180
Qy	181	HVLIMHCFVYVLPQCSIFILNSTIYVKLRKRSNFRGRSGSTCKTALIFTTISFATL	240
Db	181	HVLIMHCFVYVLPQCSIFILNSTIYVKLRKRSNFRGRSGSTCKTALIFTTISFATL	240
Qy	241	WAPRIIMLYLHVGAPIQNRMLVHIMSDIANMLALNTAINFPLYCEISKRFRTMAATL	300
Db	241	WAPRIIMLYLHVGAPIQNRMLVHIMSDIANMLALNTAINFPLYCEISKRFRTMAATL	300
Qy	301	KAPFKCKQKQPVQYTYHNHNSITSSSWISPANSHCKMLVYDQNGKPIK	350
Db	301	KAPFKCKQKQPVQYTYHNHNSITSSSWISPANSHCKMLVYDQNGKPIK	350

RESULT 14
ABR44437
ID ABR44437 standard; protein; 353 AA.
XX ABR44437;
XX
DT 25-JUL-2003 (first entry)
XX
DE Human G protein-coupled receptor #SEQ ID 2.
XX
KW Human; G protein-coupled receptor; anorectic; eating disorder; obesity.
XX
OS Homo sapiens.
XX
PN WO2003027142-A1.
XX
PD 03-APR-2003.
XX
PF 19-SEP-2002; 2002WO-JP009626.
XX
PR 21-SEP-2001; 2001JP-00288278.
XX
PA (YAMA) YAMANOUCHI PHARM CO LTD.
XX
PI Matsumoto S, Takasaki J, Kurama T, Saito T, Kamohara M, Soga T;
XX Hiyama H;
XX WPI; 2003-333291/31.
DR N-PSDB; ACC71785.
XX
PT New G protein-coupled receptor and encoded gene, useful in screening
PT preventives or remedies for eating disorders or obesity.
XX
PS Claim 1; Page 34-35; 48pp; Japanese.
XX
CC The invention relates to a novel G protein-coupled receptor. The protein
CC and its encoded gene are useful for screening preventives or remedies for
CC eating disorders or obesity. The current sequence represents a G protein
CC coupled receptor sequence
XX
SQ Sequence 353 AA;

[illegible]

Query Match	94.4%	Score 1857	DB 6	Length 353
Best Local Similarity	100.0%	Pred. No. 2.2e-197		
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Db	1	MEHTHAIIAANSLSNMSPGACGAFVWVYYSLLTCLGEPANILFYIILSQLVAROK	60	
Qy	61	SSVNYLLAALADILVFTVFVDLLFEDILNMOMPVPVKIIEVLEFSSIHFTSIWTV	120	

Db 61 SSYNTLLAALAAADIVLFFVVDLLEDFILNMQMPQVPDKIEVLEFSSIHSTIWTV 120
QY 121 PLTIDRYIAVCHPLKXHTVSPARTRKVIYSVYITCFLTSPYWMNPINWTEDYISTSVH 180
Db 121 PLTIDRYIAVCHPLKXHTVSPARTRKVIYSVYITCFLTSPYWMNPINWTEDYISTSVH 180
QY 181 HVLIMHCTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTALFTITSIFATL 240
Db 181 HVLIMHCTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTALFTITSIFATL 240
QY 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFELYCFISKRRPTMAAATL 300
Db 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFELYCFISKRRPTMAAATL 300
QY 301 KAFPKCQKQPVQFYTNHNFSTSSPWISPANSHCIKMLVYQYDKNGKPIK 350
Db 301 KAFPKCQKQPVQFYTNHNFSTSSPWISPANSHCIKMLVYQYDKNGKPIK 350

RESULT 15

ABB82499
ID ABB82499 standard; protein; 353 AA.

AC ABB82499;

DT 22-JAN-2003 (first entry)

DE Human TGR20 polypeptide.

KM G-protein coupled receptor; GPCR; antipsoriatic; antiinflammatory;
KW antileptic; nootropic; neuroprotective; antianemic; antidiabetic; human;
KW antiparkinsonian; antileptic; TGR20; receptor.

OS Homo sapiens.

PN WO200277001-A2.

PD 03-OCT-2002.

PF 08-MAR-2002; 2002WO-US007171.

PR 09-MAR-2001; 2001US-00802803.

PR 16-MAR-2001; 2001US-0276649P.

PA (TULA-) TULARIK INC.

PI Tian H, Zhao J, Chen J, Cutler G;

DR WPI; 2003-018881/01.

DR N-PSDB; ABV73364.

PT New G-protein coupled receptor polypeptides and polynucleotides useful
PT for identifying compounds for treating a TGR-associated disorder, e.g.
PT psoriasis, inflammatory bowel disease, hyperlipidemia, Parkinson's
PT disease, anemia.

PS Claim 15; Page 63; 87pp; English.

CC The invention relates to G-protein coupled receptor (GPCR) polypeptides
CC and encoding polynucleotides selected from TGR20, TGR35, TGR36, TGR183,
CC TGR341, TGR211, TGR216 and TGR79. The polypeptides and nucleic acids are
CC useful for identifying compounds for treating a TGR-associated disorder,
CC such as psoriasis, inflammatory bowel disease, hyperlipidemia,
CC Parkinson's disease, Huntington's disease, anemia, immune and blood
CC disorders, ulcerative colitis, Crohn's disease or spleen enlargement.
CC They are also useful for identifying cells such as kidney, liver,
CC hypothalamus, colon, adipose, or spleen cells, for forensics and
CC paternity determination, diagnosing diseases and examining signal
CC transduction. The present sequence represents a human TGR20 polypeptide
CC
SQ Sequence 353 AA;

Best Local Similarity 100.0%; Pred. No. 2.2e-197;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHTAHLAANGSLSMWSPGACGAFVYVYSSLLCLGLPANILTVIISQVARROK 60
Db 1 MEHTAHLAANGSLSMWSPGACGAFVYVYSSLLCLGLPANILTVIISQVARROK 60
QY 61 SSYNTLLAALAAADIVLFFVVDLLEDFILNMQMPQVPDKIEVLEFSSIHSTIWTV 120
Db 61 SSYNTLLAALAAADIVLFFVVDLLEDFILNMQMPQVPDKIEVLEFSSIHSTIWTV 120
QY 121 PLTIDRYIAVCHPLKXHTVSPARTRKVIYSVYITCFLTSPYWMNPINWTEDYISTSVH 180
Db 121 PLTIDRYIAVCHPLKXHTVSPARTRKVIYSVYITCFLTSPYWMNPINWTEDYISTSVH 180
QY 181 HVLIMHCTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTALFTITSIFATL 240
Db 181 HVLIMHCTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTALFTITSIFATL 240
QY 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFELYCFISKRRPTMAAATL 300
Db 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFELYCFISKRRPTMAAATL 300
QY 301 KAFPKCQKQPVQFYTNHNFSTSSPWISPANSHCIKMLVYQYDKNGKPIK 350
Db 301 KAFPKCQKQPVQFYTNHNFSTSSPWISPANSHCIKMLVYQYDKNGKPIK 350

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Job time : 116.714 secs

Query Match

94.4%; Score 1857; DB 6; Length 353;

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GenCore version 5.1.6
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OM protein - protein search, using SW model

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Title: US-10-712-615-103

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	241	12.3	393	1	US-07-629-1041-3 Sequence 3, Appl
2	238.5	12.1	398	1	US-08-288-663A-1 Sequence 1, Appl
3	232	11.8	415	2	US-09-545-944-2 Sequence 2, Appl
4	232	11.8	415	2	US-10-215-919-2 Sequence 2, Appl
5	231.5	11.8	355	1	US-08-012-988A-2 Sequence 5, Appl
6	231.5	11.8	355	1	US-08-450-393A-5 Sequence 5, Appl
7	231.5	11.8	355	2	US-08-446-669-5 Sequence 5, Appl
8	231.5	11.8	355	2	US-09-239-938-1 Sequence 1, Appl
9	231.5	11.8	355	2	US-09-886-319A-14 Sequence 13, Appl
10	231.5	11.8	355	2	US-10-039-659A-13 Sequence 14, Appl
11	231.5	11.8	355	2	US-09-961-068-1 Sequence 1, Appl
12	231.5	11.8	355	2	US-09-625-573-5 Sequence 9, Appl
13	231.5	11.8	355	2	US-09-960-547-1 Sequence 1, Appl
14	231.5	11.8	355	4	PCT-US95-00476-5 Sequence 10,01, A
15	228	11.6	412	2	US-09-949-016-10101 Sequence 15, Appl
16	228	11.6	412	2	US-08-288-663A-15 Sequence 15, Appl
17	226.5	11.5	398	1	US-09-341-016A-1 Sequence 1, Appl
18	226	11.5	415	2	US-09-693-746-4 Sequence 8, Appl
19	225	11.4	357	2	US-08-833-752-9 Sequence 9, Appl
20	225	11.4	355	2	US-09-938-719-9 Sequence 9, Appl
21	223.5	11.4	355	2	US-09-938-719-9 Sequence 9, Appl
22	223.5	11.4	355	2	US-09-938-719-9 Sequence 9, Appl
23	223.5	11.4	355	2	US-09-938-719-9 Sequence 9, Appl
24	223.5	11.4	355	2	US-09-938-719-9 Sequence 9, Appl
25	223	11.3	352	2	US-09-029-027B-2 Sequence 47, Appl
26	222.5	11.3	347	1	US-08-118-270-47 Sequence 47, Appl
27	222.5	11.3	347	1	PCT-US93-08528-47 Sequence 47, Appl

28	219	11.1	353	1	US-08-118-270-45 Sequence 45, Appl
29	219	11.1	353	4	PCT-US93-08528-45 Sequence 45, Appl
30	219	11.1	367	1	US-08-149-093A-4 Sequence 4, Appl
31	219	11.1	367	1	US-08-911-245-4 Sequence 4, Appl
32	219	11.1	367	1	US-08-553-058C-4 Sequence 4, Appl
33	219	11.1	367	1	US-08-514-451A-4 Sequence 4, Appl
34	219	11.1	367	2	US-09-170-331-4 Sequence 4, Appl
35	219	11.1	367	2	US-09-510-473-4 Sequence 4, Appl
36	219	11.1	367	2	US-09-048-916B-4 Sequence 4, Appl
37	219	11.1	384	2	US-09-071-434-3 Sequence 4, Appl
38	218	11.1	378	2	US-09-045-583-5 Sequence 5, Appl
39	218	11.1	378	2	US-09-534-185-5 Sequence 5, Appl
40	217	11.0	355	2	US-09-045-583-53 Sequence 53, Appl
41	217	11.0	355	2	US-09-534-185-53 Sequence 53, Appl
42	217	11.0	367	1	US-08-454-549-2 Sequence 2, Appl
43	217	11.0	367	2	US-08-454-552-2 Sequence 2, Appl
44	217	11.0	367	2	US-08-147-592A-6 Sequence 6, Appl
45	217	11.0	367	2	US-08-889-108-17 Sequence 17, Appl

ALIGNMENTS

```
RESULT 1
US-07-629-1041-3
; Sequence 3, Application US/076291041
; Patent No. 5288621
; GENERAL INFORMATION:
; APPLICANT: Gershengorn, Marvin C
; APPLICANT: Straub, Richard E
; TITLE OF INVENTION: PITUITARY TRH RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/629,1041
; FILING DATE: 19901214
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26, 824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-629-1041-3

Query Match      12.3%; Score 241; DB 1; Length 393;
Best Local Similarity 22.1%; Pred. No. 1e-13;
Matches 81; Conservative 75; Mismatches 123; Indels 88; Gaps 15;

QY 19 PSACGLGF-VPVYVYSLLC-IGLPANILFVITISOLVAROKSSYN-YLLAAADPL 75
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 16 PQAAVALBQYVTTILVYIICGLGIVGINIVLVVNR--TKMRPTTCYLSLVADIM 73
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 76 VLFVTFVDFLEDFILNMQMPQVDPKI-----IEVLFSSHSHTSIWTVPL 122
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```

```

Db      74  VL-----VAAGLPNITDSIGSWYGVGCLCTVLYGLGNABSCSITAF 113
Qy      123 TIDRIANONHPLAKHTVSYPARTRKIVSYVITCELTSPYVW-----PNWT-EDYIS 176
      120 ||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 176
Db      120 TIERIALICHPIKAOFLCTFSRRAKKIILVMA--FTSIYCMLEPFLDLNISTYKNAV 176
Qy      177 TSVHVLIVIHGCFVYLVPCSIFFLINSI---IVY-----208
      177 ||:||||:||||:||||:||||:||||:||||:||||:||||: 176
Db      177 VSCGYKISRNYSPIYLMDFGVFYVPMILATVYGFARILEPILPDPKENSXMKMN 236
Qy      209 -KLARKSNRRLG-----YSTCKTALLETISIFATLMAR-RIMILVHLYGAR 257
      237 ||:||||:||||:||||:||||:||||:||||:||||:||||: 257
Db      237 DSIHONKINLNAATNRCENSTVSSRKQVKMLAAVVILFPLLMPPKTLVAVNSPLSSP 296
Qy      258 ONRWLVHIMSDIANMLALNTALNTAINEFLYCFISKRPRTMAAATLKAFFCKQCPVQPYTN 317
      297 ||:||||:||||:||||:||||:||||:||||:||||:||||: 317
Db      297 GENWFLL----PCRICIYNSAINPIVYINLMGKFR----AARUKLCNCKQKTEKAAVY 348
Qy      318 NPSITSS 324
Db      349 SVALNYS 355

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RESULT 2
US-08-288-663A-1
: Sequence 1, Application US/082886663A

Query Match	12.1%	Score 238.5	DB 1	Length 398
Best Local Similarity	22.4%	Pred. No. 1.6e-13		
Matches	80	Conservative	70	Mismatches 120
			Indels	87
			Gaps	13
Qy	28	VPVVVYSLLC-LGPANILTVIILSQVBAROKSSYN-YLLALAAADLYLFFVIFVDF	85	
Db	26	VVTLILVLIICGLGIVGINVVLVVMR--TGMRTPTNCYLVSLAVLADMLV-----	75	
Qy	86	LLDFILMMQHPQVBDK-----IEVLEBSHTSTWITVPLTIIDRIYAVCH	132	
Db	76	-----VAAGIPNITDSYGSWVYGVCGLCTIYQYLGIVNASSCSITAFIERIYAIACH	129	
Qy	133	PLKHYTVSYPRTRKVIYSVYITGFLNSIRPYW-----PNIMT-EDYISTSVHHVLMI	186	
Db	130	PIKQFLCTFSBRAKKILIEVNA--FTSLYCMLEFLLDLINISTYKDAIVISCGKISRN	186	
Qy	187	HCFVYVLVPCSIFFILNSIIYVKL-----	215	
Db	187	YSPILYMDPEVFYVVPMLATVLYGFIARLLFLNPISDPKENSCTWKQNSTHQNTMLN	246	
Qy	216	-----FRLGYSGTGTTALLFTITSIFATLMAP-RIIMLLYHLYGAPIQNRMLVHIMS	267	
Db	247	VNTSNRCFNSVSSSRKQYTKMLAVVILFALLMMPYRFLVAVNNSLSSPQENMFLL---	303	
Qy	268	DIANMLALNNAINPELYCFISKSPRTAAATLKAFFCQKQOPQVGYNNHNSITSS	324	
Db	304	-FCRCIYLNAINPVIYNILMSQKR-----AARFLCNCKQKPEKPRANYSVALNYS	355	

```

RESULT 3
US-09-545-944-2
; Sequence 2, Application US/09545944
; Patent No. 6461836
; GENERAL INFORMATION:
; APPLICANT: AMES, ROBERT
; APPLICANT: ELSHOURBAGY, NABIL
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: SARAU, HENRY
; APPLICANT: SHABON, USMAN
; APPLICANT: VAWTER, LISA
; TITLE OF INVENTION: MOLECULAR CLONING OF
; TITLE OF INVENTION: (AXOR34) AND SCREENING
; TITLE OF INVENTION: MOLECULAR CLONING OF
; FILE REFERENCE: GP70657-1
; CURRENT APPLICATION NUMBER: US/09/545,944
; CURRENT FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 09/435,384
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-545-944-2

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Query Match	11.8%;	Score 232;	DB 2;	Length 415;
Best Local Similarity	22.4%;	Pred. No. 7.3e-13;		
Matches 79;	Conservative 77;	Mismatches 112;	Indels 84;	Gaps 15

MOLECULE TYPE: protein
US-08-288-663A-1

Db 212 ----IYNFIQTSPFLPMTVISLVLYMALRLKOKSLEADGNANTQPCRSKN 267
QY 228 AILEFTTSIFATLMARIMILYHLGAPIONRM-----LVHIMSDIANMLALNT 278
Db 268 KMLFVLVLFALICMAFPHIDLRFPSF-----VEEMTESLAANVLVHVSGV---LFTYLS 320
QY 279 AINFLYCFISKRFRTMAATLKAFFKQKQPVQFTNNFSTTSPWISPA 330
Db 321 AVNPITYNLSRFRFOAFQNVISFHK-----QMSOHD-----POLPPA 360

RESULT 4
US-10-215-619-2

; Sequence 2, Application US/10215619
; Patent No. 6881827
; GENERAL INFORMATION:
; APPLICANT: AMES, ROBERT
; APPLICANT: ELISHOURBAGY, NABIL
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: SARAU, HENRY
; APPLICANT: SHABON, USMAN
; APPLICANT: VAWTER, LISA
; TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM RECEPTOR
; FILE REFERENCE: (AXOR34) AND SCREENING METHODS THEREOF
; CURRENT APPLICATION NUMBER: US/10/215,619
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/545,944
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 09/435,384
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-215-619-2

Query Match 11.8%; Score 232; DB 2; Length 415;

Best local Similarity 22.4%; Pred. No. 7.3e-13; Matches 79; Conservative 77; Mismatches 112; Indels 84; Gaps 15;

QY 27 FVPV-VYYSLLICLGPANILTVIILSQLVARROKSSYNYLLAALADIVLFFIYVDF 85
Db 45 FLFVSVVYPIFVGVIGVNLVCLVILQHOAKTPTNY-YLFSLAVSDELVL---LLGM 99
QY 86 LLEDFLINQMPP-----QVPDKIIEVLEFSSIHSTSWITVPLTIDRYIAVCHPLKXN 137
Db 100 PLEVEMMNRYPFLFGVGCYFKTALFETVCFASI---LSITT-VSEVERVALIHHPRAK 155
QY 138 TYSYPARTRKVIYSVYITCFLTSLP-----YMMNP-----INTEDY 174
Db 156 LOSTRRARRILIGIWFGLPNTSINGIHFYFPNOSLVPGSACTVIRKPMW---- 211
QY 175 ISTSVHVLWICFTVYLWPCSIFFILNSIIVYKLR-----KSNFLRGYSTGKT 227
Db 212 ----IYNFIQTSPFLPMTVISLVLYMALRLKOKSLEADGNANTQPCRSKN 267
QY 228 AILEFTTSIFATLMARIMILYHLGAPIONRM-----LVHIMSDIANMLALNT 278
Db 268 KMLFVLVLFALICMAFPHIDLRFPSF-----VEEMTESLAANVLVHVSGV---LFTYLS 320
QY 279 AINFLYCFISKRFRTMAATLKAFFKQKQPVQFTNNFSTTSPWISPA 330
Db 321 AVNPITYNLSRFRFOAFQNVISFHK-----QMSOHD-----POLPPA 360

RESULT 5
US-08-012-988A-2

; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:

; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1
; TITLE OF INVENTION: alpha)/RANTES Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Hourie and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,988A
; FILING DATE: 19930128
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-012-988A-2

Query Match 11.8%; Score 231.5; DB 1; Length 355;

Best local Similarity 26.3%; Pred. No. 6.7e-13; Matches 81; Conservative 57; Mismatches 105; Indels 65; Gaps 13;

QY 22 ACGLGFVPPVYYSLLICLGPANILTVIILSQLVARROKSSYNYLLAALADIVLFFIYVDF 81
Db 31 AFGAQLPLPL-YSLVFIQVLGNILVAVIQYKRLKNTSI-YLLNLAISDLFLFTLP 88
QY 82 F-VDF-LLEDFLINQMPPVDPKIIIEVLEFSSIHSTSWITVPLTIDRYIAVCH---PLKX 136
Db 89 FWDYKLDKDWFGDM---CKILSGFYTGYSIFPILITLTDRIYLAIVHAFALRA 144
QY 137 HTVSYPARTRKVIYSVYITCFLTSLP---YMMNPINTEDYISTSVH----- 181
Db 145 RIVTGVITSIILMALI---LASMGLYFSKTQMEFTHHTCSLHPHESLREKLPAL 201
QY 182 -----VLIWHCTVYLWPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTALIF 231
Db 202 KNLFGVLPLVIMICYT-----GIIRLLRPBNE-----KSKAVRLIF 242
QY 232 TITSIFATLMARIMILYHLGAPIONRM-----QNRVLHIMSDIANMLALNTAIFLY 285
Db 243 VIMILFELFWTPNLTILISVQDFLTHCEQSRHL-DLAVQVEVIAVTHCCVNPVY 301
QY 286 CFISKRFR 293
Db 302 AFVGERFR 309

RESULT 6
US-08-450-393A-5

; Sequence 5, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

Qy 22 ACCLGVPVWVYSSLLLCGLPANITFTVYLSQVARRKSSSYNLAAADIVFPIV 81
Db 31 AFGAQLLPPL-XSLVPIVIGLVNITLVAVLQVYRKLKMTSI-YLNLAIISDLFFPTLP 88
Qy 82 F-YDF-LTDEFLINQMGPVBDKIIIEVBSHSITSMITVPLIDBYIVACH---PLKY 136
Db 89 FMDIYKLDQWPFGDAM---CKLISGVTYIGLSLFIILLITIDRYLIAVHAPALRA 144
Qy 137 HTVSYPAARTKRVIVSYITCELTSP-YVMPNITWEDYSTSVNH----- 181
Db 145 RYTFPGVITSIIMALAI---LASNPGLVFSKTMQEPFHNCISHPHESIREWKLFOAL 201

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QY 182 -----VIMHCFIVYLAVPCSFPIIASIIYYKLRRKSNFPLRGSTGKTAILE 231
Db 202 KLNTFGLVLPILVIMICYT-----GIKILLRPRPE-----KSKAVRLIF 242
QY 232 TITSFATLMAPRIMILYLHLYGAPI-----QNRWLVIHMSDIANMLALLNAINPELY 285
Db 243 VIMILFELPMTVYNNLTILISVFQDFLETHCEQSRHL-DLAVQVTEVIAYTHCCVNPVI 301
QY 286 CFISKRFR 293
Db 302 AFVGERFR 309

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RESULT 11-068-1
 US-09-961-068-1
 Sequence 1, Application US/09961068
 Patent No. 6723570
 GENERAL INFORMATION:
 APPLICANT: Qin, Shixin
 APPLICANT: Newman, Walter
 APPLICANT: Kassam, Nassim
 TITLE OF INVENTION: ANTI-CCR4 ANTIBODIES AND METHODS OF USE
 TITLE OF INVENTION: THEREFOR
 FILE REFERENCE: 1855.1048-011
 CURRENT APPLICATION NUMBER: US/09/961,068
 CURRENT FILING DATE: 2001-09-21
 PRIOR APPLICATION NUMBER: US 09/239,938
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 355
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-961-068-1

Query Match	11.8%;	Score 231.5;	DB 2;	Length 355;
Best Local Similarity	26.3%;	Pred. No. 6.7e-13;		
Matches	81;	Conservative	57;	Mismatches 105;
			Indels	65;
			Gaps	13

Qy	22	ACGIEFVPRVYVYSSLLCGLPANILVITISOLVAROSSVYUULAAADILVFEFV	81
Dp	31	AFGAOLLPRLXSYLFPVIGVGNILVVLVQYKRLKMTSTYLNLAISDLLEFLLP	88
Qy	82	FVDFLLEDPLNQMOPVDPKIEVLBESSIHSTIMATVPLTDRIYAVCH--PLKY	136
Dp	89	FMIDPKLKDMDWFGDAM--CKLSGFGVYTGYSSEIFPILITIDRYALVAHVAPALRA	144
Qy	137	HTVSPARTKRAIVSVYTCFLTSLPYYMMPRIMEDYISTGVNH-----	161
Dp	145	RTVTEGVITSIITMALAI--LASMGLFASKQWEPHTHTGSLHPRHESREMKLEQAL	201
Qy	182	-----VLIWTHCFVTVYLVPCSIFFTLNSIYYKLRKSNFRLRGYSTGKTAALF	231
Dp	202	KLNLGGLVPLLVIMICVY-----GIILILRRPPE-----KSKAVRLIF	242
Qy	232	TITSIFATLMAPRIIMILVLCGAPI-----QNRMLVHMDSIDANLLALTNINEFLY	285
Dp	243	VIMILFPLEWTFYNNLTILISVQDFLTHBCBSRHL-DLAVQVTEVIAIATHCCVNPVIY	301
Qy	286	CFISKRF 293	
Dp	302	AFVGERFR 309	

RESULT 12
US-09-625-573-5
; Sequence 5, Application US/09625573
; Patent No. 6730301
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; Coughlin, Shaun
;

```

1  TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
2  PROTEIN RECEPTORS
3  NUMBER OF SEQUENCES: 14
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Cooley Godward Castro Huddleston & Tatum
6  STREET: 5 Palo Alto Square
7  CITY: Palo Alto
8  STATE: California
9  COUNTRY: USA
10 ZIP: 94306-2155
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Floppy disk
13 COMPUTER: IBM PC compatible
14 OPERATING SYSTEM: PC-DOS/MS-DOS
15 SOFTWARE: Patentin Release #1.0, Version #1.25
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/09/625,573
18 FILING DATE: 25-Jul-2000
19 CLASSIFICATION: <Unknown>
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US/08/446,669
22 FILING DATE: May 25, 1995
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Neeley, Richard
25 REGISTRATION NUMBER: 30,092
26 REFERENCE/DOCKET NUMBER: UCAL-237/01US
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 415-843-5000
29 TELEFAX: 415-857-0663
30 TELEX: 380816CooleyPA
31 INFORMATION FOR SEQ ID NO: 5:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 355 amino acids
34 TYPE: amino acid
35 TOPOLOGY: linear
36 MOLECULE TYPE: protein
37 HYPOTHEICAL: NO
38 ANTI-SENSE: NO
39 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
40
41 US-09-625-573-5

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Query Match	11.8% ; Score 231.5 ; DB 2 ; Length 355 ;
Best Local Similarity	26.3% ; Pred. No. 6, 76-113 ;
Matches	81 ; Conservative 57 ; Mismatches 105 ; Indels 65 ; Gaps 13 ;
QY	22 ACGAGPVPVVYISLLCLGEPANITVYIISQVAPRQKSSVNYLLADADIVLFFIV 81
DB	31 AFGQALLPPL-YSLVAFVIGLVGNLVLVLYVQYKRLNMTSI-VLNLMAISDLLFLFTLP 88
QY	82 F-VDF-LLEDPIILMOMQPOVDKIIIEVLFEFSIHTSIMVPLRIDRYAVCH---ELKY 136
DB	89 FMIDYKLDKDDVFPDAM----CKLISGFYITGLYSELFFIILLTIDRYLMAIVHAVFPLRA 144
QY	137 HTVSVPARTKRVISVYITCEFLTSIP-YVMWNMTWEDYISTSVNH----- 181
DB	145 RTVTFGVITSIIIMALAI---LASMPLGYESKTOEWETHHTCSAHFHESLREWKLFQAL 201
QY	182 -----VLWIHCFYLVYPCSIFFILNISIYVKLRKRSNPLRGYSTGKTALIF 231
DB	202 KLANPGLVLPRLWIIICYT-----GIKKLLRRPN-----KKSAAVRLIF 242
QY	232 TITSIPATLVAERIMILMLYHGAPF-----QNRWLVIHMSIDANMLALINTAINFLFY 285
DB	243 VIMIFIFELFWPYNULIISVFODFLPETHCEGSRHL-DLAVQUTEVIAATVCCNVNVIY 301

RESULT 13
US-09-960-547-1
; Sequence 1, Application US/09960547

Best Local Similarity 22.2%; Pred. No. 1.7e-12;
 Matches 78; Conservative 77; Mismatches 113; Indels 84; Gaps 15;
 Qy 27 FVPV-VVYSLLCGLPANILTVIISQIVAROKSSVNYLALAAADILVLFIVFVDF 85
 Db 42 FLPSVVVVPFIVGVIGNVLCVILQHQAKPTNY-YLFSLAVSDLVL---LGM 96
 Qy 86 LIEDFILNMQP-----QVPDKIEVLEFSSIHSTIWITVPLTIDRYIAVCHPLKYH 137
 Db 97 PLEVEMMRNYPFLPGVGCYFKTALFETVCFASI---LSITT-VSERYVALIHPRAK 152
 Qy 138 TVSYPARTRKVVSVYITCFLTSIP-----YWMMPN-----IWTEDY 174
 Db 153 LQSTRRALRIIGIVMGFSVLFSLPNTSIHGKIFHYFPNGSLVPGSATCTVIKPMW---- 208
 Qy 175 ISTSVHVLIMHCFVYLVPCSFPIINSIIVYKLRL-----KSNFRLRGYSTGKTT 227
 Db 209 ---IYNFIIOVTSFLYLEPWTIVSVLYMALRLKDKSLADEGNANIQRPCRSVN 264
 Qy 228 AILFTTISIPATLMAPIIMILYHLYGAPIQNRW-----LVHMSDIANMLALNT 278
 Db 265 KMLFVLVLVFAICWAPFHIDRLFSPF---VEWSESLAAVFNLVHVVGCV---PFYLS 317
 Qy 279 AINFLYCFISKRERTMAAATLKAFKQKQPVQFYTNHNFISITSSPWISPA 330
 Db 318 AVNPITYNLRSRFOAPQNVISIFHK-----QWHSQHD-----POLPPA 357

Search completed: December 3, 2005, 06:37:53
 Job time : 29.9 secs

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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:31:47 ; Search time 97.65 Seconds
(without alignments)
1591.731 Million cell updates/sec

Title: US-10-712-615-103
Perfect score: 1967
Sequence: 1 MEHTAHLAANSSLSWSPG.....NDSKSYOFDAICACVILL 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1967	100.0	372	US-09-813-432-20	Sequence 20, Appl
2	1967	100.0	372	US-10-219-834-19	Sequence 19, Appl
3	1967	100.0	372	US-10-314-076-2	Sequence 2, Appl
4	1967	100.0	372	US-10-174-364-20	Sequence 20, Appl
5	1967	100.0	372	US-10-333-946-6	Sequence 6, Appl
6	1967	100.0	372	US-10-246-583-20	Sequence 20, Appl
7	1967	100.0	372	US-10-689-832-20	Sequence 20, Appl
8	1967	100.0	372	US-10-712-615-103	Sequence 103, App
9	1939.5	98.6	369	US-10-314-076-4	Sequence 4, Appl
10	1864	94.8	591	US-10-505-486-108	Sequence 108, App
11	1857	94.4	350	US-09-813-432-60	Sequence 60, Appl
12	1857	94.4	350	US-10-174-364-60	Sequence 60, Appl
13	1857	94.4	350	US-10-246-583-60	Sequence 60, Appl
14	1857	94.4	350	US-10-689-832-60	Sequence 60, Appl
15	1857	94.4	353	US-09-995-225-16	Sequence 16, Appl
16	1857	94.4	353	US-09-995-225-16	Sequence 16, Appl
17	1857	94.4	353	US-10-094-417-2	Sequence 2, Appl
18	1857	94.4	353	US-10-296-294A-5	Sequence 2, Appl
19	1857	94.4	353	US-10-450-590-2	Sequence 2, Appl
20	1857	94.4	353	US-10-779-104-2	Sequence 2, Appl
21	1857	94.4	353	US-11-086-846-2	Sequence 2, Appl
22	1853	94.2	350	US-09-813-432-59	Sequence 59, Appl
23	1853	94.2	350	US-10-174-364-59	Sequence 59, Appl
24	1853	94.2	350	US-10-246-583-59	Sequence 59, Appl
25	1853	94.2	350	US-10-689-832-59	Sequence 59, Appl
26	1853	94.2	353	US-09-813-432-22	Sequence 22, Appl
27	1853	94.2	353	US-10-174-364-22	Sequence 22, Appl

28	1853	94.2	353	4	US-10-246-583-22	Sequence 22, Appl
29	1853	94.2	353	4	US-10-689-832-22	Sequence 22, Appl
30	1829	93.0	333	4	US-10-012-140-11	Sequence 11, Appl
31	1741	88.5	345	4	US-10-094-417-20	Sequence 20, Appl
32	1741	88.5	345	6	US-11-086-846-20	Sequence 20, Appl
33	1628	82.8	318	4	US-10-174-364-85	Sequence 85, Appl
34	1628	82.8	318	4	US-10-246-583-85	Sequence 85, Appl
35	1623	82.5	333	4	US-10-079-384-26	Sequence 26, Appl
36	1623	82.5	333	4	US-10-450-590-8	Sequence 8, Appl
37	1623	82.5	356	4	US-10-450-590-7	Sequence 7, Appl
38	1623	82.5	385	4	US-10-343-650A-22	Sequence 22, Appl
39	1623	82.5	388	5	US-10-745-237-376	Sequence 376, App
40	1611	81.9	333	5	US-10-297-990A-2	Sequence 2, Appl
41	1471	74.8	287	3	US-09-791-930A-66	Sequence 66, Appl
42	1426	72.5	272	3	US-09-813-432-57	Sequence 57, Appl
43	1426	72.5	272	3	US-09-813-432-58	Sequence 58, Appl
44	1426	72.5	272	4	US-10-174-364-57	Sequence 57, Appl
45	1426	72.5	272	4	US-10-246-583-57	Sequence 57, Appl

ALIGNMENTS

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RESULT 1
US-09-813-432-20
; Sequence 20, Application US/09813432
; Publication No. US20030148485A1
; GENERAL INFORMATION:
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Majmudar, Kamud
; APPLICANT: Spaderna, Steven K
; APPLICANT: Smithson, Glenda
; APPLICANT: Mezes, Peter S
; APPLICANT: Vernet, Corine A. M.
; TITLE OF INVENTION: No. US20030148485A1el Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729
; CURRENT APPLICATION NUMBER: US/09/813,432
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/193,843
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-432-20
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Query Match 100.0%; Score 1967; DB 3; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.8e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHTAHLAANSSLSWSPGACGLFVYVYVYLLCLGLPANIITVITLSQLVAROK 60

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Db 1 MEHTAHLAANSSLSWSPGSAAGLGFVAVVYYSLLCLGLPANILTVIILISQVARRQK 60
Qy 61 SSYNVLLAAADILVLFVDFLEDFILNMQMPQVDPKIIIVLEFSSIHSTIWTIV 120
Db 61 SSYNVLLAAADILVLFVDFLEDFILNMQMPQVDPKIIIVLEFSSIHSTIWTIV 120
Qy 121 PLTIDRYAVCHPLKHTVSPARTRKIVSVYITCFILTSIPYWMWPNITWEDYISTSVH 180
Db 121 PLTIDRYAVCHPLKHTVSPARTRKIVSVYITCFILTSIPYWMWPNITWEDYISTSVH 180
Qy 181 HVLWIHCFITYLVPCSFIFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
Db 181 HVLWIHCFITYLVPCSFIFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
Qy 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFLYCFISKRFRMAAATL 300
Db 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFLYCFISKRFRMAAATL 300
Qy 301 KAFKCOQOPQVFTNNHFSITSSPWISPA NSHCKIMLVYQYDKNGKPIKSRNDSKSSYQ 360
Db 301 KAFKCOQOPQVFTNNHFSITSSPWISPA NSHCKIMLVYQYDKNGKPIKSRNDSKSSYQ 360
Qy 361 FEDAGACVITL 372
Db 361 FEDAGACVITL 372

RESULT 2
US-10-219-834-19
; Sequence 19, Application US/10219834
; Publication No. US20030096751A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THE
; FILE REFERENCE: D0191 NP
; CURRENT APPLICATION NUMBER: US/10/219, 834
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/313, 658
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/340, 703
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: US 60/318, 675
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/355, 596
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/333, 417
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/338, 367
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 19
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-834-19

Query Match 100.0%; Score 1967; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.8e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 181 HVLWIHCFITYLVPCSFIFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
Db 181 HVLWIHCFITYLVPCSFIFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
Qy 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFLYCFISKRFRMAAATL 300
Db 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFLYCFISKRFRMAAATL 300
Qy 301 KAFKCOQOPQVFTNNHFSITSSPWISPA NSHCKIMLVYQYDKNGKPIKSRNDSKSSYQ 360
Db 301 KAFKCOQOPQVFTNNHFSITSSPWISPA NSHCKIMLVYQYDKNGKPIKSRNDSKSSYQ 360
Qy 361 FEDAGACVITL 372
Db 361 FEDAGACVITL 372

RESULT 3
US-10-314-076-2
; Sequence 2, Application US/10314076
; Publication No. US20030152977A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRTMY34, AND VARIANTS A
; FILE REFERENCE: D0197NP
; CURRENT APPLICATION NUMBER: US/10/314, 076
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: U.S. 60/338, 371
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-076-2

Query Match 100.0%; Score 1967; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.8e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4

US-10-174-364-20
; Sequence 20, Application US/10174364
; Publication No. US20030216308A1
; GENERAL INFORMATION:
; APPLICANT: Anderson et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-729CIP2
; CURRENT APPLICATION NUMBER: US/10/174,364
; PRIORITY FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-364-20

Query Match 100.0%; Score 1967; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.8e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHTHAHLAANSSLSWSPGACGLGFVPPVYVYSLLCGLPANILTVIIISQVARRK 60
1 MEHTHAHLAANSSLSWSPGACGLGFVPPVYVYSLLCGLPANILTVIIISQVARRK 60
DB 1 MEHTHAHLAANSSLSWSPGACGLGFVPPVYVYSLLCGLPANILTVIIISQVARRK 60
QY 61 SSYNYLLAALADIVLFFIVFDLLEDFILNMQMPQVDPKIEVLEFSSIHSTWTV 120
61 SSYNYLLAALADIVLFFIVFDLLEDFILNMQMPQVDPKIEVLEFSSIHSTWTV 120
DB 61 SSYNYLLAALADIVLFFIVFDLLEDFILNMQMPQVDPKIEVLEFSSIHSTWTV 120
QY 121 PLTIDRYIAVCHPLKHTVSYPARTRKVIYSYITCFLTSIPYWMNPNTEDYISTSVH 180
121 PLTIDRYIAVCHPLKHTVSYPARTRKVIYSYITCFLTSIPYWMNPNTEDYISTSVH 180
DB 121 PLTIDRYIAVCHPLKHTVSYPARTRKVIYSYITCFLTSIPYWMNPNTEDYISTSVH 180
QY 181 HVLIMHCFVTVLPSCIFFILNSIIYVKLRKSNRFLGYSGTGTTALFTTISFATL 240
181 HVLIMHCFVTVLPSCIFFILNSIIYVKLRKSNRFLGYSGTGTTALFTTISFATL 240
DB 181 HVLIMHCFVTVLPSCIFFILNSIIYVKLRKSNRFLGYSGTGTTALFTTISFATL 240
QY 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFPLYCFISKRFRMAATL 300
241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFPLYCFISKRFRMAATL 300
DB 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFPLYCFISKRFRMAATL 300
QY 301 KAFKCKQKOPVQYTTNHNFSITSSPWISPAHSHCIKMLVYQYDKNGKPIKSRDSSSYQ 360
301 KAFKCKQKOPVQYTTNHNFSITSSPWISPAHSHCIKMLVYQYDKNGKPIKSRDSSSYQ 360
DB 301 KAFKCKQKOPVQYTTNHNFSITSSPWISPAHSHCIKMLVYQYDKNGKPIKSRDSSSYQ 360
QY 361 FEDAIGACVITL 372
361 FEDAIGACVITL 372
DB 361 FEDAIGACVITL 372

RESULT 5
US-10-333-946-6

; Sequence 6, Application US/10333946
; Publication No. US20040023252A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B.
; APPLICANT: ARVIZU, Chandra S.; IAL, Preeti G.
; APPLICANT: BURFORD, Neil; YUE, Henry
; APPLICANT: GANDHI, Ameena R.; ELLIOTT, Vicki S.
; APPLICANT: RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R.
; APPLICANT: KALICK, Deborah A.; CHAWLA, Nardinder K.
; APPLICANT: HAPALIA, April J.A.; YAO, Monique G.
; APPLICANT: LU, Yan; TRIBOULEY, Catherine M.
; APPLICANT: POLICKY, Jennifer L.; KEARNEY, Liam
; APPLICANT: GRAULY, Richard C.; WARREN, Bridget A.
; APPLICANT: LEE, Ernestine A.; DING, Li
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0176 USN
; CURRENT APPLICATION NUMBER: US/10/333,946
; PRIORITY FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/23433
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/221,478
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/223,268
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/227,054
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/231,121
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,243
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/232,691
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/235,146
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20040023252A1 7474767CD1
US-10-333-946-6

Query Match 100.0%; Score 1967; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.8e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHTHAHLAANSSLSWSPGACGLGFVPPVYVYSLLCGLPANILTVIIISQVARRK 60
1 MEHTHAHLAANSSLSWSPGACGLGFVPPVYVYSLLCGLPANILTVIIISQVARRK 60
DB 1 MEHTHAHLAANSSLSWSPGACGLGFVPPVYVYSLLCGLPANILTVIIISQVARRK 60
QY 61 SSYNYLLAALADIVLFFIVFDLLEDFILNMQMPQVDPKIEVLEFSSIHSTWTV 120
61 SSYNYLLAALADIVLFFIVFDLLEDFILNMQMPQVDPKIEVLEFSSIHSTWTV 120
DB 61 SSYNYLLAALADIVLFFIVFDLLEDFILNMQMPQVDPKIEVLEFSSIHSTWTV 120
QY 121 PLTIDRYIAVCHPLKHTVSYPARTRKVIYSYITCFLTSIPYWMNPNTEDYISTSVH 180
121 PLTIDRYIAVCHPLKHTVSYPARTRKVIYSYITCFLTSIPYWMNPNTEDYISTSVH 180
DB 121 PLTIDRYIAVCHPLKHTVSYPARTRKVIYSYITCFLTSIPYWMNPNTEDYISTSVH 180
QY 181 HVLIMHCFVTVLPSCIFFILNSIIYVKLRKSNRFLGYSGTGTTALFTTISFATL 240
181 HVLIMHCFVTVLPSCIFFILNSIIYVKLRKSNRFLGYSGTGTTALFTTISFATL 240
DB 181 HVLIMHCFVTVLPSCIFFILNSIIYVKLRKSNRFLGYSGTGTTALFTTISFATL 240
QY 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFPLYCFISKRFRMAATL 300
241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFPLYCFISKRFRMAATL 300
DB 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFPLYCFISKRFRMAATL 300
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301 KAFKCKQKOPVQYTTNHNFSITSSPWISPAHSHCIKMLVYQYDKNGKPIKSRDSSSYQ 360
DB 301 KAFKCKQKOPVQYTTNHNFSITSSPWISPAHSHCIKMLVYQYDKNGKPIKSRDSSSYQ 360

QY 361 FEDAIGACVITL 372
 DB 361 FEDAIGACVITL 372

RESULT 6
 US-10-246-583-20
 ; Sequence 20, Application US/10246583
 ; Publication No. US20040058862A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Majmuder
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 15366-729CIP2CON1
 ; CURRENT APPLICATION NUMBER: US/10/246,583
 ; CURRENT FILING DATE: 2002-12-06
 ; PRIOR APPLICATION NUMBER: 10/174,364
 ; PRIOR FILING DATE: 2002-06-17
 ; PRIOR APPLICATION NUMBER: 60/190,835
 ; PRIOR FILING DATE: 2000-03-20
 ; PRIOR APPLICATION NUMBER: 60/190,768
 ; PRIOR FILING DATE: 2000-03-20
 ; PRIOR APPLICATION NUMBER: 60/190,972
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 60/191,199
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 60/191,947
 ; PRIOR FILING DATE: 2000-03-24
 ; PRIOR APPLICATION NUMBER: 60/192,665
 ; PRIOR FILING DATE: 2000-03-28
 ; PRIOR APPLICATION NUMBER: 60/192,657
 ; PRIOR FILING DATE: 2000-03-28
 ; PRIOR APPLICATION NUMBER: 60/192,984
 ; PRIOR FILING DATE: 2000-03-28
 ; PRIOR APPLICATION NUMBER: 60/192,664
 ; PRIOR FILING DATE: 2000-03-28
 ; Remaining Prior Application data removed - See file wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 372
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-246-583-20

Query Match 100.0%; Score 1967; DB 4; Length 372;
 Best Local Similarity 100.0%; Pred. No. 3.8e-173;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTAHLAANSSLSWSPGACGIGFVPPVYYSLLCLGLPANILTVIISQLVARROK 60
 DB 1 MEHTAHLAANSSLSWSPGACGIGFVPPVYYSLLCLGLPANILTVIISQLVARROK 60
 QY 61 SSYNVLLAAADILVFEIYFVDLEDFILNMQMPQVPDKIEVLEFSSIHISIMTV 120
 DB 61 SSYNVLLAAADILVFEIYFVDLEDFILNMQMPQVPDKIEVLEFSSIHISIMTV 120
 QY 121 PLTIDRYIAVCHPLKHYHTVSPARTRKIVSVYITCFILTSIPYWMWPNIMWEDYISTSVH 180
 DB 121 PLTIDRYIAVCHPLKHYHTVSPARTRKIVSVYITCFILTSIPYWMWPNIMWEDYISTSVH 180
 QY 121 PLTIDRYIAVCHPLKHYHTVSPARTRKIVSVYITCFILTSIPYWMWPNIMWEDYISTSVH 180
 DB 121 PLTIDRYIAVCHPLKHYHTVSPARTRKIVSVYITCFILTSIPYWMWPNIMWEDYISTSVH 180
 QY 181 HVLWIMHCFYVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAIFTTISIFATL 240
 DB 181 HVLWIMHCFYVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAIFTTISIFATL 240
 QY 241 WAPRIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKFRMAAATL 300
 DB 241 WAPRIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKFRMAAATL 300
 QY 301 KAFKCOQOPVOFTYNNHFSITSSPWISPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
 DB 301 KAFKCOQOPVOFTYNNHFSITSSPWISPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
 QY 361 FEDAIGACVITL 372

DB 361 FEDAIGACVITL 372

RESULT 7
 US-10-689-832-20
 ; Sequence 20, Application US/10689832
 ; Publication No. US20040121380A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Majmuder, Kamud
 ; TITLE OF INVENTION: Novel Polypeptides and Amino Acids Encoding Same
 ; FILE REFERENCE: 15966-729DIV1
 ; CURRENT APPLICATION NUMBER: US/10/689,832
 ; CURRENT FILING DATE: 2003-10-20
 ; PRIOR APPLICATION NUMBER: 09/813,432
 ; PRIOR FILING DATE: 2001-03-20
 ; PRIOR APPLICATION NUMBER: 60/190,835
 ; PRIOR FILING DATE: 2000-03-20
 ; PRIOR APPLICATION NUMBER: 60/190,768
 ; PRIOR FILING DATE: 2000-03-20
 ; PRIOR APPLICATION NUMBER: 60/190,972
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 60/191,199
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 60/191,947
 ; PRIOR FILING DATE: 2000-03-24
 ; PRIOR APPLICATION NUMBER: 60/192,665
 ; PRIOR FILING DATE: 2000-03-28
 ; PRIOR APPLICATION NUMBER: 60/192,657
 ; PRIOR FILING DATE: 2000-03-28
 ; PRIOR APPLICATION NUMBER: 60/192,984
 ; PRIOR FILING DATE: 2000-03-28
 ; PRIOR APPLICATION NUMBER: 60/192,664
 ; PRIOR FILING DATE: 2000-03-28
 ; Remaining Prior Application data removed - See file wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 372
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-689-832-20

Query Match 100.0%; Score 1967; DB 4; Length 372;
 Best Local Similarity 100.0%; Pred. No. 3.8e-173;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTAHLAANSSLSWSPGACGIGFVPPVYYSLLCLGLPANILTVIISQLVARROK 60
 DB 1 MEHTAHLAANSSLSWSPGACGIGFVPPVYYSLLCLGLPANILTVIISQLVARROK 60
 QY 61 SSYNVLLAAADILVFEIYFVDLEDFILNMQMPQVPDKIEVLEFSSIHISIMTV 120
 DB 61 SSYNVLLAAADILVFEIYFVDLEDFILNMQMPQVPDKIEVLEFSSIHISIMTV 120
 QY 121 PLTIDRYIAVCHPLKHYHTVSPARTRKIVSVYITCFILTSIPYWMWPNIMWEDYISTSVH 180
 DB 121 PLTIDRYIAVCHPLKHYHTVSPARTRKIVSVYITCFILTSIPYWMWPNIMWEDYISTSVH 180
 QY 121 PLTIDRYIAVCHPLKHYHTVSPARTRKIVSVYITCFILTSIPYWMWPNIMWEDYISTSVH 180
 DB 121 PLTIDRYIAVCHPLKHYHTVSPARTRKIVSVYITCFILTSIPYWMWPNIMWEDYISTSVH 180
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 DB 181 HVLWIMHCFYVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAIFTTISIFATL 240
 QY 241 WAPRIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKFRMAAATL 300
 DB 241 WAPRIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKFRMAAATL 300
 QY 301 KAFKCOQOPVOFTYNNHFSITSSPWISPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
 DB 301 KAFKCOQOPVOFTYNNHFSITSSPWISPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
 QY 361 FEDAIGACVITL 372

Db 361 FEDAIGACV1IL 372

RESULT 8
US-10-712-615-103
; Sequence 103, Application US/10712615
; Publication No. US20040214317A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY8, EXPRESSED
; TITLE OF INVENTION: HIGHLY IN BRAIN
; FILE REFERENCE: D0047A-CIP
; CURRENT APPLICATION NUMBER: US/10/712,615
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: U.S. 09/992,238
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: U.S. 60/248,285
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: U.S. 60/268,581
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/308,285
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: U.S. 60/317,166
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 103
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-712-615-103

Query Match 100.0%; Score 1967; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 3,8e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MHTHAHLAANSSLSWSPGSAAGLGFVVVYYSLLCLGLPANILTVIILSQLVAROK 60

Qy 61 SSYNVLLAALADILVLFPIVFDLLEDFILNMQMPQVDPDKIEVLEFSSIHSTIWTIV 120
Db 61 SSYNVLLAALADILVLFPIVFDLLEDFILNMQMPQVDPDKIEVLEFSSIHSTIWTIV 120

Qy 121 PLTIDRYIAVCHPLKHTVSPARTKRVISVYITCFLSIPYMWPNMTEDYISTSVH 180
Db 121 PLTIDRYIAVCHPLKHTVSPARTKRVISVYITCFLSIPYMWPNMTEDYISTSVH 180

Qy 181 HVLWIHCFTVYLVPCSIFFILNSIIVYGLRRKSNFRLRGYSTGKTTAILFTTISIFATL 240
Db 181 HVLWIHCFTVYLVPCSIFFILNSIIVYGLRRKSNFRLRGYSTGKTTAILFTTISIFATL 240

Qy 241 WAPRIIMILYHLYGAPIQNRMLVHMSDIANNLALNTAINFPLCYFISKRRTMAAATL 300
Db 241 WAPRIIMILYHLYGAPIQNRMLVHMSDIANNLALNTAINFPLCYFISKRRTMAAATL 300

Qy 301 KAFKQKOPVOFYTNHNSITSSPWISPAHSHCIKMLVYQYDKNGKPKSRNDSKSYQ 360
Db 301 KAFKQKOPVOFYTNHNSITSSPWISPAHSHCIKMLVYQYDKNGKPKSRNDSKSYQ 360

Qy 361 FEDAIGACV1IL 372
Db 361 FEDAIGACV1IL 372

RESULT 9
US-10-314-076-4
; Sequence 4, Application US/10314076
; Publication No. US20030152977A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY34, AND VARIANTS A
; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: D0197NP
; CURRENT APPLICATION NUMBER: US/10/314,076
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: U.S. 60/338,371
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-076-4

Query Match 98.6%; Score 1939.5; DB 4; Length 369;
Best Local Similarity 99.2%; Pred. No. 1.3e-170;
Matches 369; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 MHTHAHLAANSSLSWSPGSAAGLGFVVVYYSLLCLGLPANILTVIILSQLVAROK 60
Db 1 MHTHAHLAANSSLSWSPGSAAGLGFVVVYYSLLCLGLPANILTVIILSQLVAROK 60

Qy 61 SSYNVLLAALADILVLFPIVFDLLEDFILNMQMPQVDPDKIEVLEFSSIHSTIWTIV 120
Db 61 SSYNVLLAALADILVLFPIVFDLLEDFILNMQMPQVDPDKIEVLEFSSIHSTIWTIV 120

Qy 121 PLTIDRYIAVCHPLKHTVSPARTKRVISVYITCFLSIPYMWPNMTEDYISTSVH 180
Db 121 PLTIDRYIAVCHPLKHTVSPARTKRVISVYITCFLSIPYMWPNMTEDYISTSVH 180

Qy 181 HVLWIHCFTVYLVPCSIFFILNSIIVYGLRRKSNFRLRGYSTGKTTAILFTTISIFATL 240
Db 181 HVLWIHCFTVYLVPCSIFFILNSIIVYGLRRKSNFRLRGYSTGKTTAILFTTISIFATL 240

Qy 241 WAPRIIMILYHLYGAPIQNRMLVHMSDIANNLALNTAINFPLCYFISKRRTMAAATL 300
Db 241 WAPRIIMILYHLYGAPIQNRMLVHMSDIANNLALNTAINFPLCYFISKRRTMAAATL 300

Qy 301 KAFKQKOPVOFYTNHNSITSSPWISPAHSHCIKMLVYQYDKNGKPKSRNDSKSYQ 360
Db 301 KAFKQKOPVOFYTNHNSITSSPWISPAHSHCIKMLVYQYDKNGKPKSRNDSKSYQ 357

Qy 361 FEDAIGACV1IL 372
Db 358 FEDAIGACV1IL 369

RESULT 10
US-10-505-486-108
; Sequence 108, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Determination of a ligand
; FILE REFERENCE: P03-0006PCT
; CURRENT APPLICATION NUMBER: US/10/505,486
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: JP 2002-45728
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: JP 2002-298237
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 108
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Human
US-10-505-486-108

Query Match 94.8%; Score 1864; DB 5; Length 591;
Best Local Similarity 96.7%; Pred. No. 2.1e-163;
Matches 353; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

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Db 1 MEHTAHAAANSSLSWSPGACGIFPVVYVYSSLLCLGIPANTLTVIIISQVARROK 60
QY 61 SSYNVLLAAADIVLFFIYFVDFLEDFILNMQMPQVDPKIIIEVLFSSIHSTIWTIV 120
Db 61 SSYNVLLAAADIVLFFIYFVDFLEDFILNMQMPQVDPKIIIEVLFSSIHSTIWTIV 120
QY 121 PLTIDRYAVCHPLKXHTVSPARTRKVIIVSYITCFLTSPYVWPMIWTEDYISTSVH 180
Db 121 PLTIDRYAVCHPLKXHTVSPARTRKVIIVSYITCFLTSPYVWPMIWTEDYISTSVH 180
QY 181 HVLIMHGFYTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
Db 181 HVLIMHGFYTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
QY 241 WAPRIIMLYHLYGAPIONRMLVHIMSDIANMLALNTAINFFLYCFISKRRTMAAATL 300
Db 241 WAPRIIMLYHLYGAPIONRMLVHIMSDIANMLALNTAINFFLYCFISKRRTMAAATL 300
QY 301 KAFKCOQOPVOFYTNHNFISITSPWISPA NSHCIMLVYQYDKGKPIKVSPPSKGEEL 360
Db 301 KAFKCOQOPVOFYTNHNFISITSPWISPA NSHCIMLVYQYDKGKPIKVSPPSKGEEL 360
QY 361 FEDAI 365
Db 361 FTGVV 365
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RESULT 11

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US-09-813-432-60
; Sequence 60, Application US/09813432
; Publication No. US20030148485A1
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GENERAL INFORMATION:

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; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Majmuder, Kamud
; APPLICANT: Spaderna, Steven K
; APPLICANT: Smithson, Glenda
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: No. US20030148485A1el polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729
; CURRENT APPLICATION NUMBER: US/09/813,432
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/193,843
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-813-432-60
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Query Match 94.4%; Score 1857; DB 3; Length 350;
Best Local Similarity 100.0%; Pred. No. 5.1e-163;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MEHTAHAAANSSLSWSPGACGIFPVVYVYSSLLCLGIPANTLTVIIISQVARROK 60
QY 61 SSYNVLLAAADIVLFFIYFVDFLEDFILNMQMPQVDPKIIIEVLFSSIHSTIWTIV 120
Db 61 SSYNVLLAAADIVLFFIYFVDFLEDFILNMQMPQVDPKIIIEVLFSSIHSTIWTIV 120
QY 121 PLTIDRYAVCHPLKXHTVSPARTRKVIIVSYITCFLTSPYVWPMIWTEDYISTSVH 180
Db 121 PLTIDRYAVCHPLKXHTVSPARTRKVIIVSYITCFLTSPYVWPMIWTEDYISTSVH 180
QY 181 HVLIMHGFYTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
Db 181 HVLIMHGFYTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
QY 241 WAPRIIMLYHLYGAPIONRMLVHIMSDIANMLALNTAINFFLYCFISKRRTMAAATL 300
Db 241 WAPRIIMLYHLYGAPIONRMLVHIMSDIANMLALNTAINFFLYCFISKRRTMAAATL 300
QY 301 KAFKCOQOPVOFYTNHNFISITSPWISPA NSHCIMLVYQYDKGKPIK 350
Db 301 KAFKCOQOPVOFYTNHNFISITSPWISPA NSHCIMLVYQYDKGKPIK 350
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RESULT 12

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US-10-174-364-60
; Sequence 60, Application US/10174364
; Publication No. US20030216308A1
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GENERAL INFORMATION:

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; APPLICANT: Anderson et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-729CIP2
; CURRENT APPLICATION NUMBER: US/10/174,364
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
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Query Match 94.4%; Score 1857; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 5.1e-163;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MEHTAHAAANSSLSWSPGSAACGFGFVVVYYSLLCLGLPANILTVIISQVARROK 60
Qy 61 SSYNVLLAAADIIIVLFFIVVDLLEDFILNMQMPQVPDKIEVLEFSSIHSTISWTV 120
Db 61 SSYNVLLAAADIIIVLFFIVVDLLEDFILNMQMPQVPDKIEVLEFSSIHSTISWTV 120
Qy 121 PLTIIDRYAVCHPLKXHTVSPARTKRVISVYITCFILTSIPYMMPNIMTEDYISTSVH 180
Db 121 PLTIIDRYAVCHPLKXHTVSPARTKRVISVYITCFILTSIPYMMPNIMTEDYISTSVH 180
Qy 181 HVLIMHCFVTYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTALIFTITSIFATL 240
Db 181 HVLIMHCFVTYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTALIFTITSIFATL 240
Qy 241 WAPRIIMILYHLYGAPIONRMLVHIMSDIANMLALNTAINFLVYCFISKRRRTMAAATL 300
Db 241 WAPRIIMILYHLYGAPIONRMLVHIMSDIANMLALNTAINFLVYCFISKRRRTMAAATL 300
Qy 301 KAFFCQKOPVOFYTNHNSITSSPWPISPANSHCIKMLVYOYDKNGKPIK 350
Db 301 KAFFCQKOPVOFYTNHNSITSSPWPISPANSHCIKMLVYOYDKNGKPIK 350
RESULT 13
US-10-246-583-60
; Sequence 60, Application US/10246583
; Publication No. US2004005862A1
; GENERAL INFORMATION:
; APPLICANT: Majmuder
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-729CIP2CON1
; CURRENT APPLICATION NUMBER: US/10/246,583
; CURRENT FILING DATE: 2002-12-06
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 60
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-246-583-60
Query Match 94.4%; Score 1857; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 5,1e-163;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEHTAHAAANSSLSWSPGSAACGFGFVVVYYSLLCLGLPANILTVIISQVARROK 60
Db 1 MEHTAHAAANSSLSWSPGSAACGFGFVVVYYSLLCLGLPANILTVIISQVARROK 60
Qy 61 SSYNVLLAAADIIIVLFFIVVDLLEDFILNMQMPQVPDKIEVLEFSSIHSTISWTV 120

Db 61 SSYNVLLAAADIIIVLFFIVVDLLEDFILNMQMPQVPDKIEVLEFSSIHSTISWTV 120
Qy 121 PLTIIDRYAVCHPLKXHTVSPARTKRVISVYITCFILTSIPYMMPNIMTEDYISTSVH 180
Db 121 PLTIIDRYAVCHPLKXHTVSPARTKRVISVYITCFILTSIPYMMPNIMTEDYISTSVH 180
Qy 181 HVLIMHCFVTYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTALIFTITSIFATL 240
Db 181 HVLIMHCFVTYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTALIFTITSIFATL 240
Qy 241 WAPRIIMILYHLYGAPIONRMLVHIMSDIANMLALNTAINFLVYCFISKRRRTMAAATL 300
Db 241 WAPRIIMILYHLYGAPIONRMLVHIMSDIANMLALNTAINFLVYCFISKRRRTMAAATL 300
Qy 301 KAFFCQKOPVOFYTNHNSITSSPWPISPANSHCIKMLVYOYDKNGKPIK 350
Db 301 KAFFCQKOPVOFYTNHNSITSSPWPISPANSHCIKMLVYOYDKNGKPIK 350
RESULT 14
US-10-689-832-60
; Sequence 60, Application US/10689832
; Publication No. US20040121380A1
; GENERAL INFORMATION:
; APPLICANT: Majmuder, Kamud
; TITLE OF INVENTION: Novel Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729D1V1
; CURRENT APPLICATION NUMBER: US/10/689,832
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: 09/813,432
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 60
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-832-60
Query Match 94.4%; Score 1857; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 5,1e-163;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEHTAHAAANSSLSWSPGSAACGFGFVVVYYSLLCLGLPANILTVIISQVARROK 60
Db 1 MEHTAHAAANSSLSWSPGSAACGFGFVVVYYSLLCLGLPANILTVIISQVARROK 60
Qy 61 SSYNVLLAAADIIIVLFFIVVDLLEDFILNMQMPQVPDKIEVLEFSSIHSTISWTV 120
Db 61 SSYNVLLAAADIIIVLFFIVVDLLEDFILNMQMPQVPDKIEVLEFSSIHSTISWTV 120
Qy 121 PLTIIDRYAVCHPLKXHTVSPARTKRVISVYITCFILTSIPYMMPNIMTEDYISTSVH 180

Db 121 PLTIDRYAVCHPLKHTVSYPARTRKIVSVYITCFLTISIPLYWMPINWTEIDYISTSVH 180
Qy 181 HVLIMHCFYVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
Db 181 HVLIMHCFYVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
Qy 241 WAPRIIMLYHLXGAPIONRWLVHIMSDIANMLALNTAINFPLYCFISKRFRTMAAATL 300
Db 241 WAPRIIMLYHLXGAPIONRWLVHIMSDIANMLALNTAINFPLYCFISKRFRTMAAATL 300
Qy 301 KAFKFCQKQPVQFYTNHNFISITSSPMISPA NSHCIMLVYQYDKNKGRPK 350
Db 301 KAFKFCQKQPVQFYTNHNFISITSSPMISPA NSHCIMLVYQYDKNKGRPK 350

RESULT 15
US-09-995-225-16
; Sequence 16, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huang T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Priddy, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; PRIOR FILING DATE: 2001-11-26
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 353
; TYPE: prt
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020193584A1e1 Sequence
US-09-995-225-16

Query Match 94.4%; Score 1857; DB 3: Length 353;
Best Local Similarity 100.0%; Pred. No. 5.2e-163;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEHTAHLAANSLSWMSBGSACGLGFVYVYVYSLLCGLPANITLVIISQLVARROK 60
Db 1 MEHTAHLAANSLSWMSBGSACGLGFVYVYVYSLLCGLPANITLVIISQLVARROK 60
Qy 61 SSYNYLLAALADILVLFVDFVLEDFILNMOMQVDPDKIEVLEFSSIHSTIWTIV 120

Db 61 SSYNYLLAALADILVLFVDFVLEDFILNMOMQVDPDKIEVLEFSSIHSTIWTIV 120
Qy 121 PLTIDRYAVCHPLKHTVSYPARTRKIVSVYITCFLTISIPLYWMPINWTEIDYISTSVH 180
Db 121 PLTIDRYAVCHPLKHTVSYPARTRKIVSVYITCFLTISIPLYWMPINWTEIDYISTSVH 180
Qy 181 HVLIMHCFYVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
Db 181 HVLIMHCFYVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
Qy 241 WAPRIIMLYHLXGAPIONRWLVHIMSDIANMLALNTAINFPLYCFISKRFRTMAAATL 300
Db 241 WAPRIIMLYHLXGAPIONRWLVHIMSDIANMLALNTAINFPLYCFISKRFRTMAAATL 300
Qy 301 KAFKFCQKQPVQFYTNHNFISITSSPMISPA NSHCIMLVYQYDKNKGRPK 350
Db 301 KAFKFCQKQPVQFYTNHNFISITSSPMISPA NSHCIMLVYQYDKNKGRPK 350

Search completed: December 3, 2005, 06:55:38
Job time : 98.65 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:36:57 ; Search time 5.07273 Seconds
(without alignments)
351.144 Million cell updates/sec

Title: US-10-712-615-103

Perfect score: 1967
Sequence: 1 MEHTHAHLAANSSLSWSPG.....NDSKSYQFEDAIGACVILL 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA_New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1471	74.8	287	6	US-10-980-388-66
2	912.5	46.4	313	7	US-10-980-388-63
3	205	10.4	355	7	US-11-068-686-4
4	202.5	10.3	352	7	US-11-068-686-20
5	199.5	10.1	352	7	US-11-068-686-2
6	176	8.9	417	6	US-10-992-577-44
7	158	8.0	430	6	US-10-992-577-8
8	156	7.9	358	6	US-10-980-388-96
9	156	7.9	389	6	US-10-980-388-116
10	154.5	7.9	420	6	US-10-992-577-6
11	154.5	7.9	522	6	US-10-510-018-2
12	151.5	7.7	432	6	US-10-992-577-2
13	151	7.7	409	6	US-10-627-633-4
14	149.5	7.6	415	6	US-10-627-633-2
15	145.5	7.4	352	6	US-10-627-633-6
16	138.5	7.0	360	6	US-10-851-667A-26
17	134	6.8	353	7	US-11-067-884-6
18	132	6.7	485	6	US-10-821-234-934
19	126.5	6.4	323	6	US-10-980-388-119
20	125.5	6.4	339	6	US-10-821-234-1085
21	121.5	6.2	364	7	US-11-067-884-2
22	120.5	6.1	333	6	US-10-980-388-114
23	119.5	6.1	333	6	US-10-980-388-91
24	112.5	5.7	342	6	US-10-980-388-118
25	112	5.7	340	6	US-10-980-388-117

26	105	5.3	351	7	US-11-067-884-4	Sequence 4, Appl1
27	103.5	5.3	313	7	US-11-095-093-2	Sequence 2, Appl1
28	103	5.2	211	6	US-10-980-388-97	Sequence 97, Appl1
29	100.5	5.1	508	6	US-10-980-388-112	Sequence 112, App
30	97	4.9	473	6	US-10-467-657-1874	Sequence 1874, Ap
31	96	4.9	440	6	US-10-502-893-2	Sequence 2, Appl1
32	94.5	4.8	419	7	US-11-067-884-8	Sequence 8, Appl1
33	92.5	4.7	347	6	US-10-131-826A-18	Sequence 18, Appl1
34	91	4.6	272	6	US-10-793-626-1308	Sequence 1308, Ap
35	87.5	4.4	143	6	US-10-793-626-370	Sequence 370, App
36	87	4.4	604	6	US-10-485-517-168	Sequence 168, App
37	86.5	4.4	321	6	US-10-793-626-2816	Sequence 2816, Ap
38	84.5	4.3	351	7	US-11-095-624-5	Sequence 5, Appl1
39	84	4.3	336	6	US-10-980-388-115	Sequence 120, App
40	82.5	4.2	337	6	US-10-980-388-115	Sequence 115, App
41	82.5	4.2	926	6	US-10-841-129-2	Sequence 2, Appl1
42	82	4.2	308	6	US-10-793-626-2446	Sequence 2446, Ap
43	81.5	4.1	275	7	US-11-110-977-4	Sequence 4, Appl1
44	81	4.1	350	6	US-10-502-145-1	Sequence 1, Appl1
45	80.5	4.1	433	7	US-11-082-389-332	Sequence 332, App

ALIGNMENTS

RESULT 1
US-10-980-388-66
; Sequence 66, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayes, Paul S.
; APPLICANT: Huff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related App.
; FILE REFERENCE: 00325.US1
; CURRENT FILING DATE: US/10/980,388
; PRIOR FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; TYPE: PRT
; LENGTH: 287
; ORGANISM: Homo sapiens
US-10-980-388-66
Query Match 74.8%; Score 1471; DB 6; Length 287;
Best local Similarity 99.6%; Pred. No. 1.2e-123;

Matches 281; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 43 ANILTVIILSQLVARROKSSVNYLLAALADIVLFFIVFDLLEDFILNMQMPQVDPK 102
Db 6 ANILTVIILSQLVARROKSSVNYLLAALADIVLFFIVFDLLEDFILNMQMPQVDPK 65
Qy 103 IIEVEFSSIRHSITITVPLTIDRIYAVCHPLKHTVSPARTRKIVSVYTCTLSIP 162
Db 66 IIEVEFSSIRHSITITVPLTIDRIYAVCHPLKHTVSPARTRKIVSVYTCTLSIP 125
Qy 163 YWMNINTEDEYSVHHVLIWHCFVYLVPCSIFFILNSIIVYKLRKSNFRLRGS 222
Db 126 YWMNINTEDEYSVHHVLIWHCFVYLVPCSIFFILNSIIVYKLRKSNFRLRGS 185
Qy 223 TGTCTAILFTTISIPATLWAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALTAINF 282
Db 186 TGTCTAILFTTISIPATLWAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALTAINF 245
Qy 283 FLYCFISKRFRTMAAATLKAFKCKOKOPVQPYTNHNSITSS 324
Db 246 FLYCFISKRFRTMAAATLKAFKCKOKOPVQPYTNHNSITSS 287

RESULT 2

US-10-980-388-63
; Sequence 63, Application US/10980388
; Publication No. US2005025490A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayles, Paul S.
; APPLICANT: Huff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325. US1
; CURRENT APPLICATION NUMBER: US/10/980.388
; PRIOR FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791.932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184.305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184.304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184.303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184.397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184.247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188.880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217.369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217.370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218.492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 63
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-63

Query Match 46.4%; Score 912.5; DB 6; Length 313;
Best Local Similarity 76.8%; Pred. No. 3.4e-74;
Matches 185; Conservative 6; Mismatches 21; Indels 29; Gaps 3;

Qy 5 HAHLAANSSLSWMB---GSACGLGFVPVYVYSL-----LC----- 38
Db 61 HLSMLCNISITIKYPLVGAICNAEVPQKFNHFHFGSAKTYAGPHRSQSHLCFRAX 120
Qy 39 ---IGLPAINILTVIILSQLVARROKSSVNYLLAALADIVLFFIVFDLLEDFILNMQ 95
Db 121 PVFLSTNMLITVILSQLVARROKSSVNYLLAALADIVLFFIVFDLLEDFILNMQ 180
Qy 96 MPQVDPKIEVLEFSSIRHSITITVPLTIDRIYAVCHPLKHTVSPARTRKIVSVYIT 155
Db 181 MPQVDPKIEVLEFSSIRHSITITVPLTIDRIYAVCHPLKHTVSPARTRKIVSVYIT 240
Qy 156 CFLSIPYWMNINTEDEYSVHHVLIWHCFVYLVPCSIFFILNSIIVYKLRKSN 215
Db 241 CFLSIPYWMNINTEDEYSVHHVLIWHCFVYLVPCSIFFILNSIIVYKLRKSN 300
Qy 216 F 216
Db 301 F 301

RESULT 3

US-11-068-686-4
; Sequence 4, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicki L.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068.686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Noiland, Grete E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: /= "88-28 amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-11-068-686-4

Query Match 10.4%; Score 205; DB 7; Length 355;
Best Local Similarity 24.7%; Pred. No. 1.6e-11;
Matches 81; Conservative 65; Mismatches 144; Indels 38; Gaps 13;

Qy 27 FVPVYVYSLGCTGPAIILTVIILSQLVARROKSSVNYLLAALADIVLFFIVFDL 85
Db 36 FVPVPL-YSLVFTVGLGNVVMIL--IKYRRLRIMTNIVLLNLAISDL--FLVTLPF 89


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Qy 92 LNMOMPOVDPKIEVLEFSSHTSMTWVPLTIDRYAVCH---PLKHTVSYPARTRKV 148
Db 92 AQMDGNTMCCQLTGLYFIFGFGSIFLITLITIDRYLAVHAVFALKARTYFEGVTS-- 149
Qy 149 IVSVYITCFILTSIF-----YYMMPNITWEDYISTSVHVL 184
Db 150 -VITWVAVFASLPIIFITRSGKEGLHTCSSHFYSQVQFQKNTQTLKIVLGL----- 203
Qy 185 WIHCFITVYVPCISIFILNSIIVYKLRRKSNFRLGSGTGKTTALFTTISFATLMA 244
Db 204 -----VLPLVAVICSGILKTLRLCRNEKCR-----HRAVRLIFITMIYVFLFMA 251
Qy 245 IIMIL-----YHLYGAPICRMVHIMSDIANMLALNTALINFELVCFISKPRRTMA 297
Db 252 NIVLLNTFQEFEGGLNCCSSNR--LDAQOVTEITLGMTHCCINPIIYAFVGEKFRNYLL 309
Qy 298 A-----TLKAFPKC 306
Db 310 VFQKHIAKRPCKC 323

RESULT 6
US-10-992-577-44
; Sequence 44, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; FILE REFERENCE: 57155-D/JPM
; CURRENT FILING DATE: 2004-11-18
; PRIOR FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-992-577-44

Query Match 8.9%; Score 176; DB 6; Length 417;
Best Local Similarity 22.7%; Pred. No. 7e-09; Mismatches 142; Indels 102; Gaps 18;
Matches 89; Conservative 59;

Qy 10 ANSSLSW---WSPG-----SACGLGF-----VPVY---YSLLCLGLPANILT 47
Db 7 SNSSSSWIMHSGNTOHPWSDINITWNNYLLHQPHYAVFISSYFLIFCMWGN--T 64
Qy 48 VIIISQVAKROKSSYN-YLALAAADIVLFFIYFVDFLEDFILNMOMPOVDPKIEV 106
Db 65 VVCFVAVIRRYMHTYTNFFIFMLAISDLVGIFCMPI-T-LDNIIAGMPFGSSMCKISGL 123
Qy 107 LEFSIHSTWITVPLTIDRYAVCHPLKYHTVSYPARTRK-----VIVSVYITCFLT 159
Db 124 VQGISVAASVFTLVAIVADRRCVYPRK-----PKLTVAKTAFWIYIIMGLAITIMTP 177
Qy 160 SI-----PYW-----WPNIWEDYISTSVHVLIMHCFIVYL 193
Db 178 SAIMLHVQEKYRVRLLSHNKTSTVYWCREDMPN-----QEMRRIYTTVLARATYVL 229
Qy 194 VPCSIFFILNSIIVYKLRRKSNFRLGSGTG-----KTALIFTTISFAT 239
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```
Db 230 APLSI-----VIMARIASLFTTSAHSTGQRLBGMHNSKKQKQYIKMLLVALLFTL 284
Qy 240 LMAPIIMILYHLXG--APIQNRMLVHIMSDIANMLALNTALINFELVCFISKPRRTMA 297
Db 285 SWLPLTLMMLSDVADLSPNKLAVINIYVYFPAHMLAFCNSSVNPITIGFENENR---S 341
Qy 298 ATLKAFFRCQK--QVQFY---TNNFSITSS 324
Db 342 GFODAFQFCQKVKVQEAAYGLRAKRNLDINTS 373

RESULT 7
US-10-992-577-8
; Sequence 8, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; FILE REFERENCE: 57155-D/JPM
; CURRENT FILING DATE: 2004-11-18
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-992-577-8

Query Match 8.0%; Score 158; DB 6; Length 430;
Best Local Similarity 21.7%; Pred. No. 2.8e-07; Mismatches 133; Indels 76; Gaps 14;
Matches 76; Conservative 66;

Qy 3 HTHAHLANSSLSW---SPGSACGLGFVPPVYVYSLLCGLPANILTVIISQVARR 58
Db 21 NTEATPATNLTFFSSYYQHTSPVAA---MFIYVYALIFLLCMWGNLTVCFTV--LKNRH 73
Qy 59 QKSSYN-YLALAAADIVLFFIYFVDFLEDFILNMOMPOVDPKIEVLEFSSIHSTIW 117
Db 74 MHTYTNMILMLAVSDDLVGIFCM-PTLVVNLTLMGPFMDATCKMSGLVQGMVSASVF 132
Qy 118 ITVPLTIDRYAVCHPLKYHTVSYPARTRKVIVSVYITCFLT----- 159
Db 133 TLVAIAVERFCIYVPRFKLT-----LRKALVTIAVIMALALIMCPASAVTLVTREH 187
Qy 160 -----SIPIYWMPIWITWEDYISTSVHVLIMHCFIVYVPCISFFILNSIIVYKL 210
Db 188 HPMWDARNRSYPLVSCWAMEKGM-RRVYTTVLFSH---LYLAPLALIVMVYARIARKL 243
Qy 211 -----RRKSNFRLGSGTGKTTALIFTTISFATIMAPRIIMILYHLXG 255
Db 244 COAREPAPGGEADPRASRRRAVVMHLVWVAFLEFITS--WLPDMA-LLLIDYGQLSA 300
Qy 256 PIONRMVLHNS---DIANNMLALNTALINFELVCFISKPRRTMAAATLKA 302
Db 301 P-----QHLVTVYVAFPPAHMLAFNNSGANDIIGYFENENRFRRGQAAAFRA 346

RESULT 8
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[illegible]

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RESULT 9
US-10-980-388-116
; Sequence 116, Application US/10980388
; Publication No. US2005025490A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayes, Paul S.
; APPLICANT: Huff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325, us1
CURRENT APPLICATION NUMBER: US/10/980,388
PRIOR FILING DATE: 2004-11-02
PRIOR APPLICATION NUMBER: US/09/791,932
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/184,305
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,304
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,303
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,397
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,247
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/188,880
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/217,369
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/217,370
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/218,492
PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 184
SOFTWARE: Patentin version 3.0
SEQ ID NO 116
LENGTH: 389
TYPE: PRT
ORGANISM: Homo sapiens
US-10-980-388-116

Query Match 7.9%; Score 156; DB 6; Length 389;
Best Local Similarity 22.7%; Pred. No. 3.8e-07;
Matches 71; Conservative 54; Mismatches 120; Indels 68; Gaps 12;

Cy 11 NSSLSWSPSGACGFPVYVYSLLICGLPANILTVIIS-QVARRKSSVNYLAL 69
Db 41 NETLLSKTSRATCTAFL-----LLAALLGLPGNGFVWSLACMRPRRGKPLATVLA 95
Cy 70 AAADIILVFFI-VEVDLTLEDFILNMQMPVPDKIIEVLEFSSIHNSIWTVPDITDRYI 128
Db 96 ALADGAVLLTLPFLFVALVLTRO---AWPLGQAGCKAVYVVALSMYASVLLTGLLSLQRC 152
Cy 129 AVCHPLKHTVTSVPARTRKVIIVSVYITCFLTSLIPYVWPNIMTEWDYIS----TSVHVL- 183
Db 153 AVTRPFLAPRLRSPALARRILLAWMLAALLAVPAAYRHLMRDRVCQLCHPSFVHAAD 212
Cy 184 IWHCFVYVLPVPCSIPIFILNSIIVYKLRKSNRLRG--YSTGKTPA---ILFTTISIF 237
Db 213 LSETTLTAFLVLPGLMIGCYSVTL-----ARLRGARGSGHGRVGRVLSAIVLAF 264
Cy 238 ATLAPRILMILYLVGAPIQNRLVHIMSDIANM-----LA 274
Db 265 GLMAP-----YH-----AVNLLQAVAAALAPREGALAKLGAGQARAAGTTALA 308
Cy 275 LNTAINFLPYCF 287
:::| |||

```


Db 313 ---TATWISSPSSASAKPTLYSIYANFRGKMETFCMSMKC-----YRSNAYTTT 362
QY 324 SPWISPA 331
Db 363 SSRMAKN 370

RESULT 15
US-10-627-633-6
; Sequence 6, Application US/10627633
; Publication No. US20050250720A1
; GENERAL INFORMATION:
; APPLICANT: Charles, Andrew David
; APPLICANT: Brennand, John Charles
; APPLICANT: Hart, Kevin Anthony
; TITLE OF INVENTION: Novel Compound
; FILE REFERENCE: 1991-221
; CURRENT APPLICATION NUMBER: US/10/627,633
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 09/722,342
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/172,146
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 6
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-627-633-6

Query Match 7.4%; Score 145.5; DB 6; Length 352;
Best Local Similarity 21.1%; Pred. No. 2.9e-06;
Matches 76; Conservative 68; Mismatches 154; Indels 63; Gaps 18;

QY 1 MEHTAHLAANSLSM-WSPGACGLGFVPVYYSLLCLGLPANILTVIISQVARRQ 59
Db 2 LSEHSMSNSNRDLOEYENPGEVA---TASIFGALMLFSIFGNSLVCLVYHR--SRRT 55
QY 60 KSSVYVL-LALAAADILVLF---FIVEVDPLEDFILNMQPQVDPDKIEVLEFSIHT 114
Db 56 GSTNYLVVSMACADLLISVASTPFV--LQFTGRWTLGSA-----CKVRYFOYLTPGV 110
QY 115 SIWITVPLTDRIYAVCHPLKXHTVSYPARTRKIVS-VYITCFILSIY-----163
Db 111 QIYVLISICIDRFYTIYVPLSF-KVSRKAKMIAASWILDAFVTPVFFYGSNMDSHC 169
QY 164 -YWMNPNTEDISTSVHVLWIMHCFYVYVPCSFIL-NSIIVY-----KLR 211
Db 170 NYFLPPSW-EGTAYVVIH-----FLGVFIPSVLILFYQKIKYIMRIGTDGRTL 220
QY 212 RKSNFLRGYSTGKTTALIFTTISFATLMAPRIIMILYHLYGAPIONRWLVHIMSDIAN 271
Db 221 RTMNVPR--TKVKTVKKFLLENLVFLPSMLPFHVAQLMHPHDEYKSSLVF---TAVT 275
QY 272 MLALNLTAINFLYCFISRRFT-MAAATLKAFFKOCOKOPVOFYTNHNSITSSPWISPA 330
Db 276 WVSFSSASAKFTLYSIYANFRGKMETFCMSMKC-----YRSNAYTTTSSRMMAKR 328
QY 331 N 331
Db 329 N 329

Search completed: December 3, 2005, 06:55:55
Job time : 6.07273 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:22:45 ; Search time 21.1364 Seconds
(without alignments)
1693.415 Million cell updates/sec

Title: US-10-712-615-103

Perfect score: 1967

Sequence: 1 MEHTAHLANSSLSWSPG.....NDSKSYQFEDAIGACVILL 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	242	12.3	411	2	156444
2	242	12.3	412	2	S23436
3	241	12.3	393	2	A39251
4	238.5	12.1	398	2	JN0708
5	231.5	11.8	355	2	A45177
6	226	11.5	352	2	JB0296
7	225	11.4	352	2	JC7319
8	225	11.4	423	2	JC7677
9	219.5	11.2	384	2	JN0605
10	219	11.1	384	2	A47249
11	217.5	11.1	340	2	T18704
12	217.5	11.1	394	2	JC7209
13	217.5	11.1	658	2	JC8611
14	217	11.0	367	2	JC2421
15	217	11.0	367	2	I49022
16	217	11.0	367	2	I56520
17	214.5	10.9	595	2	JC8012
18	213.5	10.9	355	2	I49339
19	213	10.8	352	2	A45747
20	213	10.8	370	2	S43087
21	212	10.8	360	2	JC4629
22	212	10.8	360	2	T23063
23	211.5	10.8	376	2	T24368
24	211.5	10.8	380	2	JC2338
25	211.5	10.8	504	2	T29338
26	210.5	10.7	380	2	S36143
27	209	10.6	424	2	JH0164
28	208.5	10.6	477	2	JC7913
29	207.5	10.5	363	2	I57940

30	207.5	10.5	399	2	A46632	bombesin-like pept
31	207.5	10.5	428	2	JN0692	cholecystokinin ty
32	206.5	10.5	380	2	A48227	kappa opioid recep
33	206.5	10.5	380	2	JC2434	kappa opioid recep
34	206.5	10.5	391	2	A41795	somatostatin recep
35	206.5	10.5	391	2	C41795	somatostatin recep
36	205.5	10.4	353	2	JC2492	G protein-coupled
37	205.5	10.4	391	2	A39297	somatostatin recep
38	205	10.4	355	2	G02436	chemokine (C-C) re
39	205	10.4	355	2	JC5067	G protein-coupled
40	205	10.4	418	2	S59601	vasopressin recep
41	205	10.4	444	2	T27866	hypothetical prote
42	204.5	10.4	352	2	S60024	bradykinin B1 rece
43	204.5	10.4	380	2	A55259	kappa opioid recep
44	204	10.4	353	2	S28787	neuropeptide y/pep
45	204	10.4	372	2	I38532	delta opioid recep

ALIGNMENTS

RESULT 1		156444		thyrotrophin-releasing hormone receptor - mouse	
C.Species: Mus sp. (mouse)		C.Date: 26-Jul-1996		#sequence_revision 26-Jul-1996 #text_change 11-Jan-2000	
C.Accession: I56444		R.Sellar, R.E.; Taylor, P.L.; Lamb, R.F.; Zabavnik, J.; Anderson, L.; Eldine, K.A.		J. Mol. Endocrinol. 10, 199-206, 1993	
A.Title: Functional expression and molecular characterization of the thyrotrophin-releas		A.Reference number: I56444; PMID:8387312		A.Accession: I56444	
A.Status: preliminary; translated from GB/EMBL/DBJ		A.Molecule type: mRNA		A.Residues: 1-411 <RES>	
A.Cross-references: UNIPARC:UPI0000170AE1; GB:S60053; NID:G300151; PIDN:AAB26491.1; PID		C.Superfamily: adenosine receptor A1			
Query Match		12.3% Score 242; DB 2; Length 411;			
Best Local Similarity 22.6% Pred. No. 1.2e-12;		Matches 83; Conservative 71; Mismatches 125; Indels 86; Gaps 14;			
QY	19	PSACGLGF-VPVVVYSLILC-LGLPANILTVIILISQVARRQKSYN-YLLALAADIL 75			
DB	16	PQVAVALBQVVTILLVVICGLVGNIMVLLVNR-TKMRRTATNCYLVSIAVADLM 73			
QY	76	VLFFIVFDLLEDFILMOMQVDPDKI-----LEVEFSIHSTITVPL 122			
DB	74	VL-----VAAGLPNITDSIVGSWVGCLCTIYQYLGINSSTGTAF 119			
QY	123	TIDRYAVCHPLKHTVSPARTRKIVSVYITCFLTSIPYMW-----PNIMT-EDYIS 176			
DB	120	TIERIYALCHPLKPAFLCTFSRAKIIIFVMA--FTSIYCMWFFLDLNIISTYKDAIV 176			
QY	177	TSVHVLWVHCFTVYLVPCSIFFILNSIIVYKL----- 210			
DB	177	ISCGYKISNNYSPIYLMFGVYVMPMLAVVLGFIARILFLNPISDPKENSMTKWN 236			
QY	211	---RRKSNFRLG-----YSTGKTALIFTTISIPATLMAP-RIIMILVHLGADI 257			
DB	237	DSTHQKNNLNTWTRCFNSTVSRSKQVTKMLAVVILFALLMMPYRLTVVNSFLSSPF 296			
QY	258	QNRVLVHMSDANMLALNTAINPFLYCFISKRPRTMAALILKAFKQKQPVQVYTTN 317			
DB	297	QNRWFL---FCRICIYLSAINPVITVLMOSQKR---AARFLCNCKQKPTKQANV 348			
QY	318	NFSITSS 324			
DB	349	SVALNYS 355			
RESULT 2		S23436			

thyrotropin receptor - rat
N:Alternate names: thyrotropin-releasing hormone receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S23436; E153279; A49168; P00326
R:de la Pena, P.; Delgado, L.M.; del Camino, D.; Barros, F.
Biochem. J. 284, 891-899, 1992
A:Title: Cloning and expression of the thyrotropin-releasing hormone receptor from GH(3)
A:Reference number: S23436; MUID:92322017; PMID:137915
A:Accession: S23436
A:Molecule type: mRNA
A:Residues: 1-412 <PDB>
A:Cross-references: UNIPROT:001717, UNIPARC:UPI0000137380, EMBL:X64630, NID:G57394; PIDN
R:Kimura, N.; Arai, K.; Sahara, Y.; Suzuki, H.; Kimura, N.
Endocrinology 134, 432-440, 1994
A:Title: Estradiol transcriptionally and posttranscriptionally up-regulates thyrotropin-
A:Reference number: 153279; MUID:94102223; PMID:8275956
A:Accession: 153279
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-412 <RES>
A:Cross-references: UNIPARC:UPI0000137380; GB:D17469; NID:9464199; PIDN:BA04289.1; PID:
R:Zhao, D.; Yang, J.; Jones, K.E.; Gerald, C.; Suzuki, Y.; Hogan, P.G.; Chin, W.W.; Tash
Endocrinology 130, 3529-3536, 1992
A:Title: Molecular cloning of a complementary deoxyribonucleic acid encoding the thyrotr
A:Reference number: A49168; MUID:92283212; PMID:1317787
A:Accession: A49168
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12, 'D', '14-290', 'K', '292-412' <ZHA>
A:Cross-references: UNIPARC:UPI00001788B0
A:Experimental source: GH cells
A:Note: Sequence extracted from NCBI backbone (NCBIN:104788, NCBI:P104795)
R:Yanada, M.; Monden, T.; Satoh, T.; Izuka, M.; Murakami, M.; Itchujima, T.; Mori, M.
Biochem. Biophys. Res. Commun. 184, 367-372, 1992
A:Title: Differential regulation of thyrotropin-releasing hormone receptor mRNA levels b
A:Reference number: P00326; MUID:92231953; PMID:1373613
A:Accession: P00326
A:Molecule type: mRNA
A:Residues: 30-58, 'P', '60-222', 'T', '224-261' <YAM>
A:Cross-references: UNIPARC:UPI00001788B1
A:Experimental source: strain Wistar
A:Note: The authors translated the codon ACA for residue 88 as Ala
C:Superfamily: adenosine receptor A1
C:Keywords: G protein-coupled receptor; transmembrane protein
F:1-22/Domain: transmembrane #status predicted <TM1>
F:32-54/Domain: transmembrane #status predicted <TM2>
F:71-92/Domain: transmembrane #status predicted <TM3>
F:116-140/Domain: transmembrane #status predicted <TM4>
F:165-186/Domain: transmembrane #status predicted <TM5>

Query Match 12.3%; Score 242; DB 2; Length 412;
Best Local Similarity 22.6%; Pred. No. 1.2e-12;
Matches 83; Conservative 71; Mismatches 125; Indels 88; Gaps 14;

QY 19 PGSAGLGF-VPVYYSLLC-LGLPANILTVILSQLVAROKSSYN-YLLALAADIL 75
DB 16 PQAAVALEQVTVILLVIIICGLGIVGNIMVLVVR--TKMRTATNCYLVSLAVADLM 73
QY 76 VLFFVFDPLLEDPILMQMPQVDPDKI-----TEVLEFSHITSMTITVPL 122
DB 74 VL-----VAAGLPNITDSYGSWVGYGCLCTITVLYQYLGINASSCSITAF 119
QY 123 TIDRYAVCHPLKHTVSPARTKRVISVYITCELTSPYVWM-----PNIMT-EDYIS 176
DB 120 TIERIALCHPDKAFLCTFSRAKKIILFVMA---FTSIYCMLEFLLDLNISTYKADALV 176
QY 177 TSVHHLWIMHCFYVLPVPCSIFFILNSIIVKL----- 210
DB 177 ISCGYKISRNYSPIYLMDFGVFVPMILATVLVGFARILFLNPISDPKENSMTWKN 236
QY 211 ---RKSKTALRFG-----YSTGKTTALFTITSITATLWAP-RIMILYHLXGAPI 257

DB 237 DSTHONKAMLNNTNRCPENSVSSRKQVTKLAAVVLLFALLMMPYRTLVVNSFLSSPF 296
QY 258 QNRMLVHIMSDIANMLALNTAINFLPYCFISKFRMTAAATLKAFFKQKQPOVQFTNH 317
DB 297 QENMFLL----FCRICIYLNAINPIVYINLMSOKFR----AAFRKLCHCKOKPTEKANY 348
QY 318 NFSITSS 324
DB 349 SVALNYS 355

RESULT 3
A39251
thyrotropin-releasing hormone receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text_change 09-Jul-2004
C:Accession: A39251
R:Straub, R.E.; Frech, G.C.; Joho, R.H.; Gerhengorn, M.C.
Proc. Natl. Acad. Sci. U.S.A. 87, 9514-9518, 1990
A:Title: Expression cloning of a cDNA encoding the mouse pituitary thyrotropin-releasing
A:Reference number: A39251; MUID:91088548; PMID:2175902
A:Accession: A39251
A:Molecule type: mRNA
A:Residues: 1-393 <STR>
A:Cross-references: UNIPROT:P21761, UNIPARC:UPI000002930A; GB:M59811; GB:M37490; NID:G20
C:Superfamily: adenosine receptor A1
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 12.3%; Score 241; DB 2; Length 393;
Best Local Similarity 22.1%; Pred. No. 1.4e-12;
Matches 81; Conservative 75; Mismatches 123; Indels 88; Gaps 15;

QY 19 PGSAGLGF-VPVYYSLLC-LGLPANILTVILSQLVAROKSSYN-YLLALAADIL 75
DB 16 PQAAVALEQVTVILLVIIICGLGIVGNIMVLVVR--TKMRTPTNCYLVSLAVADLM 73
QY 76 VLFFVFDPLLEDPILMQMPQVDPDKI-----TEVLEFSHITSMTITVPL 122
DB 74 VL-----VAAGLPNITDSYGSWVGYGCLCTITVLYQYLGINASSCSITAF 119
QY 123 TIDRYAVCHPLKHTVSPARTKRVISVYITCELTSPYVWM-----PNIMT-EDYIS 176
DB 120 TIERIALCHPDKAFLCTFSRAKKIILFVMA---FTSIYCMLEFLLDLNISTYKANV 176
QY 177 TSVHHLWIMHCFYVLPVPCSIFFILNSI---IVY----- 208
DB 177 VSCGYKISRNYSPIYLMDFGVFVPMILATVLVGFARILFLNPISDPKENSMTWKN 236
QY 209 -KLRRKSNFRLG-----YSTGKTTALFTITSITATLWAP-RIMILYHLXGAPI 257
DB 237 DSIHONKMLNNTNRCPENSVSSRKQVTKLAAVVLLFALLMMPYRTLVVNSFLSSPF 296
QY 258 QNRMLVHIMSDIANMLALNTAINFLPYCFISKFRMTAAATLKAFFKQKQPOVQFTNH 317
DB 297 QENMFLL----FCRICIYLNAINPIVYINLMSOKFR----AAFRKLCHCKOKPTEKANY 348
QY 318 NFSITSS 324
DB 349 SVALNYS 355

RESULT 4
JN0708
thyrotropin-releasing hormone receptor - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence revision 20-Aug-1994 #text_change 09-Jul-2004
C:Accession: S40682; JN0759; S50151; S50152; J38356; JN0708
R:Matre, V.; Karlsten, H.E.; Wright, M.S.; Lundell, I.; Fjeldheim, A.K.; Gabrielsen, O.S.
Biochem. Biophys. Res. Commun. 195, 179-185, 1993
A:Title: Molecular cloning of a functional human thyrotropin-releasing hormone receptor.
A:Reference number: S40682; MUID:93371401; PMID:8395824
A:Accession: S40682
A:Status: preliminary

Db 268 DIANMLALTNTAIFFLYCFISKSRFRMTAAATTLKAFPCOCOPVQFYNNHNSITSS 324
 304 -FCRICLYLMSAIPVLYNLMQKFR-----AAFKLCNCKQKPTBEKPNAYSVALNYS 355
 RESULT 5
 A45177
 chemokine (C-C) receptor 1 - human
 N/Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C/Accession: A45177; 155671
 R/Note: K. J. DiGregorio, D. J. Mak, J. Y. Horuk, R. J. Schall, T. J. Cell 72, 415-425, 1993
 A/Title: Molecular cloning, functional expression, and signaling characteristics of a C
 A/Reference number: A45177; MUID:93161416; PMID:7679328
 A/Accession: A45177
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-355 <NEO>
 A/Cross-references: UNIPROT:P32246; UNIPARC:UPI0000043584; GB:L10918; NID:g292416; PIDN:
 A/Experimental source: HL60 cells
 A/Note: sequence extracted from NCBI backbone (NCBIP:124876)
 R/Gao, J.
 J. Exp. Med. 177, 1421-1427, 1993
 A/Title: Structure and functional expression of the human macrophage inflammatory 1 al
 A/Reference number: 155671; MUID:93240122; PMID:7683036
 A/Accession: 155671
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-355 <RES>
 A/Cross-references: UNIPARC:UPI0000043584; GB:L10918; NID:g292416; PIDN:AAA6543.1; PIR
 C/Genetic8
 A/Gene: GDB:CMKBR1; CMKR-1
 A/Cross-references: GDB:138446; OMIM:601159
 A/Map position: 3p21-3p21
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; t
 F/36-60/Domain: transmembrane #status predicted <TM1>
 F/71-91/Domain: transmembrane #status predicted <TM2>
 F/108-129/Domain: transmembrane #status predicted <TM3>
 F/147-171/Domain: transmembrane #status predicted <TM4>
 F/205-223/Domain: transmembrane #status predicted <TM5>
 F/240-264/Domain: transmembrane #status predicted <TM6>
 F/268-305/Domain: transmembrane #status predicted <TM7>
 F/5/Binding site: carbonylate (Asn) (covalent) #status predicted
 F/24-273/106-183/Disulfide bonds: #status predicted
 F/345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 Query Match 11.8%; Score 231.5; DB 2; Length 355;
 Best Local Similarity 26.3%; Pred. No. 7.7e-12;
 Matches 81; Conservative 57; Mismatches 105; Indels 65; Gaps 13;
 QY 22 ACGIGFVVVYSSLLCLGPANILTVIILISQVARRKSSYNYLALAAIDLVLFPIV 81
 Db 31 AFGAGQLPPL-YSLVFIYIGLVGNILVVLVQYRKLMKMTSI-YILNLAISDLFLPLTP 88
 QY 82 F-VDF-LLEDFILNMQMPQVPDKIIEVLSESSHTSIWITVPLTDRIYANCH--PLKY 136
 Db 89 FWDYKDKDMWVFGDAM---CKILSGFYVYGLYSSEIFILITIDRYLAIHVAFLRA 144
 QY 137 HTVSYPARTRKVIYSVYITCFLTSP-YVMMPNITWEDYISTSVNH----- 181
 Db 145 RTVIFGVYITIIWALAI--LASMPLGYFSKTMQEFNHTCSLHFPESLREMKLFOAL 201
 QY 182 -----VLTIHCFYVVLVPCSIFFILNSIIVYKLRKSNFRLGSGTKTALVF 231
 Db 202 KLMNLFGLVLDLWILICYT-----GIITLLRRPNE-----KSKAVRIIF 242
 QY 232 TITSIFATLAAPRIIMLYHLYGAP-----QNRMLVHNSIDIANMLALTAINFLPY 285
 Db 243 VIMIIIFLFTPTPVNLTILISVFODFLTHEEGRNHL-DLVQVTEVIAVTHCCNVPYIY 301

Qy 286 CFIKRR 293
Db 302 AFVGERFR 309

RESULT 6

Query Match 11.5%; Score 226; DB 2; Length 352;
Best Local Similarity 23.5%; Pred. No. 2, 2e-11;
Matches 76; Conservative 61; Mismatches 104; Indels 82; Gaps 11;
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C:Accession: J02096
R:Ratdant, H.; Nakamura, T.; Itoh, J.; Iwasa, H.; Kanatani, A.; Borkowski, J.; Ihara, M.
Biochem. Biophys. Res. Commun. 250, 68-71, 1998
A:Title: Cloning and characterization of a new subtype of chytrotopin-releasing hormone
A:Reference number: J02096; MUID:98407892; PMID:9735333
A:Accession: J02096
A:Molecule type: mRNA
A:Residues: 1-352 <ITA>
A:Crosses-references: UNIPROT:088820; UNIPARC:UPI000000E6811; DDBJ:AB015645; NID:93660553;
C:Superfamily: adenosine receptor A1
F:26-48/Domain: transmembrane #status predicted <TM1>
F:58-80/Domain: transmembrane #status predicted <TM2>
F:97-118/Domain: transmembrane #status predicted <TM3>
F:147-165/Domain: transmembrane #status predicted <TM4>
F:188-209/Domain: transmembrane #status predicted <TM5>
F:252-273/Domain: transmembrane #status predicted <TM6>
F:282-304/Domain: transmembrane #status predicted <TM7>

Qy 31 VYSLLLC-LGPANILTVIISQVARRQSSYN-YLLAADAIVLFFIVFVDFLE 88
Db 26 VFLVLTCTGLGIVGAMVILV--LTSRDMHTPTNCYLVALADLVL----- 72
Qy 89 DFIAMQMPQVDPDK-----LEVEFSIHSTITVPLTIDRIYVCHPLK 135
Db 73 ---LAAGIPNVSDSLVGMHYGRACGLTTPYQIGINVSFSLAFVERVIALCHPLR 129
Qy 136 YHTVSYPARTKRVISVYITCFLSIPYWMENITEDVISTVHNLIMHCFVYLVLP 195
Db 130 AQTCTVAKARKILGINGVTSLYCLMFPLVDLVNRDQRLGEGYKPRGILYLYLD 189
Qy 196 CSIFPI---LNSIIVYK-----RRKSNFRLR 219
Db 190 FAVFPIGLVLTVLVYLHILGRILFQSPISQEMQKROPHGQSEAAPGNCRAKS----- 244
Qy 220 GYSTCKTALILFTTISATLMAP-RIMILYHLGAPIQNRWLHNSDIANMLALNT 278
Db 245 --SRQATRMALAVVLLPRAVLTPTRYTLVLLNSFVAQPLDDEWLL---FCRTCVYTNS 298
Qy 279 AINFLYCFISKRFRTMAATLK 301
Db 299 AVNPVYSLMSQKFR---AAFLK 318

RESULT 7

Query Match 11.4%; Score 225; DB 2; Length 423;
Best Local Similarity 23.5%; Pred. No. 3, 2e-11;
Matches 88; Conservative 75; Mismatches 126; Indels 86; Gaps 17;
C:Species: Drosophila melanogaster
C:Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 09-Jul-2004
C:Accession: J07319
R:Lenz, C.; Williamson, M.; Grimmelikhuijzen, C.J.P.
Biochem. Biophys. Res. Commun. 273, 571-577, 2000
A:Title: Molecular cloning and genomic organization of a second probable allatostatin re
A:Reference number: J07319
A:Accession: J07319
A:Molecule type: mRNA
A:Residues: 1-357 <LEN>
A:Crosses-references: UNIPROT:09NBC8; UNIPARC:UPI000000BFA1; GB:AF25352
A:Comment: This receptor, belonging to the insect allatostatin neuropeptide family, whic
a transmembrane glycoprotein.

C:Genetics:
A:Gene: dar-2
A:Map position: right arm of chromosome 3, 98D-E
A:Introns: 180/3; 273/3; 326/3
C:Superfamily: endothelin receptor B
C:Keywords: extracellular protein; glycoprotein; neuropeptide; transmembrane protein

Query Match 11.4%; Score 225; DB 2; Length 357;
Best Local Similarity 24.9%; Pred. No. 2, 7e-11;
Matches 87; Conservative 70; Mismatches 112; Indels 80; Gaps 18;
Qy 8 LAANSLSWMSGACGIFVPPVYVYSLLLCLG-PANILTVIISQVARRQSSYNVL 67
Db 31 LAINGTLPMW-----VGF---PFGVIAITGFFGNLVLIV--VFNNMRSTNLM 77
Qy 68 A-LAADIIVLFFIVDFLEDFIL-----NMQMPQVDPDKIEVEFSIHST 115
Db 78 VNLAAADL--MFVILCIFATDVVMVYWPGRFMSQVQ-----LIVTAFASIYT- 128
Qy 116 IWTVPPLTIDRIYVCHPLKHYVSYPARKRVISVYITCFLSIP----- 163
Db 129 --LVMSIDPFLAVVHPHRSRMKRTENITLIAVTLVIVLVSVPAFTHDVVYDA 185
Qy 164 -----YMPNMTEDVISTVHNLHCTVVLVPCSFILNSIIVYKLRK----- 213
Db 186 KKNITVGMCTTTNDPGLSPRTVQTFPI--SSYLLPMITISGLYMRIMRLMFGTGV 242
Qy 214 -SNFRLNGSYGKTALILFTTISIFATLMAP-RIMILYHLGAPIQNRWLHNSDI-A 270
Db 243 MSKSGQRK-RVTRLVVVVVIAFASLMPLVQILLLKSL--DVIENTTLTKVIQVTA 298
Qy 271 NMLALNTAINFLYCFISKRFRTMAATLKAFK--CQKQVQVPTN 316
Db 299 QTLAYSSSCINPLLYAFLENF-----KAFYKAVCSSR-QONYTS 339

RESULT 8

Query Match 11.4%; Score 225; DB 2; Length 423;
Best Local Similarity 23.5%; Pred. No. 3, 2e-11;
Matches 88; Conservative 75; Mismatches 126; Indels 86; Gaps 17;
C:Species: Periplaneta americana (American cockroach)
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: J07677
R:Auerwald, L.; Birguel, N.; Gaede, G.; Krielenkamp, H.J.; Richter, D.
Biochem. Biophys. Res. Commun. 282, 904-909, 2001
A:Title: Structural, functional, and evolutionary characterization of novel members of t
A:Reference number: J07677; MUID:21250673; PMID:11352636
A:Accession: J07677
A:Molecule type: mRNA
A:Residues: 1-423 <AUS>
A:Crosses-references: UNIPROT:0964D4; UNIPARC:UPI000017A507; GB:AF336364
C:Comment: This receptor, for the neuropeptide, is involved in the inhibition of juveni
A:Gene: Alster
C:Keywords: neuropeptide; transmembrane protein
F:73-94/Domain: transmembrane #status predicted <TM1>
F:105-127/Domain: transmembrane #status predicted <TM2>
F:143-164/Domain: transmembrane #status predicted <TM3>
F:165-167/Region: active element DRF
F:187-207/Domain: transmembrane #status predicted <TM4>
F:243-264/Domain: transmembrane #status predicted <TM5>
F:290-312/Domain: transmembrane #status predicted <TM6>
F:327-350/Domain: transmembrane #status predicted <TM7>

Qy 28 VPVYVYSLLLCLG-PANILTVIISQVARRQSSYNVLLA-DAADIVLFFIVF-VDF 85
Db 71 VPLL-FGLIVVYFGNALVVLVVA--ANQMRSTNLLINLVAADL---FIVFCVPF 124
Qy 86 LLEDIILM-QMPQVDPDKIEVEFSIHSTIWTVPPLTIDRIYVCHPLKHYVSYPAR 144

Db 125 TATDVLPEFMPGDIWICKIYOYLIVVAVASVYTLVMSLDRFLAVHPITMSIRTEEN 184
Qy 145 TRKIVSVYITCELTSPYPMNPMTEDYSTSVHYHLWIC----- 188
Db 185 AIAIAVWVIVLLASVYVLSHGEVITYT-SSAEHTACVFLPADIPINRPOCNKPFQI 243
Qy 189 ---FTVYVPCSIFFILNSIIYKLRKRSNFRLGYSFG-----KTVAILEFTI 233
Db 244 IFFATSVYTLPLALICGLYLMILLVRL-----WRGAAPGSHVASERSRGRKRVTRVVVV 296
Qy 234 TSIPFTLWAP-RITMILVHLGAPLQNRKLVHIMDIAMLLALNTAINFLYCFISGRF 292
Db 297 VAIFVAVCFPIQLILVLSVDKYEITNTSV-MIQIVSHVLAVMNSCVNPILLYAFLSDFH 354
Qy 293 RTMAATLKAFFK---C-----OKOPVQFYTNHNSITSSPWISPNASHCIRKMLVYQYDGN 345
Db 355 R-----KARKVINCSSAQAQAPGPRY-----HRASIIQQQPOAN 389
Qy 346 GKPIKS---RNDKS 357
Db 390 GRALNNECCENDNKS 404

RESULT 9
JN0605
C.Species: Homo sapiens (man)
C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C.Accession: JN0605; JN0762; A47457
R.Xu, Y.; Song, J.; Bruno, J.F.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 193, 648-652, 1993
A.Title: Molecular cloning and sequencing of a human somatostatin receptor, hSSTR4.
A.Reference number: JN0605; MUID:93290656; PMID:5512564
A.Accession: JN0605
A.Molecule type: DNA
A.Residues: 1-388 <XU>
A.Cross-references: UNIPROT:P31391; UNIPARC:UPI0000135FP9; GB:L14856; NID:g292499; PIDN:R.Yamada, Y.; Kagioto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.; I
Biochem. Biophys. Res. Commun. 195, 844-852, 1993
A.Title: Cloning, functional expression and pharmacological characterization of a fourth
A.Reference number: JN0762; MUID:93384611; PMID:8373420
A.Accession: JN0762
A.Molecule type: DNA
A.Residues: 1-388 <YAM>
A.Cross-references: UNIPARC:UPI0000135FP9; GB:D16826; NID:g693907; PIDN:BA04106.1; PID:R.Rohrer, L.; Raulf, F.; Bruns, C.; Buettner, R.; Holtschneider, F.; Schulte, R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4196-4200, 1993
A.Title: Cloning and characterization of a fourth human somatostatin receptor.
A.Reference number: A47457; MUID:93248256; PMID:8483934
A.Accession: A47457
A.Molecule type: DNA
A.Residues: 1-82, 'T', '84-364', 'K', '366-388' <ROH>
A.Cross-references: UNIPARC:UPI000050436; GB:L07833; NID:g307429; PIDN:AAA60565.1; PID:A.Nice: sequence extracted from NCBI backbone (NCBIN:110856, NCBI:110856)
C.Comment: This protein mediates the diverse actions of the tetradecapeptide somatostatin.
C.Genetics:
A.Gene: GDB:SSTR4
A.Cross-references: GDB:202662; OMIM:182454
A.Map position: 20p11.2-20p11.2
A.Introns: #status absent
C.Superfamily: vertebrate rhodopsin
C.Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; pho
F:84-109/Domain: transmembrane #status predicted <TM1>
F:121-142/Domain: transmembrane #status predicted <TM2>
F:162-184/Domain: transmembrane #status predicted <TM3>
F:208-238/Domain: transmembrane #status predicted <TM4>
F:257-284/Domain: transmembrane #status predicted <TM5>
F:291-314/Domain: transmembrane #status predicted <TM6>
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:119-196/Disulfide bonds: #status predicted
F:161,253/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pr
F:327/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 11.2%; Score 219.5; DB 2; Length 388;
Best Local Similarity 22.0%; Pred. No. 8.4e-11;
Matches 72; Conservative 75; Mismatches 130; Indels 51; Gaps 11;

Qy 19 PGSAGLGFPVY-VYSSLLCLGLPANTLYTIIISQVARRKSSYNTLLAAADIVL 77
Db 39 PGDRAAGMVAIQCIYALVLCVGNALVFLVILR-YAKKTAATNITLNLAAVDEL- 95
Qy 78 FFIVPVDELDELFI-LNNQMPQVPDKITVEVEFSSIHSTIMTVLPTIDRYAVGPKY 136
Db 96 -FMISVPPVASSAALRHPFGSVLCRAVLSVGLNMFISVCLTYLSDRYAAVHPLRA 154
Qy 137 HTVSYPARTRKIVSVYITCELTSPY-----YMPN-IWTEDYIST 177
Db 155 ATYRRPSVAKLINIGVWLASLLVTLPIAIPADTRPARGQAACNLQPHPMASAVF-- 212
Qy 178 SVHVLVIMHCFYV-YLVPCSIFFILNSIIYKLR--KSNFRLRGYSTGKTVAILEFTI 233
Db 213 -----VYTFELGLFLLPVLAIGLCYLLIVGKMAVALRAGWQORRSSEKKTITLVLMV 264
Qy 234 TSIPFTLWAPRITMILVHLGAPLQNRKLVHIMSDIAMLLALNTAINFLYCFISKPR 293
Db 265 VVFEVLCMPFYVQVLLNLVVTSLD-----ATVNHVSILISYANSCANPILYGLSDNFR 319
Qy 294 -----TMAATLKAFFKCOKOPVQFY 314
Db 320 RSFQVLCRCCLLEGAGABEPLDY 347

RESULT 10
A47249
brain-specific somatostatin receptor SSTR-4 - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C.Accession: A47249
R.Bruno, J.F.; Xu, Y.; Song, J.; Berelowitz, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 1151-1155, 1992
A.Title: Molecular cloning and functional expression of a brain-specific somatostatin re
A.Reference number: A47249; MUID:93087484; PMID:1360663
A.Accession: A47249
A.Status: preliminary
A.Molecule type: nucleic acid
A.Residues: 1-384 <BRU>
A.Cross-references: UNIPROT:P30937; UNIPARC:UPI0000135FPA; GB:M96544; NID:g207072; PIDN:A.Nice: sequence extracted from NCBI backbone (NCBIN:119731, NCBI:119732)
C.Superfamily: vertebrate rhodopsin
C.Keywords: G protein-coupled receptor; transmembrane protein

Query Match 11.1%; Score 219; DB 2; Length 384;
Best Local Similarity 20.8%; Pred. No. 9.2e-11;
Matches 75; Conservative 80; Mismatches 139; Indels 66; Gaps 11;

Qy 3 HTHAHIAANSSLSWSPG-----SACGLGFVRYV---YSSLLCLGLPAN 44
Db 2 NTPATLPIGGEPTTTPGINASWAPDEBDVRSFGTGAAGVNTIQCIYALVCLVGN 61
Qy 45 ILTVIISQLVARRKSSYNTLLAAADIVLFTVYVDLLEFIPLANMQMPQVPDKI 104
Db 62 ALVIVFVILR-YAKMKTATNITLNLAAVDELFMISVPPVASSAA--LHMPGAVLCRAV 118
Qy 105 EYLSESSIHSTIMTVLPTIDRYAVGPKYHTVSYPARTRKIVSVYITCELTSPY- 163
Db 119 LSVDELNMFISVCLTYLSDRYAAVHPLRAITRRPSVAKLINIGVWLASLLVTLPIA 178
Qy 164 -----YMPN-IWTEDYISTSVHVLVIMHCFYV-YLVPCSIFFILNS 204
Db 179 VFADTRPARGGAACNLQPHPMASAVF-----ITFELGLFLLPVLAIGLCYL 228
Qy 205 IIVYVTLR---KSNFRLRGYSTGKTVAILEFTITSFATLMAPRITMILVHLGAPIQRM 261
Db 229 IIVGKRAVALRAGWQORRSSEKKTITRLVLMVTVFVLCMPFYVQVLLNLVVTSLD--- 285

QY 262 LVHMSDIAANMLALINTINFLYCFISKRR-----TMAATLKAFFKQKQPOVY 314
Db 286 --ATVNHVSLISVANSKANPILYGLSDNFRRSQRYLCRCCLLETTGAEEBPLDY 343

RESULT 11

h18704
hypothetical protein B0334.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C:Accession: J18704
R:Swindburne, J.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19009
A:Accession: J18704
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-340 <NLS>
A:Cross-references: UNIPROT:O17478; UNIPARC:UPI0000179C62; EMBL:Z66519; NID:GI044812; PI
A:Experimental source: clone B0334
C:Genetics:
A:Gene: CESP:B0334.6
A:Map position: 2
A:Introns: 136/1; 160/3; 307/1

Query Match 11.1%; Score 217.5; DB 2; Length 340;
Best Local Similarity 23.1%; Pred. No. 1.1e-10;
Matches 84; Conservative 55; Mismatches 128; Indels 97; Gaps 13;

QY 5 HAHLAANSLSWSPSGACGLFVPPVYVYSLLCGLPANITVTIISQVARRQSSYN 64
Db 31 HEHDSQISISVWS-----NVAVLPI-----ALIGLACNLNMAVLTSNKTARRIPSN 80
QY 65 YLALAAADIVLFFIVFVDFLEDFILNMQMPQVDPKIIIEVFEFSIHITSIMIVPLTI 124
Db 81 LLIATAVCDLSFLIAT-----LDVTPLSIPS-----LASTGSHNHYSIVLYI 125
QY 125 -----DRIYAVCHPLKYHTVSYPARTRKYIVSYITCFELTSPYWMWN 168
Db 126 RLASTFYKSRNIPKSKFLANCOILE-----KIRHVNIHYR----- 164
QY 169 IWTEDYISTSVHNLIMHCFVYVLPSCIFILNSIIVYKLRKRSNPLRGYS----- 222
Db 165 --TMDYISLFAPNV-----PIIGLLYMSRIIFLTRRVVDEDSRYEETKLS 211
QY 223 -----TGKTAIFFTTSIFATLMAPRI-IMILYHLYGAPIQRMVLHMSDIA 270
Db 212 GLIQDAHNRRTMRANMLFAVVPMLFCVGGQAPARILFDNYG-QYHFKAILVYC--LS 268
QY 271 NMLALLNTAINFLYCFISKRRRTMAAATLKAFF-KCOKQPVQFYTNHNSITSSPWIS 329
Db 269 QQLVFLNLSINFLCYCVVSKRYRTLMKQTLKKFLKHLBEVDHPFOINLKQTKSSAHVTS 328
QY 330 ANSH 333
Db 329 LEDH 332

RESULT 12

JC7209
gala1an receptor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C:Accession: JC7209
R:Lenz, C.; Sondergaard, L.; Grimmelikhuisen, C.J.P.
Biochem. Biophys. Res. Commun. 269, 91-96, 2000
A:Title: Molecular cloning and genomic organization of a novel receptor from Drosophila
A:Reference number: JC7209; MUID:20160456; PMID:10694483
A:Accession: JC7209
A:Molecule type: mRNA
A:Residues: 1-394 <LEN>
A:Cross-references: UNIPROT:Q9U721; UNIPARC:UPI0000082510; GB:AF220216
C:Comment: This receptor is a G-protein-coupled receptor and a transmembrane protein.

C:Genetics:
A:Cross-references: FlyBase:FBgn0028961
A:Map position: X distal end
A:Introns: 98/1; 161/2; 193/2; 243/3; 283/2; 308/3; 360/3
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 11.1%; Score 217.5; DB 2; Length 394;
Best Local Similarity 25.9%; Pred. No. 1.3e-10;
Matches 99; Conservative 68; Mismatches 136; Indels 79; Gaps 22;

QY 2 EHT-HAHLAANSLSWSPSGAC--LGFPVYVYSLLCGLPANITVTIISQVARR 58
Db 47 EHTHSDHNAHDSMEYDIESVALERIVSTIYPVFGIIGFAGLGNGLVIV--VVAHQ 103
QY 59 Q-KSSVYVLLA-LAADIIVLFFIVF-VDFLEDFILNMQMPQV-----DKIIEVFEFS 110
Db 104 QMRSTNLLINLAVSDIL---FVIFCVPTATDYVL---PEMPFGNWKCFQVYHIV 156
QY 111 SIHTSIWTVPLTIDRYIAVCHPLKYHTVSYPARTRKYIVSYITCFELTSP----- 162
Db 157 TCHGSVYLVLMSPDRFLAVVHPVTSMSLTERNATLAIMCAWITYTTATIPVALSHSVR 216
QY 163 -YVWMPNIMEDYISTSVHNLIM-----IHCF-TYVLPSCIFILNSIIVYKLS----- 210
Db 217 IYQYHGNAGTACVFSTEEB--IWSLVGFQVSFPLSVAVADLTICFLYMGMLARKMSA 273
QY 211 -----RRKSNPLRGYSTGKTTALIFTTTSIFATLMAP-RIIMIL--YHLGAPION 259
Db 274 PGCKPSAESRKQKRRV-----TRWVVVVLAFALCWPBHVILVLKALNLVG----G 321
QY 260 RVLVHMSDIAANMLALNTAINFLYCFISKRRRTMAAATLKAFF--COKQVQRYTN 316
Db 322 SLSVITIIQISHVAVYVNSCINPILYAFLSNFR-----KARRYVWCGSP-PLMTN 373
QY 317 HNFSTSSPWISPANSHCIKWL 338
Db 374 QQVTKTTRTATGNGTSN-IEWL 394

RESULT 13

JC8784
G protein-coupled neuropeptide pyrokinin-2 receptor (CG8784) - fruit fly (Drosophila mel
C:Species: Drosophila melanogaster
C:Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004
C:Accession: JC8784
R:Rozenkild, C.; Gazzanali, G.; Williamson, M.; Hauser, F.; Sondergaard, L.; Delotto, R
Biochem. Biophys. Res. Commun. 309, 485-494, 2003
A:Title: Molecular cloning, functional expression, and gene silencing of two Drosophila
A:Reference number: JC8784; PMID: 12951076
A:Accession: JC8784
A:Molecule type: mRNA
A:Residues: 1-658 <ROS>
A:Cross-references: GB:A277898
C:Comment: This receptor is a G protein-coupled receptor and a transmembrane protein as
development, diapause, feeding, and behavior.
C:Genetics:
A:Gene: CG8784
A:Introns: 160/1; 215/2; 259/3; 326/1; 400/3
C:Keywords: G protein-coupled receptor; neuropeptide pyrokinin; transmembrane protein

Query Match 11.1%; Score 217.5; DB 2; Length 658;
Best Local Similarity 25.0%; Pred. No. 2.2e-10;
Matches 82; Conservative 63; Mismatches 132; Indels 51; Gaps 14;

QY 31 VYVSLLCGLPANITVTIISQVARRQSSVYVLLAADIIVLFFIVFVDFLEDF 90
Db 112 VCYALIFVAGVGLNLTICIVISRNPMRTATNF-YLFNLAVSDILL-----VSGIQE- 164
QY 91 ILNMQMPQV---PDKII---EVLFEFSIHITSIMIVPLTIDRYIAVCHPLKYHTVSYPAR 144
Db 165 LYNLWYPMYPTDAMCMGSLVSEMANNAIVLTITATVRYIAICHPFQHYMSKLSR 224

QY 145 TRKIVSVYITCFLTSLIPYMPNII--WTEDYISTSVHHVLIWICFTV-----YLVPQS 197
DB 225 AIKFTFAIWLALFLALPQMOFSVYVQNEGYSCTEND--FYAHFAVSGFIFGCPWT 282
QY 198 IFFINLSIIVYLRKRSNRL-----RGST--GKTAIFTTSTIPATLMAR 244
DB 283 AICVLYLVGLVLRKS--RLQSLPRRTFDANRGLNAGRYIRMLVAVAVAFPCWAF 339
QY 245 IMIIVYHLGAPIQRMWL-----VHIMSDIANMLALNTAINFLYCFISKRPRTWA 296
DB 340 HAQRLMAVYGLNLINGISRDANFYRLIDTSGVLVLTSCINPLNIMSHKREAF 399
QY 297 AATLKAFFKCKQ-----QPVQFYTNHNS 320
DB 400 KITLTFQGLARNHHQSQCH--QHNS 426

RESULT 14

JC2421

Opioid receptor homolog, MOR-C - mouse

C:Species: Mus musculus (house mouse)

C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C:Accession: J02421; 149122

R:Niimi, M.; Takeshima, H.; Mori, M.; Nakagawara, K.; Takeuchi, T.

Biochem. Biophys. Res. Commun. 205, 1353-1357, 1994

A:Title: Structure and chromosomal mapping of genes for the mouse kappa-opioid receptor

A:Reference number: J02421; PMID:9510067; PMID:7802669

A:Accession: J02421

A:Molecule type: mRNA

A:Residues: 1-367 <NIS-

A:Cross-references: UNIPROT:P35377; UNIPARC:UPI00000400E; DDBJ:D31663

J. Halford, W.P.; Gebhardt, B.M.; Carr, D.J.

J. Neuroimmunol. 59, 91-101, 1995

A:Title: Functional role and sequence analysis of a lymphocyte orphan opioid receptor.

A:Reference number: 149122; PMID:95318231; PMID:7797625

A:Accession: 149122

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-357 <RES-

A:Cross-references: UNIPARC:UPI000016CAB4; EMBL:U14165; NID:G540092; PIDN:AAA87899.1; PI

C:Genetics: MOR-C; MOR

A:Map position: 2H2-4

A:Introns: 75/2; 194/1

C:Superfamily: vertebrate rhodopsin

C:Keywords: receptor

Query Match 11.0%; Score 217; DB 2; Length 367;

Best Local Similarity 22.8%; Pred. No. 1.3e-10;

Matches 74; Conservative 65; Mismatches 117; Indels 68; Gaps 13;

QY 7 HLAANSLSWSPGACGIGF--VPVYVYSLGLCT--GLPANILTVIILSQLVARROKSSYN 64
DB 32 HLLNASHAFLP-----LGLKVTIVGLYLVAVICIGLGNCLVMYVI--LRHTKMKATN 84
QY 65 -YLLAAADIVLFFIYF--VDLLEDFILNMQMPQDPDKIEVLEFSSIHSTIWTVP 121
DB 85 IYIFNLADLTIVLTLFPGTDILGFWPFGNAL-----CKTVIAIDYNNMFTSTFTLTA 140
QY 122 LTIIDRYIACHPKHTVSPARTKRVISVYITCFLTSLIPY----- 163
DB 141 MSVDRYVACHPIRALDVRTSKAQAVNVAIMALASVGVPAINGSAQVDEBEICLVE 200
QY 164 -----YMPNITWTEDYISTSVHHVLIWICFTVYLVPCSIFFILNSIIVYLR----- 211
DB 201 IAPADYVGP-----VFALCIFLFSF---IIPVLISVCSYSLMIRLRGVRLLS 246
QY 212 --RKNFRLRGYSTGKTAIFTTSTIPATLMAPRIIMILYHLYGAPIONRMLVHIMSDI 269
DB 247 GSREKDRNLR-----RITRLVLVVAVFVGCVTPVQVFLVQGLGVQPSSETRAVAILR-F 300
QY 270 ANMLALNTAINFLYCFISKRR 293

DB 301 CTALGYVNSCLNPLIYAFLENFK 324

RESULT 15

kappa opioid receptor 3 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: 149022

R:Pan, Y.X.; Cheng, J.; Xu, J.; Rosati, G.; Jacobson, E.; Ryan-Moro, J.; Brooks, A.I.; De

Mol. Pharmacol. 47, 1180-1188, 1995

A:Title: Cloning and functional characterization through antisense mapping of a kappa 3-

A:Reference number: 149022; PMID:95327076; PMID:7603458

A:Accession: 149022

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-367 <RES-

A:Cross-references: UNIPROT:P35377; UNIPARC:UPI000016CAC8; EMBL:U09421; NID:G551484; PID

C:Superfamily: vertebrate rhodopsin

Query Match 11.0%; Score 217; DB 2; Length 367;

Best Local Similarity 22.8%; Pred. No. 1.3e-10;

Matches 74; Conservative 65; Mismatches 117; Indels 68; Gaps 13;

QY 7 HLAANSLSWSPGACGIGF--VPVYVYSLGLCT--GLPANILTVIILSQLVARROKSSYN 64
DB 32 HLLNASHAFLP-----LGLKVTIVGLYLVAVICIGLGNCLVMYVI--LRHTKMKATN 84
QY 65 -YLLAAADIVLFFIYF--VDLLEDFILNMQMPQDPDKIEVLEFSSIHSTIWTVP 121
DB 85 IYIFNLADLTIVLTLFPGTDILGFWPFGNAL-----CKTVIAIDYNNMFTSTFTLTA 140
QY 122 LTIIDRYIACHPKHTVSPARTKRVISVYITCFLTSLIPY----- 163
DB 141 MSVDRYVACHPIRALDVRTSKAQAVNVAIMALASVGVPAINGSAQVDEBEICLVE 200
QY 164 -----YMPNITWTEDYISTSVHHVLIWICFTVYLVPCSIFFILNSIIVYLR----- 211
DB 201 IAPADYVGP-----VFALCIFLFSF---IIPVLISVCSYSLMIRLRGVRLLS 246
QY 212 --RKNFRLRGYSTGKTAIFTTSTIPATLMAPRIIMILYHLYGAPIONRMLVHIMSDI 269
DB 247 GSREKDRNLR-----RITRLVLVVAVFVGCVTPVQVFLVQGLGVQPSSETRAVAILR-F 300
QY 270 ANMLALNTAINFLYCFISKRR 293
DB 301 CTALGYVNSCLNPLIYAFLENFK 324

Search completed: December 3, 2005, 06:31:40

Job time : 23.1364 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:23:01 ; Search time 125.127 seconds
(without alignments)
2097.517 Million cell updates/sec

Title: US-10-712-615-103

Perfect score: 1967

Sequence: 1 MEHTHAHLAANSLSWSPG.....NDSKSSYQEPDAGACVILL 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1857	94.4	353	2	Q6DWJ6_HUMAN
2	1623	82.5	388	2	Q8TDU8_HUMAN
3	1317	67.0	265	2	Q9BYT4_HUMAN
4	1273.5	64.7	383	2	Q7T2L1_FUGRU
5	1171	59.5	327	2	Q4RMO_TERN
6	979	49.8	186	2	Q86SP2_HUMAN
7	782	39.8	309	2	Q4S813_TERN
8	771	39.2	371	2	Q7T2L2_FUGRU
9	737	37.5	462	1	GP142_HUMAN
10	737	37.5	1464	2	Q8NGB0_HUMAN
11	713	36.2	365	1	GP142_MOUSE
12	263.5	13.4	358	2	Q4RX3_TERN
13	262.5	13.3	374	2	Q5F896_BOMMO
14	262	13.3	54	2	Q80UC8_MOUSE
15	260.5	13.2	394	2	Q17478_CABEL
16	250.5	12.7	398	1	TRFR_BOVIN
17	249.5	12.7	398	1	TRFR_SHEEP
18	249.5	12.7	440	1	Q7PYB7_ANOGA
19	248	12.6	549	1	FMAR_DROME
20	242	12.3	412	1	TRFR_RAT
21	241	12.3	393	1	TRFR_MOUSE
22	240.5	12.2	413	2	Q6Y5A_BOMMO
23	240	12.2	404	2	Q8UFZ7_XENLA
24	238.5	12.1	398	1	TRFR_HUMAN
25	238	12.1	394	2	Q620B8_CABER
26	236	12.0	488	2	Q717R7_DROME
27	235.5	12.0	395	1	TRFR_CHICK
28	234	11.9	478	2	Q717T5_DROME
29	233.5	11.9	354	2	Q6YST0_PIG
30	233	11.8	397	2	Q9DDRI_XENLA
31	233	11.8	478	2	Q9W025_DROME

32	232	11.8	435	2	Q8SMR3_DROME	Q8SMR3_drosophila
33	231.5	11.8	355	1	CCRI_HUMAN	P32246_homo sapien
34	231.5	11.8	355	2	Q5U003_HUMAN	Q5U003_homo sapien
35	231.5	11.8	355	2	Q9WJ8_CALJA	Q9WJ8_calithrix
36	231	11.7	397	2	Q8JFZ5_XENLA	Q8JFZ5_xenopus lae
37	230.5	11.7	381	2	Q7PHG5_ANOGA	Q7PHG5_anopheles g
38	230.5	11.7	427	2	Q7RTK2_ANOGA	Q7RTK2_anopheles g
39	228	11.6	415	2	Q7LC54_HUMAN	Q7LC54_homo sapien
40	228	11.6	415	2	Q96AM5_HUMAN	Q96AM5_homo sapien
41	228	11.6	415	2	Q9GZQ4_HUMAN	Q9GZQ4_homo sapien
42	226	11.5	352	2	Q88820_RAT	Q88820_rattus norv
43	226	11.5	352	2	Q9R297_RAT	Q9R297_rattus norv
44	226	11.5	488	2	Q9W027_DROME	Q9W027_drosophila
45	225.5	11.5	382	2	Q9ERT2_MOUSE	Q9ERT2_mus musc

ALIGNMENTS

RESULT 1

Q6DWJ6_HUMAN PRELIMINARY: PRT: 353 AA.

AC Q6DWJ6; 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE G protein-coupled receptor 139.
GN Name=GPR139;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Brain;
RA Bonner T.I., Nagle J.W., Kauffman D.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL: AY631579; AF65818.1; -, mRNA.
DR HNCJ: HGNC:19995; GPR139.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 353 AA, 40679 MW, CF1086FCSCG4F85 CR664;

Query Match 94.4%; Score 1857; DB 2; Length 353;

Best Local Similarity 100.0%; Pred. No. 3.2e-121;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEHTHAHLAANSLSWSPGACGIFVYVYYSLLCLGLPANITVITLSQVARRK 60		Q6DWJ6	1	MEHTHAHLAANSLSWSPGACGIFVYVYYSLLCLGLPANITVITLSQVARRK 60
DB	1	MEHTHAHLAANSLSWSPGACGIFVYVYYSLLCLGLPANITVITLSQVARRK 60		Q6DWJ6	1	MEHTHAHLAANSLSWSPGACGIFVYVYYSLLCLGLPANITVITLSQVARRK 60
QY	61	SSNYVLAALAAADIVLFFVFDLLEDFILNMQPVDPDITIEVLESSHTSIWITV 120		Q6DWJ6	61	SSNYVLAALAAADIVLFFVFDLLEDFILNMQPVDPDITIEVLESSHTSIWITV 120
DB	61	SSNYVLAALAAADIVLFFVFDLLEDFILNMQPVDPDITIEVLESSHTSIWITV 120		Q6DWJ6	61	SSNYVLAALAAADIVLFFVFDLLEDFILNMQPVDPDITIEVLESSHTSIWITV 120
QY	121	PLTIDRYAVCHPLKXHTVSPARTRKIVSYITICFLTSIPYWMWPNITEDYSTVH 180		Q6DWJ6	121	PLTIDRYAVCHPLKXHTVSPARTRKIVSYITICFLTSIPYWMWPNITEDYSTVH 180
DB	121	PLTIDRYAVCHPLKXHTVSPARTRKIVSYITICFLTSIPYWMWPNITEDYSTVH 180		Q6DWJ6	121	PLTIDRYAVCHPLKXHTVSPARTRKIVSYITICFLTSIPYWMWPNITEDYSTVH 180
QY	181	HTLIWHTCTVYLVPCSTIFLINSITVYTLARKSNFRLRGYSTGKTALFTTSTFATL 240		Q6DWJ6	181	HTLIWHTCTVYLVPCSTIFLINSITVYTLARKSNFRLRGYSTGKTALFTTSTFATL 240
DB	181	HTLIWHTCTVYLVPCSTIFLINSITVYTLARKSNFRLRGYSTGKTALFTTSTFATL 240		Q6DWJ6	181	HTLIWHTCTVYLVPCSTIFLINSITVYTLARKSNFRLRGYSTGKTALFTTSTFATL 240

[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22985413; PubMed=14623098; DOI=10.1016/S0014-5793(03)01196-7;
RA Fredriksson R., Hoeglund P.J., Giorlam D.E.I., Lagerstrom M.C.,
RA Schioeth H.B.;
RT "Seven evolutionarily conserved human rhodopsin G protein-coupled
RT receptors lacking close relatives.";
RL FEBS Lett. 554:381-388(2003).
DR EMBL, AY288414; AAP72123.1; -; mRNA.
DR Ensembl: SINFUG00000127396; Fugu rubripes.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0004872; F: receptor activity; IEA.
DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR GO: GO:0007165; P: signal transduction; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1. 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
FT NON_TER 383
SQ SEQUENCE 383 AA; 42610 MW; 761B0AA3B97ECED1 CRC64;

Query Match 64.7%; Score 1273.5; DB 2; Length 383;
Best Local Similarity 66.6%; Pred. No. 1.3e-80;
Matches 249; Conservative 34; Mismatches 66; Indels 25; Gaps 5;

QY 1 MHTTAHLAANSLSWSPG-----SACGAGFVVVYVYLLCLGLP-ANILYIIIS 52
DB 6 MEHSHIFSALPNESSTGSGHPSKATGCPGLPPLVIVYSLCLGLPVANILYIIIS 65
QY 53 OLVARROKSSNYVLLALAAADILVLFYIFVDFLEDFILNMQMPQVPPKIIIEVEFSS 112
DB 66 QLVMRROKSSNYVLLALAAADILVLLYFVDFLEDFILATPPLPSLSAAYVLEFSS 125
QY 113 HTSITVPLTIDRYAVCHPLKHTVSPARTKRVIVSVYITCPLTSPYVWPMIWE 172
DB 126 HTSITVPLTIDRYAVCHPLKHTVSPARTKRVIVSVYITCPLTSPYVWPMIWE 185
QY 173 -----DYISTSVHVLIMHCTVYLVCSPFIINSLIYKL-RRKSNFL 218
DB 186 LPTGGGGGAGGAGGNRTVAQOILVWMAHCTIVFLPCTVFFSLNAVIVHKLRRRSCFRL 245
QY 219 RGYSTGKTALIFTISIFATLWAPRIIMLYLHVGAPIONRW--LVHIMSIAMML 275
DB 246 RGYSTGKTALIFTISIFATLWAPRIIMLYLHVGAPIONRW--LVHIMSIAMML 305
QY 276 LNTAINFLYCFISKFRPTMAATLKAFFKQKQPVQFYTNHFSITSSPMISPAISHCI 335
DB 306 LNTGVNFFLYCFISKFRGMAANVLALVHCRKQPPGFYASHNFISITSSPMISPAISHCI 365
QY 336 KMLVYQYDKNGKPI 349
DB 366 KMLVYQYDKNGKPI 379

[1]
RN NUCLEOTIDE SEQUENCE.
RP Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomas N.,
RA Mauceli E., Bouneau L., Fischer C., Okou-Costaz C., Bernot A.,
RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Cascellano S.,
RA Anthouard V., Jubin C., Cascelllo V., Katinka M., Vachetie B.,
RA Biemont C., Skalli Z., Catocelli L., Poulain J., De Berardinis V.,
RA Craud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Sautin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Croillins H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN (2)
RN NUCLEOTIDE SEQUENCE.
RP Genoscope; Whitehead Institute Centre for Genome Research;
RG Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
RL -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: CA601015037; CAG11412.1; -; Genomic DNA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1. 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
FT NON_TER 327
SQ SEQUENCE 327 AA; 36754 MW; 529EDB93E8C22295 CRC64;

Query Match 59.5%; Score 1171; DB 2; Length 327;
Best Local Similarity 68.7%; Pred. No. 1.5e-73;
Matches 222; Conservative 34; Mismatches 51; Indels 16; Gaps 3;

QY 43 ANILYIIISOLVARROKSSNYVLLALAAADILVLFYIFVDFLEDFILNMQMPQVPPK 102
DB 1 ANILYVNVLSQVLKQSSNYVLLALAAADILVLLYFVDFLEDFILATPPLPSLS 60
QY 103 IIEVEFSSHTSITVPLTIDRYAVCHPLKHTVSPARTKRVIVSVYITCPLTSP 162
DB 61 AVQVLEFSSHTSITVPLTIDRYAVCHPLKHTVSPARTKRVIVSVYITCPLTSP 120
QY 163 YVWPMIWE-----TEDYISTSVHVLIMHCTVYLVCSPFIINSLIYKL 210
DB 121 YVWPMIWE-----TEDYISTSVHVLIMHCTVYLVCSPFIINSLIYKL 180
QY 211 -RRKSNFLRGYSTGKTALIFTISIFATLWAPRIIMLYLHVGAPIONRW--LVHIM 266
DB 181 RRRSCFRLRGYSTGKTALIFTISIFATLWAPRIIMLYLHVGAPIONRW--LVHIM 240
QY 267 SDIANMLALNTAINFLYCFISKFRPTMAATLKAFFKQKQPVQFYTNHFSITSSPM 326
DB 241 TDLANMLALNTGVNFFLYCFISKFRGMAANVLALVHCRKQPPGFYASHNFISITSSPM 300
QY 327 ISPAISHCIKMLVYQYDKNGKPI 349
DB 301 ISPAISHCIKMLVYQYDKNGKPI 323

RESULT 5
Q4RJM0_TETNG
ID Q4RJM0_TETNG PRELIMINARY; PRT; 327 AA.
AC Q4RJM0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 3 SCAP15037, whole genome shotgun sequence.
DE (Fragment).
DE ORFNames=GSTENG0003377001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OC NCBI_TaxId=99883;

RESULT 6
Q86SP2_HUMAN
ID Q86SP2_HUMAN PRELIMINARY; PRT; 186 AA.
AC Q86SP2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE G-protein-coupled receptor PGR3 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22584407; PubMed=12679517; DOI=10.1073/pnas.0230374100;
RA Vassiliadis D.K., Hohmann J.G., Zeng H., Li F., Rantchalis J.E.,
R Mortrud M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,
RA Bergman J.E., Galanakis G.A.;
RT "The G protein-coupled receptor repertoires of human and mouse."
RL Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908(2003).
DR EMBL: AY255545; AAC05057.1; -; mRNA.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0004872; F: receptor activity; IEA.
DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; F: G-protein coupled receptor protein signaln. . .; IEA.
DR InterPro: IPR002376; GPCR Rhodopsn.
DR PRINTS: PR00237; GPCR RHODOPSIN.
DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KM Receptor.
FT NON_TER 1 186
SQ SEQUENCE 186 AA; 21687 MW; E402AB947EC080AF CRC64;

Query Match 49.8%; Score 979; DB 2; Length 186;
Best Local Similarity 100.0%; Pred. No. 2e-60;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 168 NIMWEDYSTSVHNLWIMHCTVYLVPCISFIILNSIIYVLRKRSNRLRGSTGKT 227
DB 1 NIMWEDYSTSVHNLWIMHCTVYLVPCISFIILNSIIYVLRKRSNRLRGSTGKT 60
OY 228 AILFTTISIPATLMAPRIIMILYHLYGAPIONRWLVHMSDIANMLALNTAINFLYCF 287
DB 61 AILFTTISIPATLMAPRIIMILYHLYGAPIONRWLVHMSDIANMLALNTAINFLYCF 120
OY 268 ISKRRTMAAATLTKAFKCKQKQVQFYTNHNSITSSPISPAHSHCIKMLVQYDKXGK 347
DB 121 ISKRRTMAAATLTKAFKCKQKQVQFYTNHNSITSSPISPAHSHCIKMLVQYDKXGK 180
OY 348 PIK 350
DB 181 PIK 183

RESULT 7

Q4S813.TETNG PRELIMINARY; PRT; 309 AA.
ID Q4S813.TETNG
AC Q4S813
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 2 SCAR14705, whole genome shotgun sequence.
DE (Fragment).
GN ORRNames-GSTENG00022326001;
OS Tetradon nigrorivridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetradontiformes;
OC Tetradontidae; Tetradontidae; Tetradon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicoud S., Jaffe D., Fisher S., Dufalla G., Dosat C., Segutens B.,
RA Dabelli C., Sallanoubat M., Levy M., Boudet N., Castellano S.,
RA Aubourg V., Jubin C., Castell V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Cattelico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Broctier P., Coulanceau J.P., Guzy J.,
RA Parra G., Lardier G., Chappe C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guiso R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Laudet V., Schachter V., Quetier F., Saurin M., Scairelli C.,
RA Winkler P., Lander B.S., Weissbach J., Roest Ciolliu H.,
RT "Genome duplication in the teleost fish Tetradon nigrorivridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

DR EMBL: CA01014705; CAC03049.1; -; Genomic DNA.
DR InterPro: IPR00276; GPCR Rhodopsn.
DR Pfam: PF00001; 7em.1; 1.
DR PRINTS: PR00237; GPCR RHODOPSIN.
DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KM G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 309 309
SQ SEQUENCE 309 AA; 34931 MW; AB2PFE9E5211EF6 CRC64;

Query Match 39.8%; Score 782; DB 2; Length 309;
Best Local Similarity 48.5%; Pred. No. 1.6e-46;
Matches 141; Conservative 62; Mismatches 76; Indels 12; Gaps 4;

OY 15 SWSBPG--SACGLGFVPVYVYLLCLGLPANILTVIILSQLVARROKSSYNLLALAA 72
DB 11 SRMBPDLKACVLGHPVYVYVLLCVGPVNILTVALTSLRTKALYYLLAVYGS 70
OY 73 DILVLFVFPVDFLEPDLMMQMPQVDPDKIEVLFSSITSTWITPLTIDYIANCH 132
DB 71 DILVLFVFPVDFLEPDLMMQMPQVDPDKIEVLFSSITSTWITPLTIDYIANCH 130
OY 133 PLKYHTVSPARTKRVISVITCFLTSPYVWPNWTEIDYSTVHNLWIMHCTVY 192
DB 131 PLHKGQISPARTRIIVLVLSASGLPFVMSDMWRNHPALDAVILMHVITLY 190
OY 193 LVPCISFIILNSIIYVLRK-RKSNRLG---YST---GKTTAIIFTTISIPATLMA 242
DB 191 LVPCISFIILNSIIYVLRK-RKSNRLG---YST---GKTTAIIFTTISIPATLMA 250
OY 243 PRIMILYHLYGAPIONRWLVHMSDIANMLALNTAINFLYCFISKRF 293
DB 251 PRIMILYHLYGAPIONRWLVHMSDIANMLALNTAINFLYCFISKRF 301

RESULT 8

Q772L2.FUGRU PRELIMINARY; PRT; 371 AA.
ID Q772L2.FUGRU
AC Q772L2
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE G protein-coupled receptor 142a (Fragment).
GN Name=GPR142a;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetradontiformes;
OC Tetradontidae; Tetradontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22985413; PubMed=14623098; DOI=10.1016/S0014-5793(03)01196-7;
RA Fredriksson R., Hoeglund P.O., Gloriam D.E.I., Lagerstedt M.C.,
RA Schioeth H.B.;
RT "Seven evolutionarily conserved human rhodopsin G protein-coupled
RT receptors lacking close relatives."
RL FEBS Lett. 554:381-388(2003).
DR EMBL: AY288413; AAP72122.1; -; mRNA.
DR Ensembl: SINEFG00000154383; Fugu rubripes.
DR GO: GO:0016021; F: integral to membrane; IEA.
DR GO: GO:0004872; F: receptor activity; IEA.

DR GO; GO:0001584; Rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; G-protein coupled receptor protein signalin. . .; IEA.
 DR GO; GO:0007165; P signal transduction; IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCR_RHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 FT NON_TER 1
 FT NON_TER 371
 SQ SEQUENCE 371 AA; 42000 MW; C1A95E619681AB3 CRC64;
 Query Match 39.2%; Score 771; DB 2; Length 371;
 Best Local Similarity 47.0%; Pred. No. 1.1e-45;
 Matches 133; Conservative 65; Mismatches 75; Indels 10; Gaps 2;
 QY 21 SACGIGFVPPVYVYSLICGLGALPANITVTIISQVARRKSSVNYLLAADIIVLPFI 80
 DB 32 SACVIGFPIVYIYVYVLLCGVPPNITVAVALTRLSRTKALYYLLAATGSDILSOLF 91
 QY 81 VVDFLEDFILNMOPQVDPDKIEVLEESSIHSTSWIIVPLTIDRYIVACHPKHYTS 140
 DB 92 IFVGFLFETAVFRRVPAALLRSVSAEPAANASTISAVPLTVDRYVALCHPLHRQTS 151
 QY 141 YPARTRKVIIVSYITCFITSIPIYWPPIWTEDEYISTSVHVLWIMHCFVYLVPCSIFF 200
 DB 152 YPARTRRIIAVNLVLSLGLPFWMDMRNSHPRTALDILWIMHVIITIFLPESITL 211
 QY 201 IINSIIIVYKLRRKSNFRL---RGYST-----GKTTAILFITTSIFATLMPRIIMILY 250
 DB 212 VINSIIHITLRAKORQCSQDERGPGSAPPRLGKTTAMLAITSVFSVLMPRTVVIY 271
 QY 251 HIYGAPIQRMLVHIMSDIANMLALNTAINPFLYCFISKRR 293
 DB 272 HLIVSSVHRDMRVHLYADLSNMLAMLTAVNPFLYCFVSKPR 314
 RESULT 9
 GP142_HUMAN STANDARD; PRT; 462 AA.
 ID GP142_HUMAN
 AC Q72601; Q86SL3;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Probable G-protein coupled receptor 142 (G-protein coupled receptor
 DE PGR2).
 GN Name=GPRI42; Synonyms=PGR2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxId=9606;
 OX (1)
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP MEDLINE=22985413; PubMed=14623098; DOI=10.1016/S0014-5793(03)01196-7;
 RA Fredriksson R., Hoeglund P.J., Gloriam D.E.I., Lagerstrom M.C.,
 RA Schioeth H.B.;
 RT "Seven evolutionarily conserved human rhodopsin G protein-coupled
 RT receptors lacking close relatives.";
 RL FEBS Lett. 554:381-388(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 122-436.
 RX MEDLINE=22584407; PubMed=12679517; DOI=10.1073/pnas.0230374100;
 RA Vassiliadis D.K., Hohmann J.G., Zeng H., Li F., Rancialis J.E.,
 RA Mortrud M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,
 RA Bergmann J.E., Gaitanaris G.A.;
 RT "The G protein-coupled receptor repertoires of human and mouse.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908(2003).
 CC -1- FUNCTION: Orphan receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AY288421; AAP72130.1; -; mRNA.
 CC EMBL; AY255622; AAO85134.1; -; mRNA.
 CC Ensemble; ENSG00000197344; Homo sapiens.
 DR HGNC; HGNC:20088; GPR142.
 DR MIM; 609046; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCR_RHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 FT TOPO_DOM 1
 FT TOPO_DOM 152
 FT TRANSMEM 153
 FT TRANSMEM 173
 FT TOPO_DOM 174
 FT TOPO_DOM 195
 FT TRANSMEM 196
 FT TRANSMEM 216
 FT TOPO_DOM 217
 FT TRANSMEM 233
 FT TOPO_DOM 234
 FT TRANSMEM 255
 FT TOPO_DOM 278
 FT TRANSMEM 279
 FT TOPO_DOM 300
 FT TOPO_DOM 316
 FT TRANSMEM 317
 FT TOPO_DOM 337
 FT TOPO_DOM 357
 FT TRANSMEM 358
 FT TOPO_DOM 378
 FT TOPO_DOM 397
 FT TRANSMEM 398
 FT TOPO_DOM 418
 FT TOPO_DOM 419
 FT TOPO_DOM 462
 FT CONFLICT 132
 FT CONFLICT 132 H -> N (in Ref. 2)
 SQ SEQUENCE 462 AA; 51106 MW; E9120B52372C75CA CRC64;
 Query Match 37.5%; Score 737; DB 1; Length 462;
 Best Local Similarity 46.3%; Pred. No. 3.1e-43;
 Matches 133; Conservative 57; Mismatches 95; Indels 2; Gaps 2;
 QY 21 SACGIGFVPPVYVYSLICGLGALPANITVTIISQVARRKSSVNYLLAADIIVLPFI 80
 DB 151 SPVAGVPIVYIYVYVLLGGLVSLTAVALARLTRRPSYVYLLATASDIITQVI 210
 QY 81 VVDFLEDFILNMOPQVDPDKIEVLEESSIHSTSWIIVPLTIDRYIVACHPKHYTS 140
 DB 211 VVDFLEDFILNMOPQVDPDKIEVLEESSIHSTSWIIVPLTIDRYIVACHPKHYTS 270
 QY 201 IINSIIIVYKLRRKSNFRLRGYSTGKTTAILFITTSIFATLMPRIIMILYHYPAPIQR 260
 DB 272 SGRTRRIIAVNLVLSLGLPFWMDMRNSHPRTALDILWIMHVIITIFLPESITL 330
 QY 271 VNSAIIHITLRAKORQCSQDERGPGSAPPRLGKTTAMLAITSVFSVLMPRTVVIY 389
 QY 331 VNSAIIHITLRAKORQCSQDERGPGSAPPRLGKTTAMLAITSVFSVLMPRTVVIY 389
 DB 390 WIVHIMSDIANMLALNTAINPFLYCFISKRR-TMAAATLAFKFC 306
 DB 390 WIVHIMSDIANMLALNTAINPFLYCFISKRR-TMAAATLAFKFC 436
 RESULT 10
 O8NGBO_HUMAN PRELIMINARY; PRT; 1464 AA.
 ID O8NGBO_HUMAN
 AC Q8NGBO;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Seven transmembrane helix receptor.
 GN Name=GPRI42;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.

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OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tetsunari S., Aburatani H., Asai K., Akiyama Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
DR EMBL; AB065914; BAC06129.1; -; Genomic_DNA.
DR HGNC; HGNC:2008; GPR142.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7cm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECPE_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECPE_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transducer; Transmembrane.
KW G-PROTEIN COUPLED RECEPTOR; RECEPTOR; TRANSDUCER; TRANSMEMBRANE.
SQ
SEQUENCE 1464 AA; 156508 MW; PF8C63F8353ACF7E CRC64;

Query Match 37.5%; Score 737; DB 2; Length 1464;
Beet Local Similarity 46.3%; Pred. No. 8.7e-43;
Matches 133; Conservative 57; Mismatches 95; Indels 2; Gaps 2;

OY 21 SAGGLFVPPVYVYLLCLGLPANIILTVIISQVVARQKSSYNVLLAADAIVLFEI 80
DB 1113 SPCVAGVIVPIYVYVLLGLFVSLTAVALARLTRRPSYVYLLATASDIITQYI 1172
OY 81 VFVDLLEDFLNMQPPVDPKIIIEVLFSSIHISITVPLTIDRIYAVCHPLKHYTS 140
DB 1173 VFAGFLLOGAVILARQVPAVVNTANILEFANHASVWIAVLTVDRYVALCHPLHRAVS 1232
OY 141 YPARTRKYIVSYITCPLTISIPYWMPPNWTEDYISTSVHVLIVIHCFVTVLVPCSIFF 200
DB 1223 SPGRTRRAIAVLAVALTGLTFPVMWMDWRDTPSDPTIDEVLKNAHCLIVYFICGVFL 1292
OY 201 ILNSIIYVKLRKSNFRLRGYSTGKTTALTFTITSIFATLWAPRIIMILYHLYGAPIQNR 260
DB 1293 VTNSAIIHRLRRSGSLQRP-RVGSSTAILLGLITTLFTLWAPRVFVWLHYHYVAVPHRD 1351
OY 261 WLVIHMSDIAMMLALNTAINFPLYCFISKRR-TMAAATLKAFFKC 306
DB 1352 WRVHLADLVANVMALHTAANFGLYCFVSKTERATVRQVIDAYLPC 1398

RESULT 11
GPR142_MOUSE STANDARD; PRT; 365 AA.
AC Q7TON9;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Probable G-protein coupled receptor 142.
GN Name=Gpr142;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN NUCLEOTIDE SEQUENCE [MRNA].
RA MEDLINE=22985413; PubMed=14623098; DOI=10.1016/S0014-5793(03)01196-7;
RA Fredriksson R., Hoeglund P.J., Gloriam D.E.I., Lagerstrom M.C.,
RA Schioeth H.B.;
DE "Seven evolutionarily conserved human rhodopsin G protein-coupled
RT receptors lacking close relatives.";
RL FEBS Lett. 554:381-388(2003).
CC -1- FUNCTION: Orphan receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AY288428; AAP72137.1; -; mRNA.
DR EMBL; ENSMUSG00000034677; Mus musculus.
DR MGI; MGI:2668437; Gpr142.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7cm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPE_F1_2; 1.
DR G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
KW Transmembrane.
FT TOPO_DOM 1 66 Extracellular (Potential).
FT TRANSMEM 67 87 1 (Potential).
FT TOPO_DOM 88 102 Cytoplasmic (Potential).
FT TRANSMEM 103 123 2 (Potential).
FT TOPO_DOM 124 140 Extracellular (Potential).
FT TRANSMEM 141 161 3 (Potential).
FT TOPO_DOM 162 185 Cytoplasmic (Potential).
FT TRANSMEM 186 206 4 (Potential).
FT TOPO_DOM 207 224 Extracellular (Potential).
FT TRANSMEM 225 245 5 (Potential).
FT TOPO_DOM 246 264 Cytoplasmic (Potential).
FT TRANSMEM 265 285 6 (Potential).
FT TOPO_DOM 286 304 Extracellular (Potential).
FT TRANSMEM 305 325 7 Potential.
FT TOPO_DOM 326 365 Cytoplasmic (Potential).
FT CAROXYD 44 44 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 365 AA; 40758 MW; ACA8649245CDAE47 CRC64;

Query Match 36.2%; Score 713; DB 1; Length 365;
Beet Local Similarity 46.8%; Pred. No. 1.2e-41;
Matches 138; Conservative 51; Mismatches 96; Indels 10; Gaps 4;

OY 21 SAGGLFVPPVYVYLLCLGLPANIILTVIISQVVARQKSSYNVLLAADAIVLFEI 80
DB 64 SPCVAGVIVPIYVYVLLGLFVSLTAVALARLTRRPSYVYLLATASDIITQYI 117
OY 81 VFVDLLEDFLNMQPPVDPKIIIEVLFSSIHISITVPLTIDRIYAVCHPLKHYTS 140
DB 118 VFAGFLLOGAVILARQVPAVVNTANILEFANHASVWIAVLTVDRYVALCHPLHRAVS 177
OY 141 YPARTRKYIVSYITCPLTISIPYWMPPNWTEDYISTSVHVLIVIHCFVTVLVPCSIFF 200
DB 178 SPGRTRRAIAVLAVALTGLTFPVMWMDWRDTPSDPTIDEVLKNAHCLIVYFICGVFL 237
OY 201 ILNSIIYVKLRKSNFRLRGYSTGKTTALTFTITSIFATLWAPRIIMILYHLYGAPIQNR 260
DB 238 VTNSAIIHRLRRSGSLQRP-VSKSTAILLGLVSTLFTLWAPRIIMILYHLYVAVPHRD 296
OY 261 WLVIHMSDIAMMLALNTAINFPLYCFISKRR-TMAAATLKAFFKC--QKQPV 312
DB 297 WRVHLADLVANVMALNTAVNFGLYCFISKTERATVRQVIDVHMAKLSQPKQ 351

RESULT 12
Q4RX3_TETNG
ID Q4RX3_TETNG PRELIMINARY; PRT; 358 AA.
AC Q4RX3;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Chromosome 9 SCAR15033, whole genome shotgun sequence.
GN ORFNames=GSTENG00033238001;
OS Tetradon nigriviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetradontiformes;
OC Tetradontidae; Tetradontidae; Tetradon.

```

OK NCB1_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costat C., Bernot A.,
 RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segreus B.,
 RA Daestla C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Antouard V., Jubin C., Castellino L., Poullain J., De Berardinis V.,
 RA Bismont C., Skalli Z., Cattelico L., Coutanceau J.P., Gouzy J.,
 RA Craud C., Duprat S., Brotier P., Coullange J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Wolf J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scapellato C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope, Whitehead Institute Centre for Genome Research;
 RL Submitted (PEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC EMBL, CAEB01015033; CAG1309.1; -; Genomic DNA.
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1, 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; UNKNOW_1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 SQ SEQUENCE 358 AA; 4113 MW; B0BC8BA835CC1E CRC64;
 Query Match 13.4%; Score 263.5; DB 2; Length 358;
 Best Local Similarity 24.6%; Pred. No. 2e-10;
 Matches 88; Conservative 56; Mismatches 115; Indels 99; Gaps 13;
 QY 31 VYVSLLCGLP-----ANILVYIIISQVARQKSSNY 65
 DB 15 VEPYALAAVGLPKCKRINVSVELKKQIFDTSCFSANIVFLIILRRCKMLSKSSDY 74
 QY 66 LIALAADIIVLFFIVFVDFLL-----EDF-----ILNMQMPQVPDKIEVLEFSSIHRS 115
 DB 75 LMAISVADLVLIFFIVIELSLKHYHMEFPWSYEPWCMNR-----DIFYGAYMS 125
 QY 116 IIVTVPLTIDRYIYAVCHPKYHTVSYPARTK-----VIVSYITCEFLTSIPY 164
 DB 126 TWLVVVFIAERFIAI-----HT-----RTLTKTKVCTGRHAAWTVSVFVSHLCAIPY 174
 QY 165 WMPNITEDYISISVH-----HVLIMHCFYVLPVPCSFILNSIYKLRKSN 215
 DB 175 WSNASVNRQNGVCIYDHAALPFHITLWMLQTLQSYIVPELLIITLNGTLTLLISLR 234
 QY 216 FRLRGYSTG-----KTTAILFTTISFATLMABR-----IIMILYHLYGAP 256
 DB 235 VHTTSVHTSEVKSRIPLRSRKRSIVLVLTISMSFVLSTRAITQILIRRTTHYKAD 294
 QY 257 IONRWLV--HIMSDIANMLALNTAINFLYCFISKRFTMAATLKA--FPKQORP 310
 DB 295 -RNDYSGVGNVADIGTMLCLSNAAANMYLYVCTQCKFRREFPACVRRVIFICEAOP 351
 RESULT 13
 Q5FB96_BOMMO
 ID Q5FB96_BOMMO PRELIMINARY; PRT; 374 AA.
 AC Q5FB96;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE Myosuppressin receptor.
 GN Name=mar;

OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OK NCB1_TaxID=7091;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Kinyu x Shoua;
 RA Yamakawa N., Hua Y.J., Mizoguchi A., Watanabe K., Niwa R., Tanaka Y.,
 RA Katoka H.;
 RT "Identification of a Novel Prothoracicostatic Hormone and Its Receptor
 in the Silkmoth Bombyx mori.";
 RL J. Biol. Chem. 280:14684-14690(2005).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC EMBL, AB188257; BAD89566.1; -; mRNA.
 DR EMBL; AB188256; BAD89565.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1, 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 SQ SEQUENCE 374 AA; 41917 MW; CEA30D78BC6C6EBD CRC64;
 Query Match 13.3%; Score 262.5; DB 2; Length 374;
 Best Local Similarity 24.2%; Pred. No. 2.5e-10;
 Matches 82; Conservative 62; Mismatches 100; Indels 95; Gaps 12;
 QY 32 YVSLLC-IGLPANILTVIIISQVARQKSS--YNYLLAADIIVLFFIVFVDFLE 88
 DB 27 YIALIILCLGSAANSVNVNLVS---RKMTCTNSILGLVAVADVNV--IDYIFLAH 80
 QY 89 DFI-LNMQMPQVPDKIEVLEFSSI-----HT-SIWTIVPLTIDRYIYAVCHPKYHTVSY 141
 DB 81 LVTKGSELNONGSYGNAVFIYHHSIFSQTFFHTISITLIMLAVWRIALFKPQKNQTLGN 140
 QY 142 PARTKRVISVYITCEFLTSIPYWMNI-----MTEDYISFS----- 178
 DB 141 KENTTALIIAAVAVCVCLPIYFAMNIMERLPSDTSNGTNTLVNTSAAVSDPKQFI 200
 QY 179 -----VHVLIMHCFYVLPVPCSFILNSIYKLRKSNFLR----- 219
 DB 201 EMTNNNDLTLAIFWYISVFILKIPCVLSILSVLIMKSSDRRQKLLKKSATTTGG 260
 QY 220 -----GYSTKTTAILFTTISF-----ATLWAPRIIMILYHLYGAP 255
 DB 261 EKARLNDGCKGGRDRTTRMLVALGLFATLTELQALFGLTIAAPHLPLICYAFG- 319
 QY 256 PIQNRWLHIMSDIANMLALNTAINFLYCFISKRERT 294
 DB 320 -----EVDMLALVGSAAVFLVYCSMSRQFRT 346
 RESULT 14
 Q80UC8_MOUSE
 ID Q80UC8_MOUSE PRELIMINARY; PRT; 54 AA.
 AC Q80UC8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE G-protein-coupled receptor FGR3 (Fragment).
 GN Name=Gpr13;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath;
 OC Muridae; Murinae; Mus.
 OK NCB1_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

